

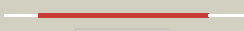





















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3255c_(manA)_3635038_3636264
Date	Thu Aug 8 16:20:46 BST 2019
Unique Job ID	a4ab85dd2c357052

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3h1yA_</a>	 Alignment		100.0	38	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mannose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of mannose 6-phosphate isomerase from 2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
2	<a href="#">d1pmia_</a>	 Alignment		100.0	30	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Type I phosphomannose isomerase
3	<a href="#">d1qwra_</a>	 Alignment		100.0	26	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Type I phosphomannose isomerase
4	<a href="#">d1zx5a1</a>	 Alignment		100.0	25	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Type I phosphomannose isomerase
5	<a href="#">c3rnsA_</a>	 Alignment		98.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> cupin 2 conserved barrel domain protein from leptotrichia buccalis
6	<a href="#">d1sfna_</a>	 Alignment		98.6	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Ylba-like
7	<a href="#">c1sefA_</a>	 Alignment		98.5	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
8	<a href="#">d1sefa_</a>	 Alignment		98.5	7	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Ylba-like
9	<a href="#">d1sq4a_</a>	 Alignment		98.4	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Ylba-like
10	<a href="#">d2d40a1</a>	 Alignment		98.4	19	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Gentisate 1,2-dioxygenase-like
11	<a href="#">c4e2sE_</a>	 Alignment		98.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> ureidoglycine aminohydrolase; <b>PDBTitle:</b> crystal structure of (s)-ureidoglycine aminohydrolase from arabidopsis2 thaliana in complex with its substrate, (s)-ureidoglycine

12	<a href="#">c2d40C_</a>	Alignment		98.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> putative gentisate 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of z3393 from escherichia coli o157:h7
13	<a href="#">c3h7yA_</a>	Alignment		98.4	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> bacilysin biosynthesis protein bacb; <b>PDBTitle:</b> crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
14	<a href="#">c5zbfA_</a>	Alignment		98.3	10	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> cupin domain protein; <b>PDBTitle:</b> crystal structure of 4-hydroxyphenylpyruvic acid bound aere from2 microcystis aeruginosa
15	<a href="#">d1rc6a_</a>	Alignment		98.3	11	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Ylba-like
16	<a href="#">d1y3ta1</a>	Alignment		98.3	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Quercetin 2,3-dioxygenase-like
17	<a href="#">d2phda1</a>	Alignment		98.1	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Gentisate 1,2-dioxygenase-like
18	<a href="#">c3myxA_</a>	Alignment		97.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein pspto_0244; <b>PDBTitle:</b> 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
19	<a href="#">d3bu7a1</a>	Alignment		97.9	23	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Gentisate 1,2-dioxygenase-like
20	<a href="#">c3bu7A_</a>	Alignment		97.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> gentisate 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure and biochemical characterization of gosp, a2 gentisate 1,2-dioxygenase from silicibacter pomeroyi
21	<a href="#">c2vqaC_</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> metal-binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> sl1358 protein; <b>PDBTitle:</b> protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.
22	<a href="#">d1juha_</a>	Alignment	not modelled	97.8	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Quercetin 2,3-dioxygenase-like
23	<a href="#">c1uijF_</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> F; <b>PDB Molecule:</b> beta subunit of beta conglycinin; <b>PDBTitle:</b> crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
24	<a href="#">c2ozjB_</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> cupin 2, conserved barrel; <b>PDBTitle:</b> crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
25	<a href="#">d1j58a_</a>	Alignment	not modelled	97.7	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
26	<a href="#">c3lwcA_</a>	Alignment	not modelled	97.6	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
27	<a href="#">d1yhfa1</a>	Alignment	not modelled	97.5	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1287-like
28	<a href="#">c4lejA_</a>	Alignment	not modelled	97.5	11	<b>PDB header:</b> allergen, plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> vicilin; <b>PDBTitle:</b> crystal structure of the korean pine (pinus koraiensis) vicilin

29	<a href="#">c5j4fB_</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the n-terminally his6-tagged hp0902, an2 uncharacterized protein from helicobacter pylori 26695
30	<a href="#">c3fjsC_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein with rmlc-like cupin fold; <b>PDBTitle:</b> crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
31	<a href="#">c3i7dB_</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar phosphate isomerase; <b>PDBTitle:</b> 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
32	<a href="#">c2pfwB_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
33	<a href="#">c2cauA_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (canavalin); <b>PDBTitle:</b> canavalin from jack bean
34	<a href="#">c4e2gE_</a>	Alignment	not modelled	97.4	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of cupin fold protein sthe2323 from sphaerobacter2 thermophilus
35	<a href="#">c5e1rC_</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> allergen <b>Chain:</b> C: <b>PDB Molecule:</b> 7s vicilin; <b>PDBTitle:</b> crystal structure of pecan (carya illinoensis) vicilin, a new food2 allergen
36	<a href="#">d1o4ta_</a>	Alignment	not modelled	97.4	9	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1287-like
37	<a href="#">c3ibmB_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of cupin 2 domain-containing protein hha1_0468 from2 halorhodospira halophila
38	<a href="#">c5fpzA_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pectin degradation protein; <b>PDBTitle:</b> the structure of kdgf from yersinia enterocolitica with2 malonate bound in the active site.
39	<a href="#">c5fq0A_</a>	Alignment	not modelled	97.4	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> kdgf; <b>PDBTitle:</b> the structure of kdgf from halomonas sp.
40	<a href="#">c2vpvA_</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein mif2; <b>PDBTitle:</b> dimerization domain of mif2p
41	<a href="#">c2gu9B_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> tetracenomycin polyketide synthesis protein; <b>PDBTitle:</b> crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
42	<a href="#">c3qacA_</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> 11s globulin seed storage protein; <b>PDBTitle:</b> structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.
43	<a href="#">c3jzvA_</a>	Alignment	not modelled	97.3	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rru_a2000; <b>PDBTitle:</b> crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
44	<a href="#">c2q30C_</a>	Alignment	not modelled	97.3	7	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
45	<a href="#">d1y9qa2</a>	Alignment	not modelled	97.2	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Probable transcriptional regulator VC1968, C-terminal domain
46	<a href="#">c5uqpA_</a>	Alignment	not modelled	97.2	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cupin; <b>PDBTitle:</b> the crystal structure of cupin protein from rhodococcus jostii rha1
47	<a href="#">d1vj2a_</a>	Alignment	not modelled	97.2	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1459-like
48	<a href="#">c3l2hD_</a>	Alignment	not modelled	97.2	9	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative sugar phosphate isomerase; <b>PDBTitle:</b> crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
49	<a href="#">c5j7mB_</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of cupin 2 conserved barrel domain protein from2 kribbella flavida dsm 17836
50	<a href="#">c5tg0A_</a>	Alignment	not modelled	97.1	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethylsulfoniopropionate lyase dddk; <b>PDBTitle:</b> crystal structure of the dimethylsulfoniopropionate (dmsp) lyase dddk2 complexed with iron and zinc
51	<a href="#">c3o14B_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> anti-ecfsigma factor, chrr; <b>PDBTitle:</b> crystal structure of an anti-ecfsigma factor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
52	<a href="#">c4i4aA_</a>	Alignment	not modelled	97.1	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> similar to unknown protein; <b>PDBTitle:</b> crystal structure of plu4264 protein from photorhabdus luminescens
53	<a href="#">c2na2A_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2720 protein;

53	<a href="#">c2o9zA</a>	Alignment	not modelled	97.1	10	<b>PDBTitle:</b> crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution <b>PDB header:</b> structural genomics, unknown function
54	<a href="#">c3kgzA</a>	Alignment	not modelled	97.1	11	<b>Chain:</b> A; <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
55	<a href="#">c2o8qA</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> 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
56	<a href="#">c4rd7A</a>	Alignment	not modelled	97.0	11	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> the crystal structure of a cupin 2 conserved barrel domain protein2 from salinispora arenicola cns-205
57	<a href="#">d2bnma2</a>	Alignment	not modelled	97.0	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> TM1459-like
58	<a href="#">c2opkC</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
59	<a href="#">c6b8wB</a>	Alignment	not modelled	96.9	14	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> xre family transcriptional regulator; <b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of cupin_2 domain (pfam2_07883) of xre family transcriptional regulator from enterobacter3 cloacae.
60	<a href="#">c2e9qA</a>	Alignment	not modelled	96.9	18	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> 11s globulin subunit beta; <b>PDBTitle:</b> recombinant pro-11s globulin of pumpkin
61	<a href="#">d1v70a</a>	Alignment	not modelled	96.9	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> TM1287-like
62	<a href="#">d2pyta1</a>	Alignment	not modelled	96.9	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> EutQ-like
63	<a href="#">c3d82A</a>	Alignment	not modelled	96.9	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
64	<a href="#">c3cewA</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized cupin protein; <b>PDBTitle:</b> crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
65	<a href="#">c5bxxA</a>	Alignment	not modelled	96.8	11	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> l-ectoine synthase; <b>PDBTitle:</b> crystal structure of the ectoine synthase from the cold-adapted marine2 bacterium sphingopyxis alaskensis
66	<a href="#">c5wxuD</a>	Alignment	not modelled	96.8	22	<b>PDB header:</b> plant protein <b>Chain:</b> D; <b>PDB Molecule:</b> 11s globulin; <b>PDBTitle:</b> 11s globulin from wrightia tinctoria reveals auxin binding site
67	<a href="#">d2b8ma1</a>	Alignment	not modelled	96.7	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> MJ0764-like
68	<a href="#">d2f4pa1</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> TM1287-like
69	<a href="#">d1dgwa</a>	Alignment	not modelled	96.7	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
70	<a href="#">c4axoA</a>	Alignment	not modelled	96.7	6	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> ethanolamine utilization protein; <b>PDBTitle:</b> structure of the clostridium difficile eutq protein
71	<a href="#">c4la3B</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> dimethylsulphoniopropionate (dmisp) lyase dddq; <b>PDBTitle:</b> crystal structure of dimethylsulphoniopropionate (dmisp) lyase dddq2 y131a in complex with dmisp
72	<a href="#">d1uika1</a>	Alignment	not modelled	96.6	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
73	<a href="#">c5oo9A</a>	Alignment	not modelled	96.5	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative cupin_2 domain-containing isomerase; <b>PDBTitle:</b> streptomyces pac13 (y55f) with uridine
74	<a href="#">c3s7eB</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> allergen <b>Chain:</b> B; <b>PDB Molecule:</b> allergen ara h 1, clone p41b; <b>PDBTitle:</b> crystal structure of ara h 1
75	<a href="#">c4b29A</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dimethylsulfoniopropionate lyase; <b>PDBTitle:</b> crystal structures of dmisp lyases rddddp and rnddddqi
76	<a href="#">d1uija1</a>	Alignment	not modelled	96.5	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
77	<a href="#">d1j3pa</a>	Alignment	not modelled	96.4	11	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Glucose-6-phosphate isomerase, GPI
78	<a href="#">c3bcwB</a>	Alignment	not modelled	96.3	11	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf861 family protein with a rmlc-

						like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
79	<a href="#">d1lr5a_</a>	Alignment	not modelled	96.3	9	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
80	<a href="#">c5cu1A_</a>	Alignment	not modelled	96.3	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dmsp lyase; <b>PDBTitle:</b> crystal structure of dmsp lyase dddq from ruegeria pomeroyi dss-3
81	<a href="#">c3h8uA_</a>	Alignment	not modelled	96.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein with double-stranded <b>PDBTitle:</b> 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
82	<a href="#">c5cadA_</a>	Alignment	not modelled	96.2	17	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> sm80.1 vicilin; <b>PDBTitle:</b> crystal structure of the vicilin from solanum melongena revealed2 existence of different anionic ligands in structurally similar3 pockets
83	<a href="#">c5yjsB_</a>	Alignment	not modelled	96.1	13	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> vicilin-like antimicrobial peptides 2-2; <b>PDBTitle:</b> structure of vicilin from capsicum annuum
84	<a href="#">c5onoA_</a>	Alignment	not modelled	96.1	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-ectoine synthase; <b>PDBTitle:</b> crystal structure of ectoine synthase from p. lautus
85	<a href="#">d1x82a_</a>	Alignment	not modelled	96.1	8	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Glucose-6-phosphate isomerase, GPI
86	<a href="#">c2i45C_</a>	Alignment	not modelled	96.1	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of protein nmb1881 from neisseria meningitidis
87	<a href="#">c2fqpD_</a>	Alignment	not modelled	96.1	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein bp2299; <b>PDBTitle:</b> crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
88	<a href="#">c3ht2A_</a>	Alignment	not modelled	95.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> remf protein; <b>PDBTitle:</b> zinc containing polyketide cyclase remf from streptomyces2 resistomycificus
89	<a href="#">c4bifC_</a>	Alignment	not modelled	95.9	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> biochemical and structural characterisation of a novel2 manganese-dependent hydroxynitrile lyase from bacteria
90	<a href="#">c2eaaB_</a>	Alignment	not modelled	95.9	14	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> 7s globulin-3; <b>PDBTitle:</b> crystal structure of adzuki bean 7s globulin-3
91	<a href="#">c2y0oA_</a>	Alignment	not modelled	95.9	31	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable d-lyxose ketol-isomerase; <b>PDBTitle:</b> the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
92	<a href="#">c1uijA_</a>	Alignment	not modelled	95.8	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta subunit of beta conglycinin; <b>PDBTitle:</b> crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
93	<a href="#">c2qnkA_</a>	Alignment	not modelled	95.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyanthranilate 3,4-dioxygenase; <b>PDBTitle:</b> crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
94	<a href="#">c5fjlk_</a>	Alignment	not modelled	95.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> quercetinase qued; <b>PDBTitle:</b> enzyme-substrate-dioxygen complex of ni-quercetinase
95	<a href="#">c3kglB_</a>	Alignment	not modelled	95.6	10	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> cruciferin; <b>PDBTitle:</b> crystal structure of procruciferin, 11s globulin from brassica napus
96	<a href="#">c5u57B_</a>	Alignment	not modelled	95.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> (s)-2-hydroxypropylphosphonic acid epoxidase; <b>PDBTitle:</b> psf4 in complex with fe2+ and (s)-2-hpp
97	<a href="#">c6b4sB_</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> allergen <b>Chain:</b> B: <b>PDB Molecule:</b> 11s globulin; <b>PDBTitle:</b> crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
98	<a href="#">d1fxza1</a>	Alignment	not modelled	95.6	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
99	<a href="#">c6nwoD_</a>	Alignment	not modelled	95.5	11	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator bgar; <b>PDBTitle:</b> structures of the transcriptional regulator bgar, a lactose sensor.
100	<a href="#">c3kscD_</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> plant protein <b>Chain:</b> D: <b>PDB Molecule:</b> lega class; <b>PDBTitle:</b> crystal structure of pea prolegumin, an 11s seed globulin from pisum2 sativum l.
101	<a href="#">c5u9eB_</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional activator rhar; <b>PDBTitle:</b> structure of the regulatory domain of the arac family transcriptional2 activator rhar
102	<a href="#">c2ozia_</a>	Alignment	not modelled	95.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rpa4178; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
103	<a href="#">d1o5ua_</a>	Alignment	not modelled	95.4	10	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Hypothetical protein TM1112

104	<a href="#">d1zvfa1</a>	Alignment	not modelled	95.4	8	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like
105	<a href="#">d1fxza2</a>	Alignment	not modelled	95.4	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
106	<a href="#">c1fxzC_</a>	Alignment	not modelled	95.4	16	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycinin g1; <b>PDBTitle:</b> crystal structure of soybean proglycinin a1ab1b homotrimer
107	<a href="#">d2phla1</a>	Alignment	not modelled	95.4	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
108	<a href="#">d1od5a2</a>	Alignment	not modelled	94.9	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
109	<a href="#">c2d5fB_</a>	Alignment	not modelled	94.9	11	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycinin a3b4 subunit; <b>PDBTitle:</b> crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
110	<a href="#">c2phlC_</a>	Alignment	not modelled	94.9	11	<b>PDB header:</b> plant seed storage protein(vicilin) <b>Chain:</b> C: <b>PDB Molecule:</b> phaseolin; <b>PDBTitle:</b> 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
111	<a href="#">d2arca_</a>	Alignment	not modelled	94.8	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Regulatory protein AraC <b>Family:</b> Regulatory protein AraC
112	<a href="#">c3es4B_</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein duf861 with a rmlc-like cupin fold; <b>PDBTitle:</b> crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
113	<a href="#">c6b9rD_</a>	Alignment	not modelled	94.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> hydroxyethylphosphonate dioxygenase; <b>PDBTitle:</b> streptomyces albus hep3 with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
114	<a href="#">c2qdrA_</a>	Alignment	not modelled	94.6	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative dioxygenase (npun_f5605) from nostoc2 punctiforme pcc 73102 at 2.60 a resolution
115	<a href="#">c1cauB_</a>	Alignment	not modelled	94.5	24	<b>PDB header:</b> seed storage protein <b>Chain:</b> B: <b>PDB Molecule:</b> canavalin; <b>PDBTitle:</b> determination of three crystal structures of canavalin by molecular2 replacement
116	<a href="#">d1yfua1</a>	Alignment	not modelled	94.5	9	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like
117	<a href="#">c5nlaA_</a>	Alignment	not modelled	94.2	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator transcription regulator <b>PDBTitle:</b> crystal structure of the arac-like transcriptional activator cuxr
118	<a href="#">c4qglA_</a>	Alignment	not modelled	94.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acireductone dioxygenase; <b>PDBTitle:</b> acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
119	<a href="#">d1uija2</a>	Alignment	not modelled	94.1	19	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
120	<a href="#">c2bnoA_</a>	Alignment	not modelled	93.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.