
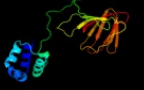





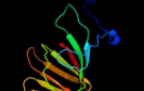













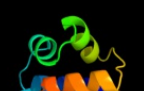


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q5H775
Date	Thu Jan 5 12:37:19 GMT 2012
Unique Job ID	197685525752e64a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bnoA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenisi.
2	c1y9qA_	 Alignment		100.0	18	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
3	c3ivpD_	 Alignment		99.7	22	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.
4	d2bnma2	 Alignment		99.7	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
5	c2kjpA_	 Alignment		99.7	14	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
6	c3op9A_	 Alignment		99.6	20	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
7	c2ewtA_	 Alignment		99.6	29	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
8	d1y9qa2	 Alignment		99.6	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
9	d1y7ya1	 Alignment		99.6	32	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
10	c3lisB_	 Alignment		99.6	24	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
11	c3clcC_	 Alignment		99.6	28	PDB header: transcription regulator/dna 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

12	c1b0nA_	Alignment		99.6	28	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
13	d1y9qa1	Alignment		99.6	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
14	d2b5aa1	Alignment		99.6	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
15	c3f52A_	Alignment		99.6	24	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
16	c3m1fC_	Alignment		99.6	25	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
17	d1x57a1	Alignment		99.6	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
18	c3b7hA_	Alignment		99.6	30	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
19	d1rioa_	Alignment		99.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
20	c3f6wE_	Alignment		99.6	20	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
21	d2r1j11	Alignment	not modelled	99.6	22	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	c3bdnB_	Alignment	not modelled	99.6	13	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
24	c3bs3A_	Alignment	not modelled	99.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
25	d1r69a_	Alignment	not modelled	99.6	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
26	d1ladra_	Alignment	not modelled	99.6	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
27	c3omtA_	Alignment	not modelled	99.6	15	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.
28	d2o38a1	Alignment	not modelled	99.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354

29	c2o38A	Alignment	not modelled	99.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
30	d2ofya1	Alignment	not modelled	99.5	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
31	d1b0na2	Alignment	not modelled	99.5	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
32	c2jvIA	Alignment	not modelled	99.5	19	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
33	c3kxaD	Alignment	not modelled	99.5	31	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
34	d1sq8a	Alignment	not modelled	99.5	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
35	d2croa	Alignment	not modelled	99.5	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
36	d2icta1	Alignment	not modelled	99.5	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
37	c3i7dB	Alignment	not modelled	99.5	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
38	c3h7yA	Alignment	not modelled	99.5	18	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
39	c2ebyA	Alignment	not modelled	99.5	20	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
40	d1lib	Alignment	not modelled	99.5	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
41	d1lmb3	Alignment	not modelled	99.5	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
42	d1utxa	Alignment	not modelled	99.5	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
43	d1sq4a	Alignment	not modelled	99.5	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
44	d1sefa	Alignment	not modelled	99.5	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
45	c1sefA	Alignment	not modelled	99.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
46	c2oa2A	Alignment	not modelled	99.5	20	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
47	c2ef8A	Alignment	not modelled	99.5	29	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
48	c3cecA	Alignment	not modelled	99.5	17	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
49	c2xcjB	Alignment	not modelled	99.5	17	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
50	d1sfna	Alignment	not modelled	99.5	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
51	c3eusB	Alignment	not modelled	99.5	19	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
52	d2a6ca1	Alignment	not modelled	99.5	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
53	c3pxpA	Alignment	not modelled	99.5	25	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
54	d1y3ta1	Alianment	not modelled	99.5	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins

					Family: Quercetin 2,3-dioxygenase-like
55	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
56	c3dnvB_	Alignment	not modelled	99.5	26 PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
57	d1vj2a_	Alignment	not modelled	99.5	16 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
58	d1rc6a_	Alignment	not modelled	99.5	14 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
59	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
60	d1o4ta_	Alignment	not modelled	99.5	24 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
61	c3trbA_	Alignment	not modelled	99.4	20 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
62	d1v70a_	Alignment	not modelled	99.4	20 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
63	c3h8uA_	Alignment	not modelled	99.4	22 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
64	c3jzvA_	Alignment	not modelled	99.4	13 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.
65	c3t76A_	Alignment	not modelled	99.4	8 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
66	c2vpvA_	Alignment	not modelled	99.4	9 PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
67	c2axzC_	Alignment	not modelled	99.4	22 PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
68	d1lr5a_	Alignment	not modelled	99.4	21 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
69	c3ht2A_	Alignment	not modelled	99.4	24 PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
70	c2fjrB_	Alignment	not modelled	99.4	11 PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
71	c3ibmB_	Alignment	not modelled	99.4	12 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
72	c3kgzA_	Alignment	not modelled	99.4	10 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	c2qfcB_	Alignment	not modelled	99.3	27 PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
74	c2wusR_	Alignment	not modelled	99.3	15 PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape2 protein rodz
75	d2b8ma1	Alignment	not modelled	99.3	13 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
76	d2f4pa1	Alignment	not modelled	99.3	17 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
77	c2pfwB_	Alignment	not modelled	99.3	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
78	d1juha_	Alignment	not modelled	99.3	12 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
79	c3fumA_	Alignment	not modelled	99.3	13 PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein;

79	c3ylnA	Alignment	not modelled	99.3	13	PDBTitle: the 1a structure of ymfM, a putative dna-binding membrane2 protein from staphylococcus aureus PDB header: metal binding protein
80	c2o8qA	Alignment	not modelled	99.3	18	Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a protein with a cupin-like fold and unknown2 function (bxe_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
81	c2vqaC	Alignment	not modelled	99.3	15	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.
82	c3fjsC	Alignment	not modelled	99.3	17	PDB header: biosynthetic protein Chain: C: PDB Molecule: uncharacterized protein with rmlc-like cupin fold; PDBTitle: crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
83	c2q30C	Alignment	not modelled	99.2	17	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
84	c2ppxA	Alignment	not modelled	99.2	18	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
85	d2ppxA1	Alignment	not modelled	99.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
86	d1j58a	Alignment	not modelled	99.1	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
87	c3fmyA	Alignment	not modelled	99.1	23	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)
88	c2fqpD	Alignment	not modelled	99.1	20	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
89	c3es1A	Alignment	not modelled	99.1	24	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
90	c2ozjB	Alignment	not modelled	99.1	16	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
91	c2d40C	Alignment	not modelled	99.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
92	c3rnsA	Alignment	not modelled	99.0	19	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
93	d1j3pa	Alignment	not modelled	99.0	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
94	c2oziA	Alignment	not modelled	99.0	22	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
95	d1yhfa1	Alignment	not modelled	99.0	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
96	c2xlfA	Alignment	not modelled	99.0	17	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)
97	d3bu7a1	Alignment	not modelled	99.0	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
98	c3bu7A	Alignment	not modelled	99.0	18	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
99	d1x82a	Alignment	not modelled	98.9	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
100	d2d40a1	Alignment	not modelled	98.9	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
101	d2et1a1	Alignment	not modelled	98.9	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
102	c3lwcA	Alignment	not modelled	98.9	15	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
103	d2phda1	Alignment	not modelled	98.9	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
						Fold: Double-stranded beta-helix

104	d1dgwa_	Alignment	not modelled	98.9	19	Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
105	c3d82A_	Alignment	not modelled	98.9	22	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
106	c3gn5B_	Alignment	not modelled	98.8	24	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)
107	d1yfua1	Alignment	not modelled	98.8	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
108	d1uika1	Alignment	not modelled	98.7	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
109	c2i45C_	Alignment	not modelled	98.7	12	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
110	d1uija1	Alignment	not modelled	98.6	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
111	d1fxza1	Alignment	not modelled	98.6	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
112	c1fxzC_	Alignment	not modelled	98.5	15	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
113	c3eqeB_	Alignment	not modelled	98.5	20	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.
114	c3bcwB_	Alignment	not modelled	98.5	16	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
115	c3kscD_	Alignment	not modelled	98.5	14	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
116	c3kglB_	Alignment	not modelled	98.5	13	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from2 brassica napus
117	d2phla2	Alignment	not modelled	98.4	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
118	c3qacA_	Alignment	not modelled	98.3	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.
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	d1fxza2	Alignment	not modelled	98.3	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein