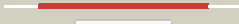



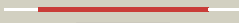
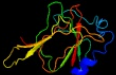















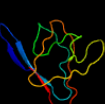








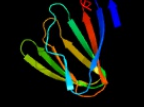


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1065_(-)_1187440_1188006
Date	Wed Jul 31 22:05:14 BST 2019
Unique Job ID	a1597112c93714c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3elna1	 Alignment		100.0	21	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Cysteine dioxygenase type I
2	d2ic1a1	 Alignment		100.0	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Cysteine dioxygenase type I
3	c3eqeB_	 Alignment		100.0	25	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.
4	c3ussA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of cysteine dioxygenase from pseudomonas aeruginosa
5	d2gm6a1	 Alignment		100.0	21	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Cysteine dioxygenase type I
6	c3h8uA_	 Alignment		99.1	21	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
7	d1v70a_	 Alignment		98.8	23	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
8	c2oa2A_	 Alignment		98.8	19	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
9	c2gu9B_	 Alignment		98.7	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
10	d1lr5a_	 Alignment		98.3	21	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
11	c2fqpD_	 Alignment		98.3	21	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

12	d2b8ma1	Alignment		98.2	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
13	c2q30C_	Alignment		98.1	20	PDB header: unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a rmlc-like cupin protein (dde_2303) from <i>Desulfovibrio desulfuricans</i> subsp. at 1.94 Å resolution
14	c4e2gE_	Alignment		98.0	20	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 <i>Sphaerobacter2 thermophilus</i>
15	c3i7dB_	Alignment		98.0	24	PDB header: isomerase Chain: B; PDB Molecule: sugar phosphate isomerase; PDBTitle: crystal structure of sugar phosphate isomerase from a cupin2 superfamily spo2919 from <i>Silicibacter pomeroyi</i> (yp_168127.1) from <i>Silicibacter pomeroyi</i> dss-3 at 2.30 Å resolution
16	c5fq0A_	Alignment		97.9	22	PDB header: lyase Chain: A; PDB Molecule: kdgf; PDBTitle: the structure of kdgf from <i>Halomonas</i> sp.
17	c2pfbB_	Alignment		97.9	23	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 <i>Shewanella2 frigidimarina</i> ncimb 400 at 1.90 Å resolution
18	c5j7mB_	Alignment		97.8	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 from <i>Kribbella flavida</i> DSM 17836
19	c5fpzA_	Alignment		97.8	17	PDB header: hydrolase Chain: A; PDB Molecule: pectin degradation protein; PDBTitle: the structure of kdgf from <i>Yersinia enterocolitica</i> with 2 malonate bound in the active site.
20	d1y9qa2	Alignment		97.8	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
21	c4e2sE_	Alignment	not modelled	97.8	12	PDB header: hydrolase Chain: E; PDB Molecule: ureidoglycine aminohydrolase; PDBTitle: crystal structure of (s)-ureidoglycine aminohydrolase from <i>Arabidopsis2 thaliana</i> in complex with its substrate, (s)-ureidoglycine
22	c3l2hD_	Alignment	not modelled	97.6	24	PDB header: isomerase Chain: D; PDB Molecule: putative sugar phosphate isomerase; PDBTitle: crystal structure of putative sugar phosphate isomerase (afe_0303)2 from <i>Acidithiobacillus ferrooxidans</i> ATCC 23270 at 1.85 Å resolution
23	d1yhfa1	Alignment	not modelled	97.6	25	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
24	c3fjsC_	Alignment	not modelled	97.6	20	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 <i>Ralstonia eutropha</i> JMP134 at 1.90 Å resolution
25	c5uqpA_	Alignment	not modelled	97.6	21	PDB header: unknown function Chain: A; PDB Molecule: cupin; PDBTitle: the crystal structure of cupin protein from <i>Rhodococcus jostii</i> rha1
26	c2ozia_	Alignment	not modelled	97.6	20	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 <i>Rhodopseudomonas palustris</i> CGA009
27	c5fljK_	Alignment	not modelled	97.5	16	PDB header: oxidoreductase Chain: K; PDB Molecule: quercetinase qued; PDBTitle: enzyme-substrate-dioxygen complex of Ni-quercetinase PDB header: unknown function

28	c4rd7A_	Alignment	not modelled	97.5	20	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
29	c3h7yA_	Alignment	not modelled	97.4	14	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
30	c3jzvA_	Alignment	not modelled	97.4	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.
31	c3cewA_	Alignment	not modelled	97.4	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
32	c4b29A_	Alignment	not modelled	97.4	20	PDB header: hydrolase Chain: A: PDB Molecule: dimethylsulfoniopropionate lyase; PDBTitle: crystal structures of dmsp lyases rddddp and rnddddqi
33	c5zbfA_	Alignment	not modelled	97.3	11	PDB header: isomerase Chain: A: PDB Molecule: cupin domain protein; PDBTitle: crystal structure of 4-hydroxyphenylpyruvic acid bound aere from2 microcystis aeruginosa
34	c2ozjB_	Alignment	not modelled	97.2	16	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
35	c4i4aA_	Alignment	not modelled	97.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: similar to unknown protein; PDBTitle: crystal structure of plu4264 protein from photorhabdus luminescens
36	c6b8wB_	Alignment	not modelled	97.1	20	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	c3kgzA_	Alignment	not modelled	97.1	10	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
38	c5j4fB_	Alignment	not modelled	96.9	11	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
39	c3rnsA_	Alignment	not modelled	96.9	10	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
40	d1j58a_	Alignment	not modelled	96.9	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
41	d1vj2a_	Alignment	not modelled	96.9	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
42	c5cu1A_	Alignment	not modelled	96.9	18	PDB header: lyase Chain: A: PDB Molecule: dmsp lyase; PDBTitle: crystal structure of dmsp lyase dddq from ruegeria pomeroyi dss-3
43	c4la3B_	Alignment	not modelled	96.9	14	PDB header: lyase Chain: B: PDB Molecule: dimethylsulphoniopropionate (dmsp) lyase dddq; PDBTitle: crystal structure of dimethylsulphoniopropionate (dmsp) lyase dddq2 y131a in complex with dmsp
44	c3es1A_	Alignment	not modelled	96.8	18	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
45	d2et1a1	Alignment	not modelled	96.7	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
46	c3ht2A_	Alignment	not modelled	96.7	18	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomyficifcus
47	c5bxxA_	Alignment	not modelled	96.7	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
48	c2vqaC_	Alignment	not modelled	96.6	24	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.
49	d1y3ta1	Alignment	not modelled	96.6	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
50	c2vpvA_	Alignment	not modelled	96.5	13	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
51	d2f4pa1	Alignment	not modelled	96.5	25	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
52	d1o4ta_	Alignment	not modelled	96.5	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
53	c1c9fA_	Alignment	not modelled	96.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein;

53	c1sefa_	Alignment	not modelled	96.3	11	PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
54	d1sefa_	Alignment	not modelled	96.3	11	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
55	d1sq4a_	Alignment	not modelled	96.3	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
56	c5onoA_	Alignment	not modelled	96.2	15	PDB header: metal binding protein Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of ectoine synthase from p. lautus
57	c4bifC_	Alignment	not modelled	95.8	15	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
58	d1dgwa_	Alignment	not modelled	95.6	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
59	c3o14B_	Alignment	not modelled	95.6	21	PDB header: gene regulation Chain: B: PDB Molecule: anti-ecsigma factor, chrr; PDBTitle: crystal structure of an anti-ecsigma factor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
60	c2d40C_	Alignment	not modelled	95.5	22	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
61	c2o8qA_	Alignment	not modelled	95.5	21	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
62	d1rc6a_	Alignment	not modelled	95.5	13	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
63	c3ibmB_	Alignment	not modelled	95.5	15	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
64	d1yfua1	Alignment	not modelled	95.4	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
65	c5tg0A_	Alignment	not modelled	95.2	14	PDB header: lyase Chain: A: PDB Molecule: dimethylsulfoniopropionate lyase dddk; PDBTitle: crystal structure of the dimethylsulfoniopropionate (dmsp) lyase dddk2 complexed with iron and zinc
66	d3bu7a1	Alignment	not modelled	95.1	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Gentisate 1,2-dioxygenase-like
67	c3bu7A_	Alignment	not modelled	95.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: gentisate 1,2-dioxygenase; PDBTitle: crystal structure and biochemical characterization of gdozp, a2 gentisate 1,2-dioxygenase from silicibacter pomeroyi
68	d1j3pa_	Alignment	not modelled	94.8	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Glucose-6-phosphate isomerase, GPI
69	d1juha_	Alignment	not modelled	94.7	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Quercetin 2,3-dioxygenase-like
70	c2xlfA_	Alignment	not modelled	94.7	11	PDB header: metal binding protein Chain: A: PDB Molecule: ssl1785 protein; PDBTitle: structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
71	d2phda1	Alignment	not modelled	94.5	12	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Gentisate 1,2-dioxygenase-like
72	d1uika1	Alignment	not modelled	94.3	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
73	c3d82A_	Alignment	not modelled	94.3	22	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 (sfrj_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
74	d1uija1	Alignment	not modelled	94.3	19	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
75	d2d40a1	Alignment	not modelled	94.1	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Gentisate 1,2-dioxygenase-like
76	c4h7lB_	Alignment	not modelled	93.8	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of plim_4148 protein from planctomyces limnophilus
77	d1sfna_	Alignment	not modelled	93.6	15	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
78	c4p9gA_	Alignment	not modelled	92.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4'-dihydroxyacetophenone dioxygenase; PDBTitle: structure of the 2,4'-dihydroxyacetophenone dioxygenase from2 alcaligenes sp.
79	d1uika2	Alignment	not modelled	92.6	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein

80	d2o1qa1	Alignment	not modelled	91.9	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acetylacetone-cleaving enzyme-like
81	c1cauB	Alignment	not modelled	91.4	11	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
82	c2z2sD	Alignment	not modelled	90.8	18	PDB header: transcription Chain: D: PDB Molecule: anti-sigma factor chrr, transcriptional activator chrr; PDBTitle: crystal structure of rhodobacter sphaeroides sigE in complex with the2 anti-sigma chrr
83	d3bb6a1	Alignment	not modelled	90.2	18	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: TehB-like
84	c5oo9A	Alignment	not modelled	90.1	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative cupin_2 domain-containing isomerase; PDBTitle: streptomyces pac13 (y55f) with uridine
85	c2i45C	Alignment	not modelled	89.5	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
86	c3cxE	Alignment	not modelled	88.4	20	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
87	d2bnma2	Alignment	not modelled	88.3	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
88	d1uija2	Alignment	not modelled	88.1	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
89	d1zvf1	Alignment	not modelled	88.0	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
90	d1x82a	Alignment	not modelled	87.7	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
91	c1fxzC	Alignment	not modelled	84.0	10	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
92	d2phla2	Alignment	not modelled	83.6	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
93	d1od5a2	Alignment	not modelled	82.9	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
94	d1fxza2	Alignment	not modelled	79.0	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
95	c3k3nA	Alignment	not modelled	78.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: phd finger protein 8; PDBTitle: crystal structure of the catalytic core domain of human phf8
96	c6b4sB	Alignment	not modelled	77.6	11	PDB header: allergen Chain: B: PDB Molecule: 11s globulin; PDBTitle: crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
97	c3lwcA	Alignment	not modelled	74.2	20	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
98	d3dl3a1	Alignment	not modelled	73.4	24	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: TehB-like
99	c3ebrA	Alignment	not modelled	72.1	20	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
100	c3bcwB	Alignment	not modelled	71.9	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
101	c3ba1B	Alignment	not modelled	70.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: acetylacetone-cleaving enzyme; PDBTitle: crystal structure of an acetylacetone dioxygenase from acinetobacter2 johnsonii
102	c3ehkC	Alignment	not modelled	69.8	12	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of prunin from prunus dulcis
103	c3kscD	Alignment	not modelled	67.2	12	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin from pismus2 sativum l.
104	c3kglB	Alignment	not modelled	65.4	10	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from brassica napus
						PDB header: allergen, plant protein

105	c4lejA_	Alignment	not modelled	62.8	21	Chain: A: PDB Molecule: vicilin; PDBTitle: crystal structure of the korean pine (pinus koraiensis) vicilin
106	c1uijA_	Alignment	not modelled	62.8	19	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)
107	c5e1rC_	Alignment	not modelled	61.6	13	PDB header: allergen Chain: C: PDB Molecule: 7s vicilin; PDBTitle: crystal structure of pecan (carya illinoensis) vicilin, a new food2 allergen
108	d1fxza1	Alignment	not modelled	60.5	10	Fold: Double-stranded beta-helix Superfamily: RmC-like cupins Family: Germin/Seed storage 7S protein
109	c2eaaB_	Alignment	not modelled	59.7	17	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
110	c5cadA_	Alignment	not modelled	58.2	16	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
111	c5yjsB_	Alignment	not modelled	57.2	13	PDB header: plant protein Chain: B: PDB Molecule: vicilin-like antimicrobial peptides 2-2; PDBTitle: structure of vicilin from capsicum annum
112	c3qacA_	Alignment	not modelled	54.5	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.
113	c1uijF_	Alignment	not modelled	53.8	20	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)
114	c3kvaA_	Alignment	not modelled	52.8	23	PDB header: h3k4me3 binding protein, transferase Chain: A: PDB Molecule: jmjc domain-containing histone demethylation protein 1d; PDBTitle: structure of kiaa1718 jumonji domain in complex with alpha-2 ketoglutarate
115	c3ejkA_	Alignment	not modelled	52.8	15	PDB header: isomerase Chain: A: PDB Molecule: dt dp sugar isomerase; PDBTitle: crystal structure of dt dp sugar isomerase (yp_390184.1) from2 desulfovibrio desulfuricans g20 at 1.95 a resolution
116	c2yu1A_	Alignment	not modelled	52.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: jmjc domain-containing histone demethylation protein 1a; PDBTitle: crystal structure of hjhdm1a complexed with a-ketoglutarate
117	c2cauA_	Alignment	not modelled	51.6	16	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
118	c3k2oB_	Alignment	not modelled	50.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional arginine demethylase and lysyl-hydroxylase PDBTitle: structure of an oxygenase
119	c3kv4A_	Alignment	not modelled	46.6	22	PDB header: h3k4me3 binding protein, transferase Chain: A: PDB Molecule: phd finger protein 8; PDBTitle: structure of phf8 in complex with histone h3
120	c3s7eB_	Alignment	not modelled	43.7	17	PDB header: allergen Chain: B: PDB Molecule: allergen ara h 1, clone p41b; PDBTitle: crystal structure of ara h 1