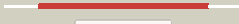



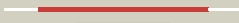



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3471c_(-) _3888987_3889520
Date	Fri Aug 9 18:20:14 BST 2019
Unique Job ID	5dfc27d7282b4609

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6b9rD_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: D; PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
2	c5u57B_	 Alignment		100.0	12	PDB header: oxidoreductase Chain: B; PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
3	c6b9rH_	 Alignment		100.0	10	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
4	c2bnoA_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
5	c1y9qA_	 Alignment		99.9	15	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
6	c4la3B_	 Alignment		99.9	15	PDB header: lyase Chain: B; PDB Molecule: dimethylsulphoniopropionate (dmsp) lyase dddq; PDBTitle: crystal structure of dimethylsulphoniopropionate (dmsp) lyase dddq2 y131a in complex with dmsp
7	c2gu9B_	 Alignment		99.9	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
8	c5fijK_	 Alignment		99.8	16	PDB header: oxidoreductase Chain: K; PDB Molecule: quercetinase qued; PDBTitle: enzyme-substrate-dioxygen complex of ni-quercetinase
9	c2oa2A_	 Alignment		99.8	25	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	d1o4ta_	 Alignment		99.8	20	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
11	c5cu1A_	 Alignment		99.8	18	PDB header: lyase Chain: A; PDB Molecule: dmsp lyase; PDBTitle: crystal structure of dmsp lyase dddq from ruegeria pomeroyi dss-3

12	c5tg0A_	Alignment		99.8	22	PDB header: lyase Chain: A; PDB Molecule: dimethylsulfoniopropionate lyase dddk; PDBTitle: crystal structure of the dimethylsulfoniopropionate (dmsp) lyase dddk2 complexed with iron and zinc
13	c3i7dB_	Alignment		99.8	20	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
14	d1sq4a_	Alignment		99.8	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Ylba-like
15	c3cewA_	Alignment		99.8	25	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
16	d1y3ta1	Alignment		99.8	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
17	c3jzvA_	Alignment		99.8	26	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.
18	d1lr5a_	Alignment		99.8	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
19	c3h8uA_	Alignment		99.8	16	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
20	d1y9qa2	Alignment		99.8	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
21	c4e2sE_	Alignment	not modelled	99.8	17	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
22	c3l2hD_	Alignment	not modelled	99.8	22	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
23	d1juha_	Alignment	not modelled	99.8	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
24	c3ht2A_	Alignment	not modelled	99.8	25	PDB header: lyase Chain: A; PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
25	c5uqpA_	Alignment	not modelled	99.8	20	PDB header: unknown function Chain: A; PDB Molecule: cupin; PDBTitle: the crystal structure of cupin protein from rhodococcus jostii rha1
26	d1sfna_	Alignment	not modelled	99.8	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Ylba-like
27	c3ibmB_	Alignment	not modelled	99.8	24	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
28	d2f4pa1	Alignment	not modelled	99.8	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like

29	d1v70a_	Alignment	not modelled	99.8	27	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
30	d1rc6a_	Alignment	not modelled	99.8	11	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
31	d1vj2a_	Alignment	not modelled	99.8	20	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1459-like
32	c2vqaC_	Alignment	not modelled	99.8	20	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.
33	c3kgzA_	Alignment	not modelled	99.8	26	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 rhodospseudomonas palustris
34	c6b8wB_	Alignment	not modelled	99.7	17	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.
35	d1sefa_	Alignment	not modelled	99.7	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
36	c1sefA_	Alignment	not modelled	99.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
37	c5bxxA_	Alignment	not modelled	99.7	21	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
38	c4b29A_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: dimethylsulfoniopropionate lyase; PDBTitle: crystal structures of dmsp lyases rddddd and rnddddii
39	d2b8ma1	Alignment	not modelled	99.7	19	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: MJ0764-like
40	d2bnma2	Alignment	not modelled	99.7	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1459-like
41	c2o8qA_	Alignment	not modelled	99.7	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
42	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
43	c4bifC_	Alignment	not modelled	99.7	22	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
44	c4rd7A_	Alignment	not modelled	99.7	17	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
45	c5fpzA_	Alignment	not modelled	99.7	16	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.
46	c5onoA_	Alignment	not modelled	99.7	20	PDB header: metal binding protein Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of ectoine synthase from p. lautus
47	c2vpvA_	Alignment	not modelled	99.7	16	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
48	c4i4aA_	Alignment	not modelled	99.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: similar to unknown protein; PDBTitle: crystal structure of plu4264 protein from photorhabdus luminescens
49	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
50	d1j58a_	Alignment	not modelled	99.7	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
51	c4e2gE_	Alignment	not modelled	99.7	19	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
52	c5fq0A_	Alignment	not modelled	99.7	18	PDB header: lyase Chain: A: PDB Molecule: kdgf; PDBTitle: the structure of kdgf from halomonas sp.
53	c5j7mB_	Alignment	not modelled	99.7	20	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
54	d1j3pa_	Alignment	not modelled	99.7	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Glucose-6-phosphate isomerase, GPI

55	c4h7IB_	Alignment	not modelled	99.7	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of plim_4148 protein from planctomyces limnophilus
56	c2oziA_	Alignment	not modelled	99.7	18	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
57	c2pfwB_	Alignment	not modelled	99.7	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
58	c5oo9A_	Alignment	not modelled	99.7	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative cupin_2 domain-containing isomerase; PDBTitle: streptomyces pac13 (y55f) with uridine
59	c3h7yA_	Alignment	not modelled	99.6	15	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
60	c3fjsC_	Alignment	not modelled	99.6	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
61	d1x82a_	Alignment	not modelled	99.6	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
62	c2xifA_	Alignment	not modelled	99.6	15	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)
63	d1dgwa_	Alignment	not modelled	99.6	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
64	d2et1a1	Alignment	not modelled	99.6	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
65	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
66	c2q30C_	Alignment	not modelled	99.6	24	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
67	d1uika1	Alignment	not modelled	99.6	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
68	c2d40C_	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
69	c5e1rC_	Alignment	not modelled	99.5	16	PDB header: allergen Chain: C: PDB Molecule: 7s vicilin; PDBTitle: crystal structure of pecan (carya illinoensis) vicilin, a new food2 allergen
70	c2ozjB_	Alignment	not modelled	99.5	19	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
71	d2phda1	Alignment	not modelled	99.5	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
72	d1fxza2	Alignment	not modelled	99.5	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
73	d2d40a1	Alignment	not modelled	99.5	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
74	c4axoA_	Alignment	not modelled	99.5	17	PDB header: structural protein Chain: A: PDB Molecule: ethanolamine utilization protein; PDBTitle: structure of the clostridium difficile eutq protein
75	d3bu7a1	Alignment	not modelled	99.5	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
76	c3bu7A_	Alignment	not modelled	99.5	20	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
77	c5j4fB_	Alignment	not modelled	99.5	23	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
78	c4lejA_	Alignment	not modelled	99.5	16	PDB header: allergen, plant protein Chain: A: PDB Molecule: vicilin; PDBTitle: crystal structure of the korean pine (pinus koraiensis) vicilin
79	c1fxzC_	Alignment	not modelled	99.5	16	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
80	c3rnsA_	Alignment	not modelled	99.5	20	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
81	c3d82A	Alignment	not modelled	99.4	28	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
82	d1uija1	Alignment	not modelled	99.4	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
83	c3lwcA	Alignment	not modelled	99.4	24	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
84	d1yhfa1	Alignment	not modelled	99.4	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
85	c2i45C	Alignment	not modelled	99.4	16	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
86	c5yjsB	Alignment	not modelled	99.4	15	PDB header: plant protein Chain: B: PDB Molecule: vicilin-like antimicrobial peptides 2-2; PDBTitle: structure of vicilin from capsicum annuum
87	c3kglB	Alignment	not modelled	99.4	19	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from brassica napus
88	c3kscD	Alignment	not modelled	99.4	17	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin from pisum2 sativum l.
89	c5cadA	Alignment	not modelled	99.4	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
90	d1fxza1	Alignment	not modelled	99.3	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
91	c3qacA	Alignment	not modelled	99.3	13	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin seed storage protein; PDBTitle: structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.
92	d1od5a2	Alignment	not modelled	99.3	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
93	c5wpwA	Alignment	not modelled	99.3	15	PDB header: allergen Chain: A: PDB Molecule: 11s globulin isoform 1; PDBTitle: crystal structure of coconut allergen cocosin
94	c1cauB	Alignment	not modelled	99.3	18	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
95	c6b4sB	Alignment	not modelled	99.3	12	PDB header: allergen Chain: B: PDB Molecule: 11s globulin; PDBTitle: crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
96	c3c3vA	Alignment	not modelled	99.3	19	PDB header: allergen Chain: A: PDB Molecule: arachin arah3 isoform; PDBTitle: crystal structure of peanut major allergen ara h 3
97	d1uika2	Alignment	not modelled	99.3	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
98	c2e9qA	Alignment	not modelled	99.3	15	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin subunit beta; PDBTitle: recombinant pro-11s globulin of pumpkin
99	c2cauA	Alignment	not modelled	99.3	17	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
100	d1yfua1	Alignment	not modelled	99.3	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
101	d2phla2	Alignment	not modelled	99.3	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
102	d1uija2	Alignment	not modelled	99.3	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
103	c2d5fB	Alignment	not modelled	99.2	20	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
104	c4p9gA	Alignment	not modelled	99.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4'-dihydroxyacetophenone dioxygenase; PDBTitle: structure of the 2,4'-dihydroxyacetophenone dioxygenase from2 alcaligenes sp.
105	c3ehkC	Alignment	not modelled	99.2	18	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
106	c1uijA	Alignment	not modelled	99.2	17	PDB header: sugar binding protein Chain: A: PDB Molecule: beta subunit of beta conglycinin;

106	c1uijA_	Alignment	not modelled	99.2	17	PDBTitle: crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
107	c2eaaB_	Alignment	not modelled	99.2	18	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
108	d1od5a1	Alignment	not modelled	99.2	21	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
109	c1uijF_	Alignment	not modelled	99.2	16	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)
110	c5wxuD_	Alignment	not modelled	99.2	18	PDB header: plant protein Chain: D: PDB Molecule: 11s globulin; PDBTitle: 11s globulin from wrightia tinctoria reveals auxin binding site
111	c4qglA_	Alignment	not modelled	99.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: acireductone dioxygenase; PDBTitle: acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
112	c3s7eB_	Alignment	not modelled	99.1	18	PDB header: allergen Chain: B: PDB Molecule: allergen ara h 1, clone p41b; PDBTitle: crystal structure of ara h 1
113	c3bcwB_	Alignment	not modelled	99.1	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
114	c3eqeB_	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putative cystein dioxygenase; PDBTitle: crystal structure of a yubc protein from bacillus subtilis.2 northeast structural genomics consortium target sr112.
115	c6nwoD_	Alignment	not modelled	99.0	13	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator bgar; PDBTitle: structures of the transcriptional regulator bgar, a lactose sensor.
116	d2phla1	Alignment	not modelled	98.9	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
117	c2zklA_	Alignment	not modelled	98.9	22	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
118	c2phlC_	Alignment	not modelled	98.9	17	PDB header: plant seed storage protein(vicilin) Chain: C: PDB Molecule: phaseolin; PDBTitle: the structure of phaseolin at 2.2 angstroms resolution: implications2 for a common vicilin(/slash)legumin structure and the genetic3 engineering of seed storage proteins
119	c3ebrA_	Alignment	not modelled	98.9	17	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
120	d2pyta1	Alignment	not modelled	98.9	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: EutQ-like