Phyre^2

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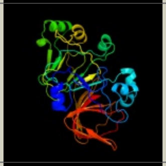
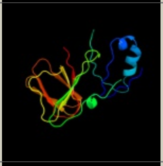
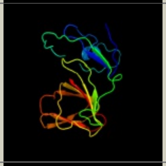
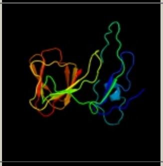
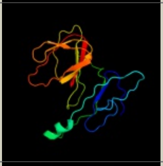
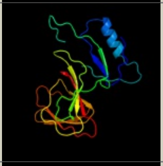
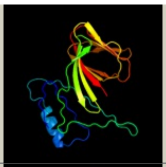
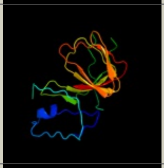
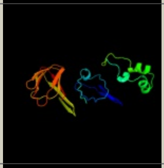
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h1yA_	Alignment		100.0	87	**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)
2	d1pmia_	Alignment		100.0	32	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
3	d1qwra_	Alignment		100.0	26	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
4	d1zx5a1	Alignment		100.0	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
5	c3rnsA_	Alignment		98.9	14	**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
6	d1sfna_	Alignment		98.8	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
7	c1sefA_	Alignment		98.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
8	d1sefa_	Alignment		98.8	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
9	d1rc6a_	Alignment		98.7	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
10	d1sq4a_	Alignment		98.6	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
11	d2d40a1	Alignment		98.6	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like

12	c3h7yA_	Alignment		98.5	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
13	d1y3ta1	Alignment		98.5	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
14	c2d40C_	Alignment		98.5	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
15	d2phda1	Alignment		98.3	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
16	c3myxA_	Alignment		98.2	16	**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
17	c2cauA_	Alignment		98.1	19	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
18	c2eaaB_	Alignment		98.1	18	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
19	c3bu7A_	Alignment		98.1	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
20	d3bu7a1	Alignment		98.1	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
21	c2vqaC_	Alignment	not modelled	98.1	15	**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.
22	c2pfwB_	Alignment	not modelled	98.1	12	**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
23	c2ozjB_	Alignment	not modelled	98.0	16	**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
24	d1j58a_	Alignment	not modelled	98.0	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
25	c3lwcA_	Alignment	not modelled	97.9	8	**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
26	c3s7eB_	Alignment	not modelled	97.9	16	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
27	d1yhfa1	Alignment	not modelled	97.8	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
						PDB header:biosynthetic protein **Chain:** C: **PDB Molecule:**uncharacterized protein with rmlc-like

28	c3fjsC_	Alignment	not modelled	97.7	13	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
29	d1juha_	Alignment	not modelled	97.7	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
30	c1uijA_	Alignment	not modelled	97.7	22	**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)
31	d2pyta1	Alignment	not modelled	97.6	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
32	c2q30C_	Alignment	not modelled	97.6	8	**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
33	c3ibmB_	Alignment	not modelled	97.6	14	**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
34	c3bcwB_	Alignment	not modelled	97.6	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
35	c2gu9B_	Alignment	not modelled	97.5	12	**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	c2oa2A_	Alignment	not modelled	97.4	17	**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
37	d1dgwa_	Alignment	not modelled	97.3	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
38	c2o8qA_	Alignment	not modelled	97.3	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
39	d1vj2a_	Alignment	not modelled	97.3	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
40	d1v70a_	Alignment	not modelled	97.3	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
41	d1y9qa2	Alignment	not modelled	97.3	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
42	c3jzvA_	Alignment	not modelled	97.3	11	**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.
43	c3d82A_	Alignment	not modelled	97.2	16	**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
44	d1uika1	Alignment	not modelled	97.2	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
45	c2vpvA_	Alignment	not modelled	97.1	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
46	d2b8ma1	Alignment	not modelled	97.1	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
47	d1uija1	Alignment	not modelled	97.1	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
48	d2f4pa1	Alignment	not modelled	97.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
49	d1o5ua_	Alignment	not modelled	97.1	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
50	c3h8uA_	Alignment	not modelled	97.1	11	**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
51	d1o4ta_	Alignment	not modelled	97.0	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like

52	d1lr5a_	Alignment	not modelled	97.0	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
53	c3qacA_	Alignment	not modelled	96.9	15	**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.
54	c3i7dB_	Alignment	not modelled	96.9	13	**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
55	c3kgzA_	Alignment	not modelled	96.9	9	**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
56	d1yfua1	Alignment	not modelled	96.9	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
57	c2qnkA_	Alignment	not modelled	96.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyanthranilate 3,4-dioxygenase; **PDBTitle:** crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
58	c3l2hD_	Alignment	not modelled	96.8	13	**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
59	c3cewA_	Alignment	not modelled	96.7	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
60	c2i45C_	Alignment	not modelled	96.7	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
61	c3es4B_	Alignment	not modelled	96.6	20	**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
62	c2fqpD_	Alignment	not modelled	96.6	16	**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
63	d2phla1	Alignment	not modelled	96.6	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
64	c3ehkC_	Alignment	not modelled	96.4	12	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
65	d2phla2	Alignment	not modelled	96.3	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
66	c3o14B_	Alignment	not modelled	96.3	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
67	d2bnma2	Alignment	not modelled	96.2	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
68	c3kscD_	Alignment	not modelled	96.1	11	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
69	d1fxza1	Alignment	not modelled	96.1	7	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
70	c3ht2A_	Alignment	not modelled	96.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
71	c2oziA_	Alignment	not modelled	96.0	19	**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
72	c2e9qA_	Alignment	not modelled	95.9	15	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
73	c2y0oA_	Alignment	not modelled	95.9	26	**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
74	c1cauB_	Alignment	not modelled	95.9	20	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
75	c2opkC_	Alignment	not modelled	95.8	8	**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
76	c3kglB	Alignment	not modelled	95.8	9	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin;

76	c3kglB_	Alignment	not modelled	95.8	9	**PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
77	d2arca_	Alignment	not modelled	95.5	8	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
78	c1fxzC_	Alignment	not modelled	95.5	11	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
79	d1od5a1	Alignment	not modelled	95.4	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
80	c3c3vA_	Alignment	not modelled	95.4	12	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
81	d1uija2	Alignment	not modelled	95.2	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
82	d1uika2	Alignment	not modelled	95.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
83	d1fxza2	Alignment	not modelled	95.0	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
84	d1od5a2	Alignment	not modelled	94.7	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
85	c2d5fB_	Alignment	not modelled	94.5	11	**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
86	d2et1a1	Alignment	not modelled	94.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
87	d1j3pa_	Alignment	not modelled	94.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
88	c2qdrA_	Alignment	not modelled	94.1	13	**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
89	d1zvfa1	Alignment	not modelled	94.0	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
90	d1x82a_	Alignment	not modelled	93.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
91	c3kv4A_	Alignment	not modelled	93.1	21	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** structure of phf8 in complex with histone h3
92	c3k3nA_	Alignment	not modelled	93.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** crystal structure of the catalytic core domain of human phf8
93	c3kv5D_	Alignment	not modelled	93.0	21	**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
94	c2qjvB_	Alignment	not modelled	92.7	18	**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
95	c3pu3A_	Alignment	not modelled	92.7	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 2; **PDBTitle:** phf2 jumonji domain-nog complex
96	c2yu1A_	Alignment	not modelled	92.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 1a; **PDBTitle:** crystal structure of hjhdm1a complexed with a-ketoglutarate
97	d1vrba1	Alignment	not modelled	91.9	33	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
98	c3kvaA_	Alignment	not modelled	91.8	21	**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
99	d1xrua1	Alignment	not modelled	91.6	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like
100	c1ywkE_	Alignment	not modelled	91.6	10	**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
101	d1ywka1	Alignment	not modelled	91.6	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like
						PDB header:oxidoreductase

102	c3uyjA_	Alignment	not modelled	91.6	32	**Chain:** A: **PDB Molecule:**lysine-specific demethylase 8; **PDBTitle:** crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg
103	c3hqxA_	Alignment	not modelled	91.5	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0345 protein aciad0356; **PDBTitle:** crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1
104	d1zrra1	Alignment	not modelled	91.4	26	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
105	d2oyza1	Alignment	not modelled	90.7	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**VPA0057-like
106	c3al6A_	Alignment	not modelled	90.7	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
107	c3eo6B_	Alignment	not modelled	90.5	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of unknown function (duf1255); **PDBTitle:** crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455 at3 0.97 a resolution
108	c3n9mC_	Alignment	not modelled	90.5	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** cekdm7a from c.elegans, alone
109	c2bnoA_	Alignment	not modelled	90.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
110	c3mpbA_	Alignment	not modelled	90.1	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
111	c3k2oB_	Alignment	not modelled	90.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional arginine demethylase and lysyl-hydroxylase **PDBTitle:** structure of an oxygenase
112	c3esgA_	Alignment	not modelled	89.5	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of hutd from pseudomonas fluorescens sbw25
113	d1tq5a1	Alignment	not modelled	89.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
114	c2xdvA_	Alignment	not modelled	88.7	29	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
115	d1h2ka_	Alignment	not modelled	86.6	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
116	c2xxzA_	Alignment	not modelled	85.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of the human jmjd3 jumonji domain
117	c3es1A_	Alignment	not modelled	82.9	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
118	c2vecA_	Alignment	not modelled	81.7	20	**PDB header:**cytosolic protein **Chain:** A: **PDB Molecule:**pirin-like protein yhak; **PDBTitle:** the crystal structure of the protein yhak from escherichia2 coli
119	c1y9qA_	Alignment	not modelled	81.3	12	**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
120	d1ylla1	Alignment	not modelled	80.6	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**PA5104-like