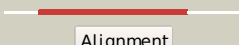

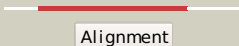

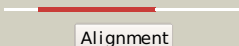

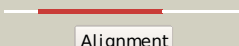



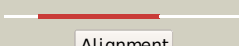

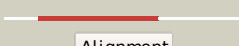









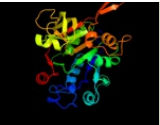


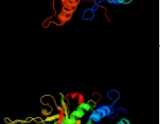






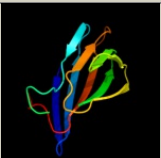
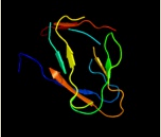


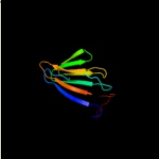


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2x5sB_	 Alignment		100.0	40	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
2	c2cu2A_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: putative mannose-1-phosphate guanylyl transferase; PDBTitle: crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
3	c2qh5B_	 Alignment		100.0	36	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
4	d2cu2a2	 Alignment		100.0	38	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
5	c2pa4B_	 Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
6	d1mc3a_	 Alignment		100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
7	d1h5ra_	 Alignment		100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
8	d1fxoa_	 Alignment		100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
9	d1lvwa_	 Alignment		100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
10	c2e3dB_	 Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
11	d1iina_	 Alignment		100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase

12	c2ux8G	Alignment		100.0	17	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
13	c1yp3C	Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenyllyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
14	d1yp2a2	Alignment		100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyllyltransferase
15	c1hm8A	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridylyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
16	c3brkX	Alignment		100.0	18	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyllyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
17	c3d98A	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
18	c3pnnA	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
19	c3jukA	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
20	c2qkxA	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridylyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
21	c2v0hA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridylyltransferase (glmu)
22	c1fwyA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcnac
23	c3hl3A	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyllyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidyllyltransferase from bacillus anthracis in complex with a3 sucrose.
24	c2oi6A	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
25	d1g97a2	Alignment	not modelled	100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
26	d2oi6a2	Alignment	not modelled	100.0	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
27	c2ggqA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyllyltransferase from2 sulfolobus tokodaii
						Fold: Nucleotide-diphospho-sugar transferases

28	d1tzfa_	Alignment	not modelled	99.9	18	Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
29	d1jyka_	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
30	c1jylC_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidylyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (licc)
31	d1vica_	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
32	c3oamD_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: crystal structure of cytidylyltransferase from vibrio cholerae
33	c2xmhB_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidylyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate2 cytidylyltransferase from archaeoglobus fulgidus
34	c2xwlB_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
35	c3polA_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidylyltransferase (kdsb) from acinetobacter baumannii.
36	d1vpaa_	Alignment	not modelled	99.8	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
37	d1h7ea_	Alignment	not modelled	99.8	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
38	d2cu2a1	Alignment	not modelled	99.8	34	Fold: Single-stranded left-handed beta-helix Superfamily: Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain Family: Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain
39	d1eyra_	Alignment	not modelled	99.7	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
40	d1i52a_	Alignment	not modelled	99.7	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
41	c2y6pC_	Alignment	not modelled	99.7	16	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the2 kdo-cytidylyltransferase kdsb
42	c3tqdA_	Alignment	not modelled	99.7	17	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidylyltransferase2 (kdsb) from coxiella burnetii
43	c2fqpD_	Alignment		99.7	19	PDB header: metal binding protein Chain: D: PDB Molecule: hypothetical protein bp2299; PDBTitle: crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohamia i at 1.80 a resolution
44	d1w55a1	Alignment	not modelled	99.7	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
45	d1vh1a_	Alignment	not modelled	99.7	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
46	c2gu9B_	Alignment		99.7	22	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	c3i7dB_	Alignment		99.7	19	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

48	c2oa2A	Alignment		99.7	24	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
49	c3f1cB	Alignment	not modelled	99.6	13	PDB header: transferase Chain: B: PDB Molecule: putative 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from listeria monocytogenes
50	c2wawA	Alignment	not modelled	99.6	21	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
51	d1qwja	Alignment	not modelled	99.6	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
52	d1w77a1	Alignment	not modelled	99.6	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
53	d1vh3a	Alignment	not modelled	99.6	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
54	c3h8uA	Alignment		99.6	19	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
55	c3cewA	Alignment		99.6	20	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
56	c3d82A	Alignment	not modelled	99.6	20	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
57	c2we9A	Alignment	not modelled	99.6	16	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
58	d2dpwa1	Alignment	not modelled	99.6	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
59	c2o8qA	Alignment	not modelled	99.6	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 (bx_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
60	c3jzvA	Alignment	not modelled	99.5	16	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.
61	d1vgwa	Alignment	not modelled	99.5	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
62	c3l2hD	Alignment	not modelled	99.5	21	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
63	d1e5ka	Alignment	not modelled	99.5	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
64	d1v70a	Alignment	not modelled	99.5	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
65	d1x82a	Alignment	not modelled	99.5	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
66	d2b8ma1	Alignment	not modelled	99.5	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
67	c2oziA	Alignment	not modelled	99.5	16	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
68	c3rsbB	Alignment	not modelled	99.5	16	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
69	c3ibmB	Alignment	not modelled	99.4	28	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
70	c2e8bA_	Alignment	not modelled	99.4	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of the putative protein (aq1419) from aquifex2 aeolicus vf5
71	c2vshB_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
72	c3kgzA_	Alignment	not modelled	99.4	16	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
73	c2vpvA_	Alignment	not modelled	99.4	13	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
74	c3okrA_	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
75	c1w57A_	Alignment	not modelled	99.4	13	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
76	d1lr5a_	Alignment	not modelled	99.4	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
77	d1o4ta_	Alignment	not modelled	99.4	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
78	d1j3pa_	Alignment	not modelled	99.4	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
79	c2i45C_	Alignment	not modelled	99.4	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
80	c3ngwA_	Alignment	not modelled	99.4	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein a PDBTitle: crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189
81	d1y9qa2	Alignment	not modelled	99.4	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
82	c2px7A_	Alignment	not modelled	99.3	19	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
83	d1vj2a_	Alignment	not modelled	99.3	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
84	d1rc6a_	Alignment	not modelled	99.3	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
85	c3fjsC_	Alignment	not modelled	99.2	16	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
86	c3ht2A_	Alignment	not modelled	99.2	20	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
87	c2ozjB_	Alignment	not modelled	99.2	19	PDB header: unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel; PDBTitle: crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
88	c1sefA_	Alignment	not modelled	99.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
89	d1sefa_	Alignment	not modelled	99.2	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
90	d1sfna_	Alignment	not modelled	99.2	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
91	c3rnsA_	Alignment	not modelled	99.2	15	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
92	c2pfwB_	Alignment	not modelled	99.2	26	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
93	d2f4pa1	Alignment	not modelled	99.2	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
						PDB header: unknown function

94	c2q30C	Alignment	not modelled	99.1	15	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
95	d1sq4a	Alignment	not modelled	99.1	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
96	d1yhfa1	Alignment	not modelled	99.1	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
97	d1y3ta1	Alignment	not modelled	99.1	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
98	c2vqaC	Alignment	not modelled	99.1	24	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.
99	d2icya2	Alignment	not modelled	99.0	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
100	c3lwcA	Alignment	not modelled	99.0	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
101	c3h7yA	Alignment	not modelled	99.0	16	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
102	c3okrC	Alignment	not modelled	99.0	17	PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
103	d1j58a	Alignment	not modelled	98.9	25	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
104	c2y0oA	Alignment	not modelled	98.9	23	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
105	c2d40C	Alignment	not modelled	98.8	24	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
106	c3d5nB	Alignment	not modelled	98.8	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from2 sulfobolus solfataricus. nesg target ssr125.
107	d2et1a1	Alignment	not modelled	98.8	25	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
108	d1vm8a	Alignment	not modelled	98.8	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
109	c2i5kB	Alignment	not modelled	98.8	10	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of ugp1p
110	d2d40a1	Alignment	not modelled	98.8	27	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
111	d1dgwa	Alignment	not modelled	98.8	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
112	c2zklA	Alignment	not modelled	98.7	27	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
113	c2q4iB	Alignment	not modelled	98.7	13	PDB header: transferase Chain: B: PDB Molecule: probable utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
114	d1uika1	Alignment	not modelled	98.7	27	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
115	d1juha	Alignment	not modelled	98.7	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
116	d2phda1	Alignment	not modelled	98.7	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
117	d1fxza1	Alignment	not modelled	98.6	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
118	c3ogzA	Alignment	not modelled	98.6	19	PDB header: transferase Chain: A: PDB Molecule: udp-sugar pyrophosphorylase; PDBTitle: protein structure of usp from l. major in apo-form
119	c3mpbA	Alignment	not modelled	98.6	25	PDB header: isomerase Chain: A: PDB Molecule: sugar isomerase; PDBTitle: z5688 from e. coli o157:h7 bound to fructose

120	c3gueB	<div><div></div><div>Alignment</div></div>	not modelled	98.6	13	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
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