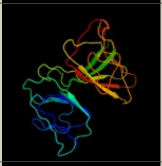
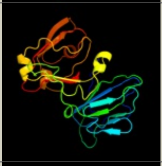
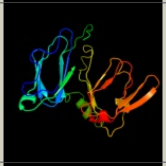
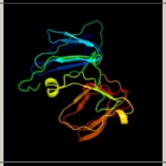
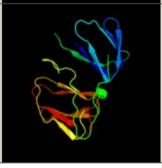
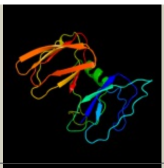
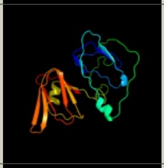
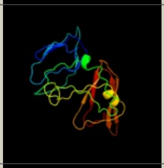
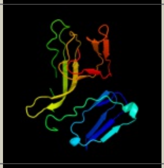
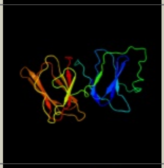
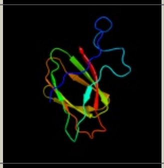
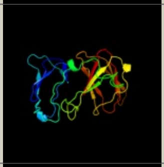
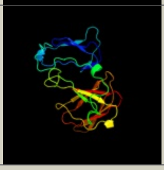
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q46938
Date	Thu Jan 5 12:35:57 GMT 2012
Unique Job ID	4aad2dc4166e23c8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xrua1	Alignment		100.0	95	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like
2	d1ywka1	Alignment		100.0	54	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like
3	c1ywkE_	Alignment		100.0	54	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**4-deoxy-l-threo-5-hexosulose-uronate ketol- **PDBTitle:** crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
4	c2qjvB_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**uncharacterized iolb-like protein; **PDBTitle:** crystal structure of an iolb-like protein (stm4420) from salmonella2 typhimurium lt2 at 1.90 a resolution
5	d1sq4a_	Alignment		98.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
6	d1rc6a_	Alignment		98.9	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
7	c1sefA_	Alignment		98.8	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
8	d1sefa_	Alignment		98.8	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
9	d1sfna_	Alignment		98.6	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
10	d1y3ta1	Alignment		98.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
11	c3rnsA_	Alignment		98.3	13	**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

12	c2d40C_	Alignment		98.1	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
13	d2phda1	Alignment		98.1	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
14	d2d40a1	Alignment		98.0	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
15	c3h7yA_	Alignment		98.0	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
16	c3myxA_	Alignment		97.8	13	**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
17	c2vqaC_	Alignment		97.5	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.
18	c2vpvA_	Alignment		97.4	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
19	c3bu7A_	Alignment		97.4	20	**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
20	d3bu7a1	Alignment		97.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
21	c2gu9B_	Alignment	not modelled	97.4	15	**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
22	d1j58a_	Alignment	not modelled	97.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
23	c3cewA_	Alignment	not modelled	97.1	22	**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
24	c2cauA_	Alignment	not modelled	97.0	13	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
25	c3ht2A_	Alignment	not modelled	96.9	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
26	c3jzvA_	Alignment	not modelled	96.9	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.
27	c3i7dB_	Alignment	not modelled	96.9	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

28	d2pyta1	Alignment	not modelled	96.9	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
29	c3lwcA_	Alignment	not modelled	96.8	28	**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
30	d1y9qa2	Alignment	not modelled	96.8	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
31	d2arca_	Alignment	not modelled	96.7	20	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
32	c2oa2A_	Alignment	not modelled	96.7	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
33	d1v70a_	Alignment	not modelled	96.6	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
34	d1lr5a_	Alignment	not modelled	96.6	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
35	c3kgzA_	Alignment	not modelled	96.5	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
36	c3ibmB_	Alignment	not modelled	96.5	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 hhal_0468 from2 halorhodospira halophila
37	c3h8uA_	Alignment	not modelled	96.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein with double-stranded **PDBTitle:** crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
38	c3l2hD_	Alignment	not modelled	96.3	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
39	c2pfwB_	Alignment	not modelled	96.2	16	**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
40	c3fjsC_	Alignment	not modelled	96.1	24	**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
41	d1o4ta_	Alignment	not modelled	96.1	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
42	d2b8ma1	Alignment	not modelled	95.7	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
43	c3d82A_	Alignment	not modelled	95.5	15	**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
44	c2o8qA_	Alignment	not modelled	95.4	10	**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 (bxe_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
45	d1yhfa1	Alignment	not modelled	94.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
46	d2f4pa1	Alignment	not modelled	94.6	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
47	c2eaaB_	Alignment	not modelled	94.5	12	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
48	c2q30C_	Alignment	not modelled	94.2	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
49	c3bcwB_	Alignment	not modelled	94.0	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
50	c2i45C_	Alignment	not modelled	94.0	11	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
						Fold: Double-stranded beta-helix

51	d1uika1	Alignment	not modelled	93.8	20	**Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
52	c2ozjB_	Alignment	not modelled	93.6	18	**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
53	d1o5ua_	Alignment	not modelled	93.5	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
54	d1dgwa_	Alignment	not modelled	93.4	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
55	d1vj2a_	Alignment	not modelled	93.1	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
56	d1uija1	Alignment	not modelled	92.6	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
57	c1ey2A_	Alignment	not modelled	92.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
58	d1eyba_	Alignment	not modelled	92.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
59	d1pmia_	Alignment	not modelled	92.1	26	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
60	c2oziA_	Alignment	not modelled	91.9	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
61	d1j3pa_	Alignment	not modelled	91.3	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
62	c2fqpD_	Alignment	not modelled	90.7	11	**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
63	c3s7eB_	Alignment	not modelled	88.1	14	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
64	c1uijA_	Alignment	not modelled	87.6	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta subunit of beta conglycinin; **PDBTitle:** crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
65	c3h1yA_	Alignment	not modelled	87.4	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
66	d1juha_	Alignment	not modelled	86.5	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
67	d1zx5a1	Alignment	not modelled	86.2	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
68	d1x82a_	Alignment	not modelled	86.1	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
69	c2opkC_	Alignment	not modelled	85.3	20	**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
70	d1qwra_	Alignment	not modelled	85.1	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
71	c3kglB_	Alignment	not modelled	83.8	21	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
72	c3es4B_	Alignment	not modelled	83.2	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein duf861 with a rmlc-like cupin fold; **PDBTitle:** crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
73	c2bnoA_	Alignment	not modelled	78.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
74	c1y9qA_	Alignment	not modelled	70.8	12	**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
75	d1od5a2	Alignment	not modelled	68.5	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
76	c3eo6B_	Alignment	not modelled	64.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of unknown function (duf1255); **PDBTitle:** crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455

						at3 0.97 a resolution
77	c2qnkA_	Alignment	not modelled	64.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyanthranilate 3,4-dioxygenase; **PDBTitle:** crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
78	d1yfua1	Alignment	not modelled	63.0	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
79	c2xlfA_	Alignment	not modelled	61.7	19	**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)
80	c3es1A_	Alignment	not modelled	61.6	19	**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
81	c1cauB_	Alignment	not modelled	61.4	28	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
82	d2phla2	Alignment	not modelled	59.5	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
83	c3qacA_	Alignment	not modelled	57.9	17	**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.
84	d2et1a1	Alignment	not modelled	53.6	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
85	d1fxza1	Alignment	not modelled	51.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
86	d1uija2	Alignment	not modelled	48.4	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
87	d2bnma2	Alignment	not modelled	48.3	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
88	c2xdvA_	Alignment	not modelled	43.2	15	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
89	c2k5hA_	Alignment	not modelled	32.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
90	d2oyza1	Alignment	not modelled	32.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**VPA0057-like
91	c3hqxA_	Alignment	not modelled	31.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0345 protein aciad0356; **PDBTitle:** crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1
92	d1zrra1	Alignment	not modelled	30.8	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
93	d2exda1	Alignment	not modelled	30.7	13	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
94	d1vrba1	Alignment	not modelled	30.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
95	c2ko2A_	Alignment	not modelled	29.0	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**reticulon-4; **PDBTitle:** nogo66
96	c3kscD_	Alignment	not modelled	28.7	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.
97	c3al6A_	Alignment	not modelled	26.3	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
98	d1fxza2	Alignment	not modelled	25.4	7	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
99	c2d5fB_	Alignment	not modelled	23.9	10	**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
100	d1od5a1	Alignment	not modelled	23.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
101	c2b9sB_	Alignment	not modelled	21.4	50	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex