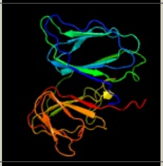
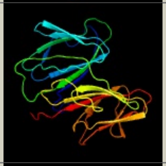
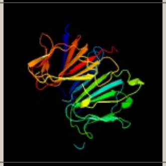
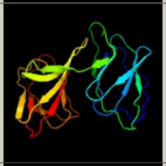
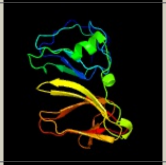
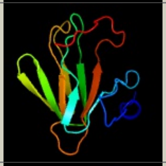
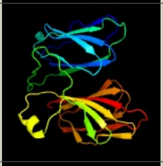
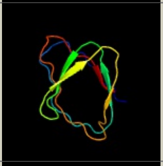
Email	mdejesus@rockefeller.edu
Description	RVBD0181c_(-)_212275_213009
Date	Tue Jul 23 14:50:23 BST 2019
Unique Job ID	e5126a5bd549ff83

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tq5a1	Alignment		100.0	35	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
2	c2vecA_	Alignment		100.0	25	**PDB header:**cytosolic protein **Chain:** A: **PDB Molecule:**pirin-like protein yhak; **PDBTitle:** the crystal structure of the protein yhak from escherichia2 coli
3	c6d0gA_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pirin family protein; **PDBTitle:** 1.78 angstrom resolution crystal structure of quercetin 2,3-2 dioxygenase from acinetobacter baumannii
4	c2p17A_	Alignment		100.0	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pirin-like protein; **PDBTitle:** crystal structure of gk1651 from geobacillus kaustophilus
5	d1j1la_	Alignment		100.0	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
6	c6d0pC_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pirin family protein; **PDBTitle:** 1.88 angstrom resolution crystal structure of quercetin 2,3-2 dioxygenase from acinetobacter baumannii
7	c4e2sE_	Alignment		99.2	15	**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
8	c5zbfA_	Alignment		98.9	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**cupin domain protein; **PDBTitle:** crystal structure of 4-hydroxyphenylpyruvic acid bound aere from2 microcystis aeruginosa
9	c3o14B_	Alignment		98.9	24	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**anti-ecfsigma factor, chrr; **PDBTitle:** crystal structure of an anti-ecfsigma factor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
10	d1sfna_	Alignment		98.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
11	d1sq4a_	Alignment		98.9	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like

12	d1sefa_	Alignment		98.9	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
13	c1sefA_	Alignment		98.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
14	d1rc6a_	Alignment		98.8	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
15	c3h8uA_	Alignment		98.6	25	**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
16	c3h7yA_	Alignment		98.6	12	**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
17	c2d40C_	Alignment		98.5	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
18	c2oziA_	Alignment		98.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa4178; **PDBTitle:** structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
19	c3rnsA_	Alignment		98.4	11	**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
20	c2vqaC_	Alignment		98.4	19	**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.
21	d2d40a1	Alignment	not modelled	98.4	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
22	d1y3ta1	Alignment	not modelled	98.4	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
23	d2phda1	Alignment	not modelled	98.1	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
24	c3i7dB_	Alignment	not modelled	98.0	23	**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
25	c4rd7A_	Alignment	not modelled	97.9	19	**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
26	c4i4aA_	Alignment	not modelled	97.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**similar to unknown protein; **PDBTitle:** crystal structure of plu4264 protein from photorhabdus luminescens
27	c2fqpD_	Alignment	not modelled	97.9	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
28	c5uqpA_	Alignment	not modelled	97.9	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cupin; **PDBTitle:** the crystal structure of cupin protein from rhodococcus jostii rha1

29	d2f4pa1	Alignment	not modelled	97.8	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
30	c3l2hD_	Alignment	not modelled	97.8	23	**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
31	c5wxuD_	Alignment	not modelled	97.8	19	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**11s globulin; **PDBTitle:** 11s globulin from wrightia tinctoria reveals auxin binding site
32	c5j7mB_	Alignment	not modelled	97.8	12	**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
33	c3es1A_	Alignment	not modelled	97.8	21	**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
34	c5tg0A_	Alignment	not modelled	97.7	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dimethylsulfoniopropionate lyase dddk; **PDBTitle:** crystal structure of the dimethylsulfoniopropionate (dmsp) lyase dddk2 complexed with iron and zinc
35	d1o4ta_	Alignment	not modelled	97.7	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
36	d1j58a_	Alignment	not modelled	97.6	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
37	c2oa2A_	Alignment	not modelled	97.6	18	**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
38	c2vpvA_	Alignment	not modelled	97.5	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
39	c6b4sB_	Alignment	not modelled	97.5	15	**PDB header:**allergen **Chain:** B: **PDB Molecule:**11s globulin; **PDBTitle:** crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
40	d1v70a_	Alignment	not modelled	97.5	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
41	c3ibmB_	Alignment	not modelled	97.4	20	**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
42	c6b8wB_	Alignment	not modelled	97.4	24	**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.
43	c2cauA_	Alignment	not modelled	97.4	18	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
44	d1vj2a_	Alignment	not modelled	97.4	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
45	c5cu1A_	Alignment	not modelled	97.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dmsp lyase; **PDBTitle:** crystal structure of dmsp lyase dddq from ruegeria pomeroyi dss-3
46	c2gu9B_	Alignment	not modelled	97.3	18	**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
47	c4b29A_	Alignment	not modelled	97.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dimethylsulfoniopropionate lyase; **PDBTitle:** crystal structures of dmsp lyases rddddp and rndddqii
48	c4bifC_	Alignment	not modelled	97.1	20	**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
49	c4p9gA_	Alignment	not modelled	97.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4'-dihydroxyacetophenone dioxygenase; **PDBTitle:** structure of the 2,4'-dihydroxyacetophenone dioxygenase from2 alcaligenes sp.
50	c3myxA_	Alignment	not modelled	97.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pspto_0244; **PDBTitle:** crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
51	d1yhfa1	Alignment	not modelled	97.0	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
52	c3ht2A_	Alignment	not modelled	97.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
53	c3kgzA_	Alignment	not modelled	97.0	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris

54	c3fjsC_	Alignment	not modelled	97.0	17	**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
55	c2pfwB_	Alignment	not modelled	96.9	14	**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
56	c2phlC_	Alignment	not modelled	96.9	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
57	c1uijF_	Alignment	not modelled	96.9	21	**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)
58	c2q30C_	Alignment	not modelled	96.9	14	**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
59	c4la3B_	Alignment	not modelled	96.9	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
60	c2ozjB_	Alignment	not modelled	96.9	9	**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
61	c5j4fB_	Alignment	not modelled	96.8	20	**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
62	d3bu7a1	Alignment	not modelled	96.8	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
63	c3bu7A_	Alignment	not modelled	96.8	14	**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
64	c3ebrA_	Alignment	not modelled	96.8	18	**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
65	c3jzvA_	Alignment	not modelled	96.7	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.
66	c3cewA_	Alignment	not modelled	96.7	18	**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
67	c1fxzC_	Alignment	not modelled	96.7	16	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
68	c5fq0A_	Alignment	not modelled	96.7	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**kdgf; **PDBTitle:** the structure of kdgf from halomonas sp.
69	d2b8ma1	Alignment	not modelled	96.7	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
70	d1juha_	Alignment	not modelled	96.7	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
71	c5fpzA_	Alignment	not modelled	96.6	12	**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.
72	d1lr5a_	Alignment	not modelled	96.6	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
73	c3c3vA_	Alignment	not modelled	96.6	19	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
74	c2z2sD_	Alignment	not modelled	96.6	33	**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
75	c3kglB_	Alignment	not modelled	96.6	14	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from brassica napus
76	c5onoA_	Alignment	not modelled	96.5	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**l-ectoine synthase; **PDBTitle:** crystal structure of ectoine synthase from p. lautus
77	c5fljK_	Alignment	not modelled	96.4	14	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**quercetinase qued; **PDBTitle:** enzyme-substrate-dioxygen complex of ni-quercetinase
78	c4lejA_	Alignment	not modelled	96.3	16	**PDB header:**allergen, plant protein **Chain:** A: **PDB Molecule:**vicilin; **PDBTitle:** crystal structure of the korean pine (pinus koraiensis)

						vicilin
79	d1y9qa2	Alignment	not modelled	96.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
80	c2i45C_	Alignment	not modelled	96.2	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
81	c5bxxA_	Alignment	not modelled	96.1	14	**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
82	c2xlfA_	Alignment	not modelled	96.1	22	**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)
83	c3bcwB_	Alignment	not modelled	96.1	21	**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
84	c2o8qA_	Alignment	not modelled	96.1	19	**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
85	c3qacA_	Alignment	not modelled	96.0	18	**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.
86	d3elna1	Alignment	not modelled	95.9	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
87	c5wpwA_	Alignment	not modelled	95.9	20	**PDB header:**allergen **Chain:** A: **PDB Molecule:**11s globulin isoform 1; **PDBTitle:** crystal structure of coconut allergen cocosin
88	c4axoA_	Alignment	not modelled	95.8	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ethanolamine utilization protein; **PDBTitle:** structure of the clostridium difficile eutq protein
89	c3s7eB_	Alignment	not modelled	95.8	16	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
90	d2et1a1	Alignment	not modelled	95.7	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
91	d1fxza1	Alignment	not modelled	95.5	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
92	c4e2gE_	Alignment	not modelled	95.5	17	**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
93	d1uika1	Alignment	not modelled	95.3	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
94	c2eaaB_	Alignment	not modelled	95.3	18	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
95	d1j3pa_	Alignment	not modelled	95.1	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
96	d1yfua1	Alignment	not modelled	95.0	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
97	c2d5fB_	Alignment	not modelled	94.8	15	**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
98	d1x82a_	Alignment	not modelled	94.7	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
99	c5e1rC_	Alignment	not modelled	94.4	20	**PDB header:**allergen **Chain:** C: **PDB Molecule:**7s vicilin; **PDBTitle:** crystal structure of pecan (carya illinoinensis) vicilin, a new food2 allergen
100	c6b9rD_	Alignment	not modelled	94.3	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**hydroxyethylphosphonate dioxygenase; **PDBTitle:** streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
101	c3kscD_	Alignment	not modelled	94.2	18	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin from pisum2 sativum l.
102	d2gm6a1	Alignment	not modelled	94.2	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
103	c6nwoD_	Alignment	not modelled	94.1	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator bgar; **PDBTitle:** structures of the transcriptional regulator bgar, a lactose sensor.
104	d1dgwa_	Alignment	not modelled	93.7	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins

						Family: Germin/Seed storage 7S protein
105	c3lwcA_	Alignment	not modelled	93.7	17	**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
106	c3esgA_	Alignment	not modelled	93.5	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of hutd from pseudomonas fluorescens sbw25
107	c3cjxE_	Alignment	not modelled	93.3	11	**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
108	d1uija1	Alignment	not modelled	93.3	28	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
109	c3d82A_	Alignment	not modelled	93.3	12	**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
110	d1fxza2	Alignment	not modelled	93.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
111	c1uijA_	Alignment	not modelled	93.2	21	**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)
112	c5cadA_	Alignment	not modelled	93.2	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
113	d2o1qa1	Alignment	not modelled	92.9	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acetylacetone-cleaving enzyme-like
114	d2phla2	Alignment	not modelled	92.8	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
115	c3balB_	Alignment	not modelled	92.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acetylacetone-cleaving enzyme; **PDBTitle:** crystal structure of an acetylacetone dioxygenase from acinetobacter2 johnsonii
116	d2phla1	Alignment	not modelled	92.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
117	d1od5a2	Alignment	not modelled	92.3	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
118	c5yjsB_	Alignment	not modelled	92.2	18	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**vicilin-like antimicrobial peptides 2-2; **PDBTitle:** structure of vicilin from capsicum annuum
119	c5oo9A_	Alignment	not modelled	91.8	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative cupin_2 domain-containing isomerase; **PDBTitle:** streptomyces pac13 (y55f) with uridine
120	d1o5ua_	Alignment	not modelled	91.7	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112