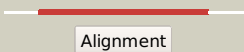

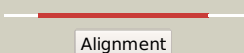

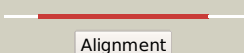

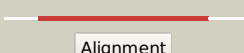


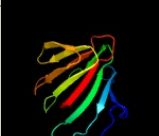

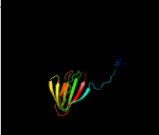
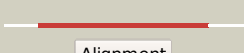

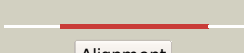









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1717_(-)_1944413_1944763
Date	Fri Aug 2 13:30:32 BST 2019
Unique Job ID	4b06814eee09e2bf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5tg0A_	 Alignment		99.9	13	PDB header: lyase Chain: A; PDB Molecule: dimethylsulfonylpropionate lyase dddk; PDBTitle: crystal structure of the dimethylsulfonylpropionate (dmsp) lyase dddk2 complexed with iron and zinc
2	d1lr5a_	 Alignment		99.9	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
3	d1vj2a_	 Alignment		99.8	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
4	c3ht2A_	 Alignment		99.8	18	PDB header: lyase Chain: A; PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomyficicus
5	d1o4ta_	 Alignment		99.8	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
6	c5uqpA_	 Alignment		99.8	13	PDB header: unknown function Chain: A; PDB Molecule: cupin; PDBTitle: the crystal structure of cupin protein from rhodococcus jostii rha1
7	c3jzvA_	 Alignment		99.8	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.
8	c3i7dB_	 Alignment		99.8	26	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
9	c2oa2A_	 Alignment		99.8	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
10	c4i4aA_	 Alignment		99.8	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: similar to unknown protein; PDBTitle: crystal structure of plu4264 protein from photorhabdus luminescens
11	c3ibmB_	 Alignment		99.8	23	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 domain-containing protein hha1_0468 from2 halorhodospira halophila

12	c5j7mB_	Alignment		99.8	18	PDB header: unknown function Chain: B: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 conserved barrel domain protein from2 kribbella flavida dsm 17836
13	c4bifC_	Alignment		99.8	16	PDB header: lyase Chain: C: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: biochemical and structural characterisation of a novel2 manganese-dependent hydroxynitrile lyase from bacteria
14	d2f4pa1	Alignment		99.8	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
15	d1sq4a_	Alignment		99.8	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Ylba-like
16	d1v70a_	Alignment		99.8	25	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
17	c3kqzA_	Alignment		99.8	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
18	c3l2hD_	Alignment		99.8	21	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
19	c5bxxA_	Alignment		99.8	13	PDB header: lyase Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of the ectoine synthase from the cold-adapted marine2 bacterium sphingopyxis alaskensis
20	c2gu9B_	Alignment		99.8	20	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
21	c4rd7A_	Alignment	not modelled	99.8	20	PDB header: unknown function Chain: A: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: the crystal structure of a cupin 2 conserved barrel domain protein2 from salinispora arenicola cns-205
22	c5fljK_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: K: PDB Molecule: quercetinase qucd; PDBTitle: enzyme-substrate-dioxygen complex of ni-quercetinase
23	d1y9qa2	Alignment	not modelled	99.8	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
24	c4e2gE_	Alignment	not modelled	99.8	12	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of cupin fold protein sthe2323 from sphaerobacter2 thermophilus
25	c3cewA_	Alignment	not modelled	99.8	19	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
26	c3h8uA_	Alignment	not modelled	99.8	18	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
27	c5onoA_	Alignment	not modelled	99.8	14	PDB header: metal binding protein Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of ectoine synthase from p. lautus
						Fold: Double-stranded beta-helix

28	d2b8ma1	Alignment	not modelled	99.7	16	Superfamily: RmlC-like cupins Family: MJ0764-like
29	c5zbfA_	Alignment	not modelled	99.7	15	PDB header: isomerase Chain: A: PDB Molecule: cupin domain protein; PDBTitle: crystal structure of 4-hydroxyphenylpyruvic acid bound aere from2 microcystis aeruginosa
30	c2pfbB_	Alignment	not modelled	99.7	18	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
31	c1sefA_	Alignment	not modelled	99.7	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
32	d1sefa_	Alignment	not modelled	99.7	9	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Ylba-like
33	c2d40C_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
34	d1sfna_	Alignment	not modelled	99.7	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Ylba-like
35	c2vpvA_	Alignment	not modelled	99.7	17	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
36	c6b8wB_	Alignment	not modelled	99.7	21	PDB header: transcription Chain: B: PDB Molecule: xre family transcriptional regulator; PDBTitle: 1.9 angstrom resolution crystal structure of cupin_2 domain (pfam2_07883) of xre family transcriptional regulator from enterobacter3 cloacae.
37	c3h7yA_	Alignment	not modelled	99.7	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: bacilysin biosynthesis protein bacb; PDBTitle: crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
38	c4e2sE_	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: E: PDB Molecule: ureidoglycine aminohydrolase; PDBTitle: crystal structure of (s)-ureidoglycine aminohydrolase from arabidopsis2 thaliana in complex with its substrate, (s)-ureidoglycine
39	d1y3ta1	Alignment	not modelled	99.7	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
40	c3fjsC_	Alignment	not modelled	99.7	23	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
41	c5fpzA_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: pectin degradation protein; PDBTitle: the structure of kdgf from yersinia enterocolitica with2 malonate bound in the active site.
42	d1rc6a_	Alignment	not modelled	99.7	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Ylba-like
43	c2vqaC_	Alignment	not modelled	99.7	19	PDB header: metal-binding protein Chain: C: PDB Molecule: sl1358 protein; PDBTitle: protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.
44	d2bnma2	Alignment	not modelled	99.7	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
45	d2d40a1	Alignment	not modelled	99.7	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
46	c5fq0A_	Alignment	not modelled	99.7	11	PDB header: lyase Chain: A: PDB Molecule: kdgf; PDBTitle: the structure of kdgf from halomonas sp.
47	c2ozjB_	Alignment	not modelled	99.7	18	PDB header: unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel; PDBTitle: crystal structure of a cupin superfamily protein (dsv2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
48	c4b29A_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: dimethylsulfoniopropionate lyase; PDBTitle: crystal structures of dmsp lyases rddddp and rndddqii
49	d1j58a_	Alignment	not modelled	99.7	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
50	d1juha_	Alignment	not modelled	99.7	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
51	c2fqpD_	Alignment	not modelled	99.7	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
52	c3bu7A_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: gentisate 1,2-dioxygenase; PDBTitle: crystal structure and biochemical characterization of gdosp, a2 gentisate 1,2-dioxygenase from silicibacter pomeroyi
53	d3bu7a1	Alignment	not modelled	99.6	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like

54	c2q30C	Alignment	not modelled	99.6	19	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
55	d2phda1	Alignment	not modelled	99.6	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
56	c5cu1A	Alignment	not modelled	99.6	20	PDB header: lyase Chain: A: PDB Molecule: dmisp lyase; PDBTitle: crystal structure of dmisp lyase dddq from ruegeria pomeroyi dss-3
57	d1x82a	Alignment	not modelled	99.6	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
58	c3rnsA	Alignment	not modelled	99.6	21	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
59	d1j3pa	Alignment	not modelled	99.6	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
60	c4la3B	Alignment	not modelled	99.6	17	PDB header: lyase Chain: B: PDB Molecule: dimethylsulphonio propionate (dmisp) lyase dddq; PDBTitle: crystal structure of dimethylsulphonio propionate (dmisp) lyase dddq2 y131a in complex with dmisp
61	c3es1A	Alignment	not modelled	99.6	16	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
62	c2oziA	Alignment	not modelled	99.6	17	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
63	d1yhfa1	Alignment	not modelled	99.6	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
64	d2et1a1	Alignment	not modelled	99.6	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
65	c5u57B	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
66	c5oo9A	Alignment	not modelled	99.6	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative cupin_2 domain-containing isomerase; PDBTitle: streptomyces pac13 (y55f) with uridine
67	c5j4fB	Alignment	not modelled	99.6	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the n-terminally his6-tagged hp0902, an2 uncharacterized protein from helicobacter pylori 26695
68	c4h7lB	Alignment	not modelled	99.6	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of plim_4148 protein from planctomyces limnophilus
69	c3lwcA	Alignment	not modelled	99.6	25	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
70	c2o8gA	Alignment	not modelled	99.5	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 (bx_e_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
71	c6b9rD	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
72	c2xlfA	Alignment	not modelled	99.5	13	PDB header: metal binding protein Chain: A: PDB Molecule: sl1785 protein; PDBTitle: structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
73	d1dgwa	Alignment	not modelled	99.4	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
74	c2bnoA	Alignment	not modelled	99.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
75	c4axoA	Alignment	not modelled	99.4	20	PDB header: structural protein Chain: A: PDB Molecule: ethanolamine utilization protein; PDBTitle: structure of the clostridium difficile eutq protein
76	d1uika1	Alignment	not modelled	99.4	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
77	c1y9gA	Alignment	not modelled	99.4	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
78	c3d82A	Alignment	not modelled	99.4	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

79	c4p9gA	Alignment	not modelled	99.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4'-dihydroxyacetophenone dioxygenase; PDBTitle: structure of the 2,4'-dihydroxyacetophenone dioxygenase from2 alcaligenes sp.
80	d1yfua1	Alignment	not modelled	99.4	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
81	c2i45C	Alignment	not modelled	99.4	15	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
82	c4qglA	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: acireductone dioxygenase; PDBTitle: acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
83	d1fxza1	Alignment	not modelled	99.3	9	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
84	d1uija1	Alignment	not modelled	99.3	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
85	d1fxza2	Alignment	not modelled	99.3	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
86	c1fxzC	Alignment	not modelled	99.2	9	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
87	c3bcwB	Alignment	not modelled	99.2	17	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
88	c6b4sB	Alignment	not modelled	99.2	20	PDB header: allergen Chain: B: PDB Molecule: 11s globulin; PDBTitle: crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
89	c3kgLB	Alignment	not modelled	99.2	11	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from brassica napus
90	d1od5a2	Alignment	not modelled	99.2	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
91	d2phla2	Alignment	not modelled	99.2	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
92	c3ebrA	Alignment	not modelled	99.2	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
93	d1od5a1	Alignment	not modelled	99.2	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
94	c6nwoD	Alignment	not modelled	99.2	16	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator bgar; PDBTitle: structures of the transcriptional regulator bgar, a lactose sensor.
95	c1cauB	Alignment	not modelled	99.1	14	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
96	c2d5fB	Alignment	not modelled	99.1	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
97	c5wpwA	Alignment	not modelled	99.1	14	PDB header: allergen Chain: A: PDB Molecule: 11s globulin isoform 1; PDBTitle: crystal structure of coconut allergen cocosin
98	c2e9gA	Alignment	not modelled	99.1	16	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin subunit beta; PDBTitle: recombinant pro-11s globulin of pumpkin
99	c5e1rC	Alignment	not modelled	99.1	10	PDB header: allergen Chain: C: PDB Molecule: 7s vicilin; PDBTitle: crystal structure of pecan (carya illinoensis) vicilin, a new food2 allergen
100	c3qacA	Alignment	not modelled	99.1	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.
101	d1uika2	Alignment	not modelled	99.1	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
102	c3kscD	Alignment	not modelled	99.1	9	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin from pismus2 sativum l.
103	c5wxuD	Alignment	not modelled	99.1	18	PDB header: plant protein Chain: D: PDB Molecule: 11s globulin; PDBTitle: 11s globulin from wrightia tinctoria reveals auxin binding site
104	c3cxE	Alignment	not modelled	99.1	12	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
105	d1zrra1	Alignment	not modelled	99.1	9	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Acireductone dioxygenase
106	c1uijF_	Alignment	not modelled	99.1	22	PDB header: sugar binding protein Chain: F: PDB Molecule: beta subunit of beta conglycinin; PDBTitle: crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
107	c2cauA_	Alignment	not modelled	99.0	17	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
108	c3ehkC_	Alignment	not modelled	99.0	13	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
109	c4lejA_	Alignment	not modelled	99.0	17	PDB header: allergen, plant protein Chain: A: PDB Molecule: vicilin; PDBTitle: crystal structure of the korean pine (pinus koraiensis) vicilin
110	c5yjsB_	Alignment	not modelled	99.0	21	PDB header: plant protein Chain: B: PDB Molecule: vicilin-like antimicrobial peptides 2-2; PDBTitle: structure of vicilin from capsicum annum
111	c5cadA_	Alignment	not modelled	99.0	19	PDB header: plant protein Chain: A: PDB Molecule: sm80.1 vicilin; PDBTitle: crystal structure of the vicilin from solanum melongena revealed2 existence of different anionic ligands in structurally similar3 pockets
112	c3c3vA_	Alignment	not modelled	99.0	12	PDB header: allergen Chain: A: PDB Molecule: arachin arah3 isoform; PDBTitle: crystal structure of peanut major allergen ara h 3
113	c6b9tH_	Alignment	not modelled	99.0	9	PDB header: oxidoreductase Chain: H: PDB Molecule: methylphosphonate synthase; PDBTitle: crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
114	d1zvfa1	Alignment	not modelled	99.0	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
115	d1uija2	Alignment	not modelled	99.0	12	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
116	c2eaaB_	Alignment	not modelled	99.0	22	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
117	c3o14B_	Alignment	not modelled	99.0	13	PDB header: gene regulation Chain: B: PDB Molecule: anti-ecfsigma factor, chrr; PDBTitle: crystal structure of an anti-ecfsigma factor, chrr (magu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
118	c3eqeB_	Alignment	not modelled	99.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative cystein dioxygenase; PDBTitle: crystal structure of the yubc protein from bacillus subtilis.2 northeast structural genomics consortium target sr112.
119	c1uijA_	Alignment	not modelled	99.0	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)
120	d2o1qa1	Alignment	not modelled	99.0	10	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Acetylacetone-cleaving enzyme-like