


Phyre2

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Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yhfa1	 Alignment		99.8	27	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
2	c5j4fB_	 Alignment		99.8	24	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
3	c3fjsC_	 Alignment		99.8	19	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
4	c2ozjB_	 Alignment		99.8	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
5	c3rnsA_	 Alignment		99.8	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
6	c2q30C_	 Alignment		99.8	21	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
7	d1v70a_	 Alignment		99.8	24	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
8	c2pfwB_	 Alignment		99.7	20	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
9	c4e2gE_	 Alignment		99.7	26	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 sphaerobacter2 thermophilus
10	d2b8ma1	 Alignment		99.7	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: MJ0764-like
11	c3h8uA_	 Alignment		99.6	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 klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution

12	c3jzvA_	Alignment		99.6	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.
13	c2oa2A_	Alignment		99.6	18	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
14	c2gu9B_	Alignment		99.6	14	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
15	c5bxxA_	Alignment		99.6	18	PDB header: lyase Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of the ectoine synthase from the cold-adapted marine2 bacterium sphingopyxis alaskensis
16	c5fpzA_	Alignment		99.6	16	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.
17	c5fq0A_	Alignment		99.6	19	PDB header: lyase Chain: A: PDB Molecule: kdgf; PDBTitle: the structure of kdgf from halomonas sp.
18	d1vj2a_	Alignment		99.6	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1459-like
19	c5onoA_	Alignment		99.6	13	PDB header: metal binding protein Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of ectoine synthase from p. lautus
20	c3kgzA_	Alignment		99.6	15	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
21	c5j7mB_	Alignment	not modelled	99.5	15	PDB header: unknown function Chain: B: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 conserved barrel domain protein from2 kribbella flavida dsm 17836
22	d1sfna_	Alignment	not modelled	99.5	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
23	c5tg0A_	Alignment	not modelled	99.5	18	PDB header: lyase Chain: A: PDB Molecule: dimethylsulfoniopropionate lyase dddk; PDBTitle: crystal structure of the dimethylsulfoniopropionate (dmsp) lyase dddk2 complexed with iron and zinc
24	c4bifC_	Alignment	not modelled	99.5	17	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
25	c5zbfA_	Alignment	not modelled	99.5	13	PDB header: isomerase Chain: A: PDB Molecule: cupin domain protein; PDBTitle: crystal structure of 4-hydroxyphenylpyruvic acid bound aere from2 microcystis aeruginosa
26	d1sq4a_	Alignment	not modelled	99.5	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
27	c3h7yA_	Alignment	not modelled	99.5	11	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
28	d2f4pa1	Alignment	not modelled	99.5	23	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
						Fold: Double-stranded beta-helix

29	d1y9qa2	Alignment	not modelled	99.5	16	Superfamily: RmIC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
30	c3ibmB	Alignment	not modelled	99.5	14	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
31	c5uqpA	Alignment	not modelled	99.5	21	PDB header: unknown function Chain: A: PDB Molecule: cupin; PDBTitle: the crystal structure of cupin protein from rhodococcus jostii rha1
32	d1sefa	Alignment	not modelled	99.5	13	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
33	c1sefA	Alignment	not modelled	99.5	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
34	d1lr5a	Alignment	not modelled	99.5	19	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
35	c3cewA	Alignment	not modelled	99.5	21	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
36	c4e2sE	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: E: PDB Molecule: ureidoglycine aminohydrolase; PDBTitle: crystal structure of (s)-ureidoglycine aminohydrolase from arabidopsis2 thaliana in complex with its substrate, (s)-ureidoglycine
37	c3ht2A	Alignment	not modelled	99.4	16	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomyficus
38	d1o4ta	Alignment	not modelled	99.4	15	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
39	c4rd7A	Alignment	not modelled	99.4	18	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 salinispora arenicola cns-205
40	d1y3ta1	Alignment	not modelled	99.4	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Quercetin 2,3-dioxygenase-like
41	c3d82A	Alignment	not modelled	99.4	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
42	c4la3B	Alignment	not modelled	99.4	18	PDB header: lyase Chain: B: PDB Molecule: dimethylsulphoniopropionate (dmsp) lyase dddq; PDBTitle: crystal structure of dimethylsulphoniopropionate (dmsp) lyase dddq2_y131a in complex with dmsp
43	c6b8wB	Alignment	not modelled	99.4	11	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.
44	c4i4aA	Alignment	not modelled	99.4	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: similar to unknown protein; PDBTitle: crystal structure of plu4264 protein from photorhabdus luminescens
45	c4b29A	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: A: PDB Molecule: dimethylsulphoniopropionate lyase; PDBTitle: crystal structures of dmsp lyases rddddp and rndddqii
46	c5cu1A	Alignment	not modelled	99.4	21	PDB header: lyase Chain: A: PDB Molecule: dmsp lyase; PDBTitle: crystal structure of dmsp lyase dddq from ruegeria pomeroyi dss-3
47	d2phda1	Alignment	not modelled	99.4	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Gentisate 1,2-dioxygenase-like
48	d1rc6a	Alignment	not modelled	99.4	13	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
49	c2vpvA	Alignment	not modelled	99.4	17	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
50	c5fijk	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: K: PDB Molecule: quercetinase qued; PDBTitle: enzyme-substrate-dioxygen complex of ni-quercetinase
51	c3i7dB	Alignment	not modelled	99.4	20	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
52	c3lwcA	Alignment	not modelled	99.4	17	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
53	c2d40C	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7

54	c3l2hD	Alignment	not modelled	99.3	20	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
55	d2d40a1	Alignment	not modelled	99.3	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
56	c2i45C	Alignment	not modelled	99.3	20	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
57	c5oo9A	Alignment	not modelled	99.3	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative cupin_2 domain-containing isomerase; PDBTitle: streptomyces pac13 (y55f) with uridine
58	d1yfua1	Alignment	not modelled	99.3	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
59	c2fqpD	Alignment	not modelled	99.3	13	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
60	c4h7lB	Alignment	not modelled	99.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of plim_4148 protein from planctomyces limnophilus
61	c4p9gA	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4'-dihydroxyacetophenone dioxygenase; PDBTitle: structure of the 2,4'-dihydroxyacetophenone dioxygenase from2 alcaligenes sp.
62	d3bu7a1	Alignment	not modelled	99.3	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
63	c3bu7A	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: gentisate 1,2-dioxygenase; PDBTitle: crystal structure and biochemical characterization of gdosp, a2 gentisate 1,2-dioxygenase from silicibacter pomeroyi
64	c2oziA	Alignment	not modelled	99.3	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 rhodospseudomonas palustris cga009
65	d1zvfA1	Alignment	not modelled	99.2	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
66	d2bnma2	Alignment	not modelled	99.2	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
67	c2o8qA	Alignment	not modelled	99.2	20	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
68	c2vqaC	Alignment	not modelled	99.2	22	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.
69	c4axoA	Alignment	not modelled	99.2	7	PDB header: structural protein Chain: A: PDB Molecule: ethanolamine utilization protein; PDBTitle: structure of the clostridium difficile eutq protein
70	c4qglA	Alignment	not modelled	99.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: acireductone dioxygenase; PDBTitle: acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
71	d1j3pa	Alignment	not modelled	99.1	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
72	c5u57B	Alignment	not modelled	99.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
73	d1dgwa	Alignment	not modelled	99.1	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
74	c6b9rD	Alignment	not modelled	99.1	13	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
75	d1juha	Alignment	not modelled	99.1	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
76	d2et1a1	Alignment	not modelled	99.1	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
77	d1x82a	Alignment	not modelled	99.1	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
78	c1y9qA	Alignment	not modelled	99.1	15	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
79	d1uika1	Alignment	not modelled	99.0	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
						PDB header: unknown function

80	c3bcwB	Alignment	not modelled	99.0	13	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
81	d1j58a	Alignment	not modelled	99.0	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
82	c3es1A	Alignment	not modelled	99.0	16	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
83	c3ebrA	Alignment	not modelled	99.0	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized rmlc-like cupin; PDBTitle: crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
84	d1uija1	Alignment	not modelled	99.0	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
85	d2o1qa1	Alignment	not modelled	98.9	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acetylacetone-cleaving enzyme-like
86	c3cjxE	Alignment	not modelled	98.9	14	PDB header: unknown function Chain: E: PDB Molecule: protein of unknown function with a cupin-like fold; PDBTitle: crystal structure of a protein of unknown function with a cupin-like2 fold (reut_b4571) from ralstonia eutropha jmp134 at 2.60 a resolution
87	c2bnoA	Alignment	not modelled	98.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
88	d1fxza1	Alignment	not modelled	98.8	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
89	c3balB	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: acetylacetone-cleaving enzyme; PDBTitle: crystal structure of an acetylacetone dioxygenase from acinetobacter2 johnsonii
90	d2phla2	Alignment	not modelled	98.8	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
91	d1zrra1	Alignment	not modelled	98.8	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
92	c3o14B	Alignment	not modelled	98.8	23	PDB header: gene regulation Chain: B: PDB Molecule: anti-ecfsigma factor, chrr; PDBTitle: crystal structure of an anti-ecfsigma factor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
93	c2xlfA	Alignment	not modelled	98.8	10	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	c2eaaB	Alignment	not modelled	98.7	21	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
95	c1cauB	Alignment	not modelled	98.7	18	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
96	c5u9eB	Alignment	not modelled	98.7	17	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional activator rhar; PDBTitle: structure of the regulatory domain of the arac family transcriptional2 activator rhar
97	c1fxzC	Alignment	not modelled	98.7	16	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
98	c2cauA	Alignment	not modelled	98.7	20	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
99	c1uijF	Alignment	not modelled	98.7	24	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)
100	c5yjsB	Alignment	not modelled	98.7	16	PDB header: plant protein Chain: B: PDB Molecule: vicilin-like antimicrobial peptides 2-2; PDBTitle: structure of vicilin from capsicum annuum
101	c6b4sB	Alignment	not modelled	98.7	14	PDB header: allergen Chain: B: PDB Molecule: 11s globulin; PDBTitle: crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
102	d1uika2	Alignment	not modelled	98.7	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
103	c5e1rC	Alignment	not modelled	98.7	15	PDB header: allergen Chain: C: PDB Molecule: 7s vicilin; PDBTitle: crystal structure of pecan (carya illinoensis) vicilin, a new food2 allergen
104	c5cadA	Alignment	not modelled	98.6	18	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
105	c1uijA	Alignment	not modelled	98.6	24	PDB header: sugar binding protein Chain: A: PDB Molecule: beta subunit of beta conglycinin;

105	c1uijA_	Alignment	not modelled	98.6	24	PDBTitle: crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
106	c4lejA_	Alignment	not modelled	98.6	15	PDB header: allergen, plant protein Chain: A: PDB Molecule: vicilin; PDBTitle: crystal structure of the korean pine (pinus koraiensis) vicilin
107	d1od5a1	Alignment	not modelled	98.6	19	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
108	d1uija2	Alignment	not modelled	98.6	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
109	c3kglB_	Alignment	not modelled	98.6	11	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from brassica napus
110	d1fxza2	Alignment	not modelled	98.6	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
111	c3kscD_	Alignment	not modelled	98.6	14	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin from pismus2 sativum l.
112	d1od5a2	Alignment	not modelled	98.6	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
113	c5wpaA_	Alignment	not modelled	98.6	11	PDB header: allergen Chain: A: PDB Molecule: 11s globulin isoform 1; PDBTitle: crystal structure of coconut allergen cocosin
114	c3myxA_	Alignment	not modelled	98.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pspto_0244; PDBTitle: crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
115	c2e9qA_	Alignment	not modelled	98.5	20	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin subunit beta; PDBTitle: recombinant pro-11s globulin of pumpkin
116	d2pyta1	Alignment	not modelled	98.5	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: EutQ-like
117	c6nwoD_	Alignment	not modelled	98.5	12	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator bgar; PDBTitle: structures of the transcriptional regulator bgar, a lactose sensor.
118	c3ehkC_	Alignment	not modelled	98.5	20	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
119	c5wxuD_	Alignment	not modelled	98.5	21	PDB header: plant protein Chain: D: PDB Molecule: 11s globulin; PDBTitle: 11s globulin from wrightia tinctoria reveals auxin binding site
120	c3qacA_	Alignment	not modelled	98.5	15	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.