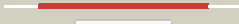



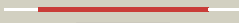



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3465_(rmlC)_3883013_3883621
Date	Fri Aug 9 18:20:14 BST 2019
Unique Job ID	b57e85536dd68100

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ixca1	Alignment 		100.0	100	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
2	c1upiA_	Alignment 		100.0	99	PDB header: epimerase Chain: A: PDB Molecule: dtdp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: mycobacterium tuberculosis rmlc epimerase (rv3465)
3	d1oi6a_	Alignment 		100.0	40	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
4	d2c0za1	Alignment 		100.0	49	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
5	c2c0zA_	Alignment 		100.0	49	PDB header: isomerase Chain: A: PDB Molecule: novw; PDBTitle: the 1.6 a resolution crystal structure of novw: a 4-keto-6-2 deoxy sugar epimerase from the novobiocin biosynthetic3 gene cluster of streptomyces spheroides
6	c4hmzD_	Alignment 		100.0	45	PDB header: unknown function Chain: D: PDB Molecule: putative 3-epimerase in d-allose pathway; PDBTitle: crystal structure of chmj, a 3'-monoepimerase from streptomyces2 bikiniensis in complex with dtdp-quinovose
7	c6ndrA_	Alignment 		100.0	40	PDB header: sugar binding protein Chain: A: PDB Molecule: dtdp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: crystal structure of dtdp-6-deoxy-d-glucose-3,5-epimerase rmlc from2 legionella pneumophila philadelphia 1 in complex with dtdp-4-keto-l-3 rhamnose
8	d1dzra_	Alignment 		100.0	38	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
9	c6c46E_	Alignment 		100.0	37	PDB header: isomerase Chain: E: PDB Molecule: dtdp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: crystal structure of dtdp-4-dehydrorhamnose 3,5-epimerase from2 elizabethkingia anophelis nuhp1
10	d2ixha1	Alignment 		100.0	40	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
11	d1ep0a_	Alignment 		100.0	37	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase

12	c3rykB_	Alignment		100.0	35	PDB header: isomerase Chain: B: PDB Molecule: dtdp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: 1.63 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 3,5-epimerase (rfbc) from bacillus anthracis str. ames with tdp and3 ppi bound
13	c5buvc_	Alignment		100.0	34	PDB header: isomerase Chain: C: PDB Molecule: putative epimerase; PDBTitle: x-ray structure of wbca from yersinia enterocolitica
14	d1wlta1	Alignment		100.0	34	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: dTDP-sugar isomerase
15	d1nxma_	Alignment		100.0	28	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: dTDP-sugar isomerase
16	c3ejkA_	Alignment		100.0	19	PDB header: isomerase Chain: A: PDB Molecule: dtdp sugar isomerase; PDBTitle: crystal structure of dtdp sugar isomerase (yp_390184.1) from2 desulfovibrio desulfuricans g20 at 1.95 a resolution
17	c5tpuB_	Alignment		100.0	13	PDB header: isomerase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: x-ray structure of the wlarb tdp-quinovose 3,4-ketoisomerase from2 campylobacter jejuni
18	c2zklA_	Alignment		100.0	20	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
19	c4o9gA_	Alignment		100.0	14	PDB header: isomerase Chain: A: PDB Molecule: qdtoa; PDBTitle: crystal structure of the h51n mutant of the 3,4-ketoisomerase qdtoa2 from thermoanaerobacterium thermosaccharolyticum in complex with tdp-3 4-keto-6-deoxyglucose
20	d2pa7a1	Alignment		99.9	20	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: dTDP-sugar isomerase
21	c5tpvB_	Alignment	not modelled	99.9	9	PDB header: isomerase Chain: B: PDB Molecule: wlara, tdp-fucose-3,4-ketoisomerase; PDBTitle: x-ray structure of wlara (tdp-fucose-3,4-ketoisomerase) from2 campylobacter jejuni
22	c4mzuG_	Alignment	not modelled	99.4	18	PDB header: isomerase, transferase Chain: G: PDB Molecule: wxcm-like protein; PDBTitle: crystal structure of fdtd, a bifunctional ketoisomerase/n-2 acetyltransferase from shewanella denitrificans
23	c2vqaC_	Alignment	not modelled	97.8	14	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.
24	d1j58a_	Alignment	not modelled	97.8	22	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
25	d2phla2	Alignment	not modelled	97.4	11	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
26	d1juha_	Alignment	not modelled	97.3	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Quercetin 2,3-dioxygenase-like
27	d1uija2	Alignment	not modelled	97.3	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
28	c1cauB_	Alignment	not modelled	97.3	14	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
29	c2o8qA_	Alignment	not modelled	97.2	24	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
30	c5f1jK_	Alignment	not modelled	97.2	18	PDB header: oxidoreductase Chain: K: PDB Molecule: quercetinase qucd; PDBTitle: enzyme-substrate-dioxygen complex of ni-quercetinase
31	c4leja_	Alignment	not modelled	97.2	10	PDB header: allergen, plant protein Chain: A: PDB Molecule: vicilin; PDBTitle: crystal structure of the korean pine (pinus koraiensis) vicilin
32	c3kgjB_	Alignment	not modelled	97.2	11	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from brassica napus
33	d1x82a_	Alignment	not modelled	97.1	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Glucose-6-phosphate isomerase, GPI
34	c2d5fB_	Alignment	not modelled	97.1	11	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
35	d1uika2	Alignment	not modelled	97.1	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
36	d2et1a1	Alignment	not modelled	97.0	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
37	c5cadA_	Alignment	not modelled	97.0	13	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
38	c1fxzC_	Alignment	not modelled	97.0	16	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
39	d1y3ta1	Alignment	not modelled	97.0	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Quercetin 2,3-dioxygenase-like
40	c3c3vA_	Alignment	not modelled	96.9	16	PDB header: allergen Chain: A: PDB Molecule: arachin arah3 isoform; PDBTitle: crystal structure of peanut major allergen ara h 3
41	c5yjsB_	Alignment	not modelled	96.9	15	PDB header: plant protein Chain: B: PDB Molecule: vicilin-like antimicrobial peptides 2-2; PDBTitle: structure of vicilin from capsicum annuum
42	d1fxza2	Alignment	not modelled	96.9	15	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
43	c3ehkC_	Alignment	not modelled	96.9	12	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
44	c6b4sB_	Alignment	not modelled	96.8	11	PDB header: allergen Chain: B: PDB Molecule: 11s globulin; PDBTitle: crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
45	c5wxuD_	Alignment	not modelled	96.8	9	PDB header: plant protein Chain: D: PDB Molecule: 11s globulin; PDBTitle: 11s globulin from wrightia tinctoria reveals auxin binding site
46	d1j3pa_	Alignment	not modelled	96.7	15	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Glucose-6-phosphate isomerase, GPI
47	d1od5a2	Alignment	not modelled	96.7	9	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
48	c3kscD_	Alignment	not modelled	96.6	13	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin from pisum2 sativum l.
49	c2gu9B_	Alignment	not modelled	96.6	16	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
50	c2oa2A_	Alignment	not modelled	96.6	17	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
51	c5fpzA_	Alignment	not modelled	96.6	21	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.
52	c2phlC_	Alignment	not modelled	96.5	12	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
53	c3qacA_	Alignment	not modelled	96.5	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.
54	c5e1rC_	Alignment	not modelled	96.4	17	PDB header: allergen Chain: C: PDB Molecule: 7s vicilin; PDBTitle: crystal structure of pecan (carya illinoensis) vicilin, a

						new food2 allergen
55	c5wpwA_	Alignment	not modelled	96.4	12	PDB header: allergen Chain: A: PDB Molecule: 11s globulin isoform 1; PDBTitle: crystal structure of coconut allergen cocosin
56	c4nubA_	Alignment	not modelled	96.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 50s ribosomal protein l16 arginine hydroxylase; PDBTitle: crystal structure of escherichia coli ribosomal oxygenase ycfD
57	c3s7eB_	Alignment	not modelled	96.4	15	PDB header: allergen Chain: B: PDB Molecule: allergen ara h 1, clone p41b; PDBTitle: crystal structure of ara h 1
58	c1uijA_	Alignment	not modelled	96.3	16	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)
59	c2e9qA_	Alignment	not modelled	96.3	8	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin subunit beta; PDBTitle: recombinant pro-11s globulin of pumpkin
60	d1v70a_	Alignment	not modelled	96.2	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
61	c1uijF_	Alignment	not modelled	96.2	17	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)
62	c2eaaB_	Alignment	not modelled	96.0	15	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
63	c4e2gE_	Alignment	not modelled	95.9	13	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>
64	c5tg0A_	Alignment	not modelled	95.7	15	PDB header: lyase Chain: A: PDB Molecule: dimethylsulfoniopropionate lyase dddk; PDBTitle: crystal structure of the dimethylsulfoniopropionate (dmsp) lyase dddk2 complexed with iron and zinc
65	d1zvfa1	Alignment	not modelled	95.7	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
66	c5fq0A_	Alignment	not modelled	95.7	18	PDB header: lyase Chain: A: PDB Molecule: kdgf; PDBTitle: the structure of kdgf from <i>halomonas</i> sp.
67	c2q30C_	Alignment	not modelled	95.7	13	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 a resolution
68	c3uyjA_	Alignment	not modelled	95.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 8; PDBTitle: crystal structure of jmjd5 catalytic core domain in complex with 2 nickel and alpha-kg
69	c2i45C_	Alignment	not modelled	95.4	21	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from <i>neisseria meningitidis</i>
70	c3h8uA_	Alignment	not modelled	95.4	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 <i>klebsiella3 pneumoniae</i> subsp. <i>pneumoniae</i> mgh 78578 at 1.80 a resolution
71	c4b29A_	Alignment	not modelled	95.1	19	PDB header: hydrolase Chain: A: PDB Molecule: dimethylsulfoniopropionate lyase; PDBTitle: crystal structures of dmsp lyases rddddp and rndddqii
72	d1yfua1	Alignment	not modelled	95.1	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
73	c3jzvA_	Alignment	not modelled	95.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rru_a2000; PDBTitle: crystal structure of rru_a2000 from <i>rhodospirillum rubrum</i> : a cupin-22 domain.
74	c2pfwB_	Alignment	not modelled	95.0	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 <i>shewanella2 frigidimarina</i> ncimb 400 at 1.90 a resolution
75	c3al6A_	Alignment	not modelled	94.9	13	PDB header: unknown function Chain: A: PDB Molecule: jmjc domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5
76	c5j7mB_	Alignment	not modelled	94.8	13	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
77	c4qglA_	Alignment	not modelled	94.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: acireductone dioxygenase; PDBTitle: acireductone dioxygenase from <i>bacillus anthracis</i> with three cadmium2 ions
78	d1fxza1	Alignment	not modelled	94.7	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
79	d1lr5a_	Alignment	not modelled	94.7	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
						Fold: Double-stranded beta-helix

80	d1yhfa1	Alignment	not modelled	94.6	22	Superfamily: RmIC-like cupins Family: TM1287-like
81	d2b8ma1	Alignment	not modelled	94.4	15	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: MJ0764-like
82	d2f4pa1	Alignment	not modelled	94.3	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
83	d1o4ta	Alignment	not modelled	94.2	13	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
84	c4cswA	Alignment	not modelled	94.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cupin 4 family protein; PDBTitle: rhodothermus marinus ycf-d-like ribosomal protein I16 arginyl2 hydroxylase
85	c2y0oA	Alignment	not modelled	94.1	18	PDB header: isomerase Chain: A: PDB Molecule: probable d-lyxose ketol-isomerase; PDBTitle: the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
86	c2ozjB	Alignment	not modelled	94.1	10	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
87	c6b8wB	Alignment	not modelled	94.0	10	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.
88	c2cauA	Alignment	not modelled	94.0	15	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
89	d1dgwa	Alignment	not modelled	93.9	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
90	c3fjsC	Alignment	not modelled	93.9	26	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
91	c5j4fB	Alignment	not modelled	93.8	18	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
92	c2d40C	Alignment	not modelled	93.8	15	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
93	c2xlfA	Alignment	not modelled	93.7	16	PDB header: metal binding protein Chain: A: PDB Molecule: sl1785 protein; PDBTitle: structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
94	c3ibmB	Alignment	not modelled	93.7	21	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
95	c3d82A	Alignment	not modelled	93.6	13	PDB header: metal binding protein Chain: A: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
96	d1uija1	Alignment	not modelled	93.5	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
97	d1rc6a	Alignment	not modelled	93.4	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
98	d1od5a1	Alignment	not modelled	93.2	13	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
99	c5oo9A	Alignment	not modelled	93.2	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative cupin_2 domain-containing isomerase; PDBTitle: streptomyces pac13 (y55f) with uridine
100	c5zbfA	Alignment	not modelled	93.1	10	PDB header: isomerase Chain: A: PDB Molecule: cupin domain protein; PDBTitle: crystal structure of 4-hydroxyphenylpyruvic acid bound aere from2 microcystis aeruginosa
101	d1y9qa2	Alignment	not modelled	93.0	13	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
102	c3k3nA	Alignment	not modelled	92.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: phd finger protein 8; PDBTitle: crystal structure of the catalytic core domain of human phf8
103	c3kgzA	Alignment	not modelled	92.7	14	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
104	d2d40a1	Alignment	not modelled	92.6	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Gentisate 1,2-dioxygenase-like
105	c3al6C	Alignment	not modelled	92.6	15	PDB header: unknown function Chain: C: PDB Molecule: jmjc domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5

106	c2eceA_	Alignment	not modelled	92.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 462aa long hypothetical selenium-binding protein; PDBTitle: x-ray structure of hypothetical selenium-binding protein2 from <i>sulfolobus tokodaii</i> , st0059
107	c3i7dB_	Alignment	not modelled	92.2	15	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 a resolution
108	c3rnsA_	Alignment	not modelled	92.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: cupin 2 conserved barrel domain protein from <i>leptotrichia buccalis</i>
109	d1vj2a_	Alignment	not modelled	92.1	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1459-like
110	c4rd7A_	Alignment	not modelled	92.0	20	PDB header: unknown function Chain: A: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: the crystal structure of a cupin 2 conserved barrel domain protein2 from <i>salinispora arenicola</i> cns-205
111	d1sq4a_	Alignment	not modelled	91.9	12	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
112	d1sfna_	Alignment	not modelled	91.8	13	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
113	c3cewA_	Alignment	not modelled	91.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized cupin protein; PDBTitle: crystal structure of a cupin protein (bf4112) from <i>bacteroides2 fragilis</i> . northeast structural genomics consortium target bfr205
114	c3k2oB_	Alignment	not modelled	91.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional arginine demethylase and lysyl-hydroxylase PDBTitle: structure of an oxygenase
115	d1uika1	Alignment	not modelled	91.4	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
116	c4h7lB_	Alignment	not modelled	91.4	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of plim_4148 protein from <i>planctomyces limnophilus</i>
117	c4bifC_	Alignment	not modelled	91.2	9	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
118	d1vrba1	Alignment	not modelled	90.9	16	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Asparaginyl hydroxylase-like
119	c5onoA_	Alignment	not modelled	90.7	15	PDB header: metal binding protein Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of ectoine synthase from <i>p. lautus</i>
120	c3ht2A_	Alignment	not modelled	90.5	18	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from <i>streptomyces2 resistomyficifus</i>