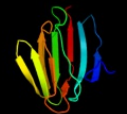


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y9qa_	 Alignment		100.0	39	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
2	c2bnoA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
3	d1y9qa2	 Alignment		99.8	34	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
4	c3ivpD_	 Alignment		99.7	23	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
5	c2ewtA_	 Alignment		99.7	29	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
6	c3op9A_	 Alignment		99.7	18	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
7	d1y9qa1	 Alignment		99.7	54	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
8	c3clcC_	 Alignment		99.7	27	PDB header: transcription regulator/dna binding protein Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
9	d1y7ya1	 Alignment		99.7	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
10	c2kpiA_	 Alignment		99.7	15	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
11	d2b5aa1	 Alignment		99.7	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like

12	c3f52A_	Alignment		99.7	27	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
13	d2bnma2	Alignment		99.7	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
14	c3b7hA_	Alignment		99.7	23	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
15	c1b0nA_	Alignment		99.7	35	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
16	c3lisB_	Alignment		99.7	26	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
17	c3f6wE_	Alignment		99.7	19	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
18	c3mlfC_	Alignment		99.6	21	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
19	d2ofya1	Alignment		99.6	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
20	d1rioA_	Alignment		99.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
21	d2r1j11	Alignment	not modelled	99.6	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
22	c2gu9B_	Alignment	not modelled	99.6	20	PDB header: immune system Chain: B: PDB Molecule: tetracenomycin polyketide synthesis protein; PDBTitle: crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
23	d1adra_	Alignment	not modelled	99.6	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
24	c2o38A_	Alignment	not modelled	99.6	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
25	d2o38a1	Alignment	not modelled	99.6	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
26	c3i7dB_	Alignment	not modelled	99.6	18	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
27	d1b0na2	Alignment	not modelled	99.6	36	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
28	c3hc3A_	Alignment	not modelled	99.6	28	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein;

28	c3us3A	Alignment	not modelled	99.6	28	PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
29	d1x57a1	Alignment	not modelled	99.6	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
30	d1sq4a	Alignment	not modelled	99.6	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
31	c3omtA	Alignment	not modelled	99.6	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
32	c3kxaD	Alignment	not modelled	99.6	27	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
33	d1rc6a	Alignment	not modelled	99.6	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
34	c2jvlA	Alignment	not modelled	99.6	20	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
35	d1r69a	Alignment	not modelled	99.6	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
36	d1sq8a	Alignment	not modelled	99.6	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
37	d2icta1	Alignment	not modelled	99.6	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
38	d2croa	Alignment	not modelled	99.6	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
39	d1utxa	Alignment	not modelled	99.6	31	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
40	c3eusB	Alignment	not modelled	99.6	18	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
41	d1lmb3	Alignment	not modelled	99.6	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
42	c3bdnB	Alignment	not modelled	99.6	13	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
43	d1llib	Alignment	not modelled	99.5	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
44	c1sefA	Alignment	not modelled	99.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
45	d1sefa	Alignment	not modelled	99.5	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
46	c2ebyA	Alignment	not modelled	99.5	14	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
47	c3dnnB	Alignment	not modelled	99.5	32	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
48	c2xcjB	Alignment	not modelled	99.5	20	PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
49	c3l2hd	Alignment	not modelled	99.5	19	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
50	c3pxpA	Alignment	not modelled	99.5	23	PDB header: transcription regulator Chain: A: PDB Molecule: helix-turn-helix domain protein; PDBTitle: crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
51	d2a6ca1	Alignment	not modelled	99.5	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
52	c3cecA	Alignment	not modelled	99.5	15	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
53	c2vpvA	Alignment	not modelled	99.5	10	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
						PDB header: transcription regulator

54	c2ef8A_	Alignment	not modelled	99.5	23	Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
55	d1vj2a_	Alignment	not modelled	99.5	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
56	c3t76A_	Alignment	not modelled	99.5	29	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
57	c3cewA_	Alignment	not modelled	99.5	19	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
58	c3trbA_	Alignment	not modelled	99.5	17	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
59	c3h7yA_	Alignment	not modelled	99.5	13	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
60	c2axzC_	Alignment	not modelled	99.5	25	PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
61	c3jzvA_	Alignment	not modelled	99.5	17	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.
62	d1sfna_	Alignment	not modelled	99.5	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
63	d1o4ta_	Alignment	not modelled	99.5	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
64	c3ht2A_	Alignment	not modelled	99.4	16	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
65	c2qfcB_	Alignment	not modelled	99.4	27	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
66	c2oa2A_	Alignment	not modelled	99.4	14	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
67	c3fjsC_	Alignment	not modelled	99.4	14	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
68	c3kgzA_	Alignment	not modelled	99.4	20	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
69	d1v70a_	Alignment	not modelled	99.4	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
70	c3ibmB_	Alignment	not modelled	99.4	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
71	c3fymA_	Alignment	not modelled	99.4	29	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of ymfM, a putative dna-binding membrane2 protein from staphylococcus aureus
72	c2wusR_	Alignment	not modelled	99.4	18	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape2 protein rodz
73	d1lr5a_	Alignment	not modelled	99.4	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
74	c2pfwB_	Alignment	not modelled	99.4	18	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
75	c3h8uA_	Alignment	not modelled	99.4	18	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
76	c2fjrB_	Alignment	not modelled	99.4	7	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
77	d1y3ta1	Alignment	not modelled	99.3	23	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
78	d2b8ma1	Alignment	not modelled	99.3	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like

79	d2f4pa1	Alignment	not modelled	99.3	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
80	d1juha	Alignment	not modelled	99.3	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
81	c3es1A	Alignment	not modelled	99.2	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
82	c2q30C	Alignment	not modelled	99.2	15	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
83	c2ppxA	Alignment	not modelled	99.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
84	d2ppxa1	Alignment	not modelled	99.2	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
85	c3fmyA	Alignment	not modelled	99.1	11	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
86	d1yhfa1	Alignment	not modelled	99.1	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
87	c2d40C	Alignment	not modelled	99.1	18	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
88	c2ozjB	Alignment	not modelled	99.1	14	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
89	c3rnsA	Alignment	not modelled	99.1	22	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
90	c2o8qA	Alignment	not modelled	99.1	14	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
91	c2fqpD	Alignment	not modelled	99.1	16	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
92	d3bu7a1	Alignment	not modelled	99.0	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
93	c3bu7A	Alignment	not modelled	99.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: gentisate 1,2-dioxygenase; PDBTitle: crystal structure and biochemical characterization of gdosp_2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi
94	d2d40a1	Alignment	not modelled	99.0	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
95	d1j3pa	Alignment	not modelled	99.0	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
96	c2oziA	Alignment	not modelled	99.0	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
97	c2vqaC	Alignment	not modelled	99.0	15	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.
98	d2phda1	Alignment	not modelled	99.0	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
99	c3gn5B	Alignment	not modelled	98.9	10	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
100	c3lwcA	Alignment	not modelled	98.9	22	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	d1x82a	Alignment	not modelled	98.9	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
102	d2et1a1	Alignment	not modelled	98.9	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
103	c3d82A	Alignment	not modelled	98.9	23	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
104	d1j58a_	Alignment	not modelled	98.8	14 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
105	c2xlfA_	Alignment	not modelled	98.8	15 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)
106	d1yfua1	Alignment	not modelled	98.8	17 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
107	c2i45C_	Alignment	not modelled	98.8	20 PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
108	d1dgwa_	Alignment	not modelled	98.7	15 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
109	c3bcwB_	Alignment	not modelled	98.6	18 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
110	d1fxza1	Alignment	not modelled	98.6	9 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
111	d1uika1	Alignment	not modelled	98.6	18 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
112	c3eqeB_	Alignment	not modelled	98.6	18 PDB header: oxidoreductase Chain: B: PDB Molecule: putative cystein deoxygenase; PDBTitle: crystal structure of the yubc protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr112.
113	d1uija1	Alignment	not modelled	98.5	21 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
114	c1fxzC_	Alignment	not modelled	98.5	9 PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
115	c3r1fO_	Alignment	not modelled	98.5	19 PDB header: transcription Chain: O: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
116	c3kglB_	Alignment	not modelled	98.4	13 PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from2 brassica napus
117	c3kscD_	Alignment	not modelled	98.4	9 PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
118	d1fxza2	Alignment	not modelled	98.3	14 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
119	c2d5fB_	Alignment	not modelled	98.3	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
120	c2opkC_	Alignment	not modelled	98.3	14 PDB header: isomerase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution