Phyre^2

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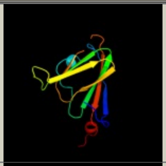
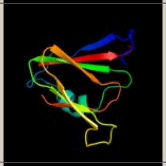
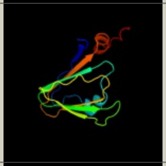
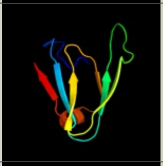
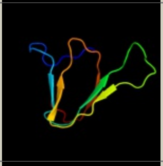
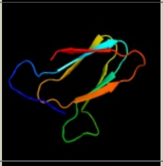
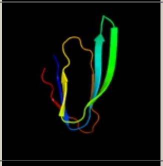
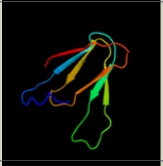
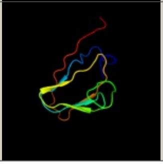
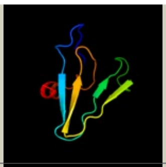
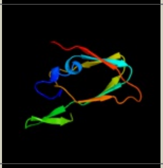
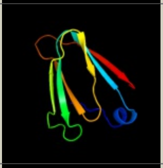
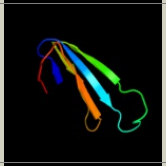
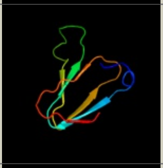
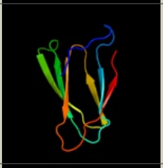
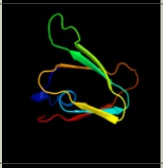
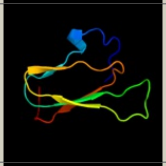
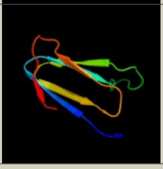
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3bb6a1	Alignment		100.0	96	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
2	d3dl3a1	Alignment		100.0	41	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
3	c3m70A_	Alignment		100.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
4	c3eqeB_	Alignment		96.8	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.
5	c2gu9B_	Alignment		96.6	19	**PDB header:**immune system **Chain:** B: **PDB Molecule:**tetracenomycin polyketide synthesis protein; **PDBTitle:** crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
6	c2o8qA_	Alignment		96.5	30	**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
7	d1juha_	Alignment		95.8	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
8	d1y3ta1	Alignment		95.7	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
9	d1v70a_	Alignment		95.6	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
10	c2q30C_	Alignment		95.5	28	**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
11	c3fjsC_	Alignment		95.5	15	**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

12	c3d82A_	Alignment		95.4	26	**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
13	d2gm6a1	Alignment		95.4	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
14	d2ic1a1	Alignment		95.3	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
15	c3rnsA_	Alignment		95.1	26	**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
16	c2i45C_	Alignment		95.1	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
17	d1x82a_	Alignment		95.1	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
18	d3elna1	Alignment		95.0	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
19	c2ozjB_	Alignment		95.0	17	**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
20	d1y9qa2	Alignment		94.8	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
21	d1rc6a_	Alignment	not modelled	94.8	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
22	c2oa2A_	Alignment	not modelled	94.6	14	**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
23	c3ibmB_	Alignment	not modelled	94.5	21	**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
24	d1yhfa1	Alignment	not modelled	94.4	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
25	c3h8uA_	Alignment	not modelled	93.8	17	**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
26	c2zklA_	Alignment	not modelled	93.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
27	d2pa7a1	Alignment	not modelled	93.8	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase

28	d1o4ta_	Alignment	not modelled	93.7	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
29	d1vj2a_	Alignment	not modelled	93.7	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
30	d1j58a_	Alignment	not modelled	93.6	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
31	d2et1a1	Alignment	not modelled	93.1	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
32	c3h7yA_	Alignment	not modelled	93.1	13	**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
33	c2vqaC_	Alignment	not modelled	93.0	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.
34	d1vrba1	Alignment	not modelled	93.0	16	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
35	d1j3pa_	Alignment	not modelled	93.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
36	c3kgzA_	Alignment	not modelled	92.5	18	**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
37	c3k2oB_	Alignment	not modelled	92.3	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional arginine demethylase and lysyl-hydroxylase **PDBTitle:** structure of an oxygenase
38	d1sfna_	Alignment	not modelled	92.1	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
39	d1yfua1	Alignment	not modelled	91.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
40	c3cewA_	Alignment	not modelled	91.5	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
41	c3kv4A_	Alignment	not modelled	91.3	23	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** structure of phf8 in complex with histone h3
42	c3pu3A_	Alignment	not modelled	91.0	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 2; **PDBTitle:** phf2 jumonji domain-nog complex
43	c3al6A_	Alignment	not modelled	90.9	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
44	c2opkC_	Alignment	not modelled	90.1	11	**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
45	c3uyjA_	Alignment	not modelled	90.1	21	**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
46	c3kvaA_	Alignment	not modelled	90.1	19	**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
47	d1zvfa1	Alignment	not modelled	89.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
48	c2yu1A_	Alignment	not modelled	89.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 1a; **PDBTitle:** crystal structure of hjhdm1a complexed with a-ketoglutarate
49	c2pfwB_	Alignment	not modelled	89.6	19	**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
50	c3jzvA_	Alignment	not modelled	89.5	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.
51	d2o1qa1	Alignment	not modelled	89.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acetylacetone-cleaving enzyme-like
52	d2f4pa1	Alignment	not modelled	89.3	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
53	d2bnma2	Alignment	not modelled	89.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins

						Family:TM1459-like
54	d1sefa_	Alignment	not modelled	89.2	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
55	c1sefA_	Alignment	not modelled	89.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
56	d1sq4a_	Alignment	not modelled	89.2	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
57	c3k3nA_	Alignment	not modelled	88.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** crystal structure of the catalytic core domain of human phf8
58	c3kv5D_	Alignment	not modelled	88.3	18	**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
59	d2b8ma1	Alignment	not modelled	87.7	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
60	d1lr5a_	Alignment	not modelled	87.4	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
61	c2d40C_	Alignment	not modelled	86.5	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
62	c1y9qA_	Alignment	not modelled	85.6	22	**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
63	d1dgwa_	Alignment	not modelled	85.3	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
64	c2vpvA_	Alignment	not modelled	84.8	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
65	d1uika1	Alignment	not modelled	84.5	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
66	c3lwcA_	Alignment	not modelled	84.5	12	**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	d1h2ka_	Alignment	not modelled	84.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
68	c3n9mC_	Alignment	not modelled	83.7	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** cekdm7a from c.elegans, alone
69	c2xdvA_	Alignment	not modelled	83.2	13	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
70	c3i7dB_	Alignment	not modelled	83.0	21	**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
71	c2fqpD_	Alignment	not modelled	81.5	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
72	d1uija1	Alignment	not modelled	81.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
73	c3bcwB_	Alignment	not modelled	80.8	15	**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
74	d1zrra1	Alignment	not modelled	79.8	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
75	d2d40a1	Alignment	not modelled	79.7	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
76	c2bnoA_	Alignment	not modelled	79.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
77	d1od5a2	Alignment	not modelled	78.8	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
78	d2phla2	Alignment	not modelled	78.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
						PDB header:isomerase

79	c3ejkA_	Alignment	not modelled	75.5	22	**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
80	d1fxza2	Alignment	not modelled	74.2	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
81	c3balB_	Alignment	not modelled	74.1	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acetylacetone-cleaving enzyme; **PDBTitle:** crystal structure of an acetylacetone dioxygenase from2 acinetobacter johnsonii
82	c3dkqB_	Alignment	not modelled	72.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pkhd-type hydroxylase sbal_3634; **PDBTitle:** crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
83	c2y0oA_	Alignment	not modelled	72.1	17	**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
84	c3ht2A_	Alignment	not modelled	70.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
85	d2phda1	Alignment	not modelled	70.0	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
86	d1uika2	Alignment	not modelled	68.8	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
87	c3es1A_	Alignment	not modelled	64.7	17	**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
88	c2cauA_	Alignment	not modelled	64.3	17	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
89	c2oziA_	Alignment	not modelled	62.2	9	**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
90	c1cauB_	Alignment	not modelled	61.0	15	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
91	c3mpbA_	Alignment	not modelled	57.2	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
92	d3bu7a1	Alignment	not modelled	57.0	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
93	c3bu7A_	Alignment	not modelled	57.0	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
94	c3ehkC_	Alignment	not modelled	48.8	15	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
95	d1wlta1	Alignment	not modelled	46.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
96	d1o5ua_	Alignment	not modelled	46.3	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
97	c3ka5A_	Alignment	not modelled	44.7	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**ribosome-associated protein y (psrp-1); **PDBTitle:** crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
98	c3l2hD_	Alignment	not modelled	43.6	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
99	c3kglB_	Alignment	not modelled	40.5	12	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
100	c3bvcA_	Alignment	not modelled	38.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ism_01780; **PDBTitle:** crystal structure of uncharacterized protein ism_01780 from2 roseovarius nubinhibens ism
101	c1fxzC_	Alignment	not modelled	35.0	9	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
102	d2arca_	Alignment	not modelled	34.9	18	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
103	c3ebrA_	Alignment	not modelled	34.2	16	**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
104	d1uija2	Alignment	not modelled	34.0	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins

						Family: Germin/Seed storage 7S protein
105	c3mlhA_	Alignment	not modelled	33.8	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of the 2009 h1n1 influenza virus hemagglutinin2 receptor-binding domain
106	d1gl0i_	Alignment	not modelled	33.7	30	**Fold:**PMP inhibitors **Superfamily:**PMP inhibitors **Family:**PMP inhibitors
107	c1ey2A_	Alignment	not modelled	33.6	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
108	d1eyba_	Alignment	not modelled	33.6	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
109	d1a6ca1	Alignment	not modelled	32.8	20	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
110	d1w9ya1	Alignment	not modelled	31.4	14	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
111	d1ep0a_	Alignment	not modelled	29.9	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
112	c1upiA_	Alignment	not modelled	29.1	14	**PDB header:**epimerase **Chain:** A: **PDB Molecule:**dtdp-4-dehydrorhamnose 3,5-epimerase; **PDBTitle:** mycobacterium tuberculosis rmlc epimerase (rv3465)
113	c2f91B_	Alignment	not modelled	28.8	30	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**serine protease inhibitor i/ii; **PDBTitle:** 1.2a resolution structure of a crayfish trypsin complexed2 with a peptide inhibitor, sgti
114	c3c3vA_	Alignment	not modelled	28.7	11	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
115	d2ixca1	Alignment	not modelled	27.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
116	d2phla1	Alignment	not modelled	27.6	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
117	c3d0jA_	Alignment	not modelled	25.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ca_c3497; **PDBTitle:** crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
118	d2ixha1	Alignment	not modelled	24.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
119	c2d5fB_	Alignment	not modelled	23.5	14	**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
120	d2bdra1	Alignment	not modelled	23.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA