
















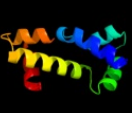















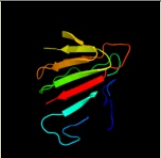
# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A4UR77
Date	Thu Jan 5 10:55:05 GMT 2012
Unique Job ID	48dfafd19ed8ae98

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gbgA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tcp pilus virulence regulatory protein; <b>PDBTitle:</b> crystal structure of toxT from vibrio cholerae o395
2	<a href="#">c1d5yD_</a>	 Alignment		99.9	22	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> rob transcription factor; <b>PDBTitle:</b> crystal structure of the e. coli rob transcription factor2 in complex with dna
3	<a href="#">c3ooaA_</a>	 Alignment		99.9	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2118 protein; <b>PDBTitle:</b> the structure of a protein with unkown function from listeria innocua
4	<a href="#">c3oioA_</a>	 Alignment		99.9	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (arac-type dna-binding domain- <b>PDBTitle:</b> crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
5	<a href="#">c1bl0A_</a>	 Alignment		99.9	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (multiple antibiotic resistance protein); <b>PDBTitle:</b> multiple antibiotic resistance protein (mara)/dna complex
6	<a href="#">c3mn2B_</a>	 Alignment		99.9	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable arac family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
7	<a href="#">c3mklB_</a>	 Alignment		99.9	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator gadx; <b>PDBTitle:</b> crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
8	<a href="#">c2k9sA_</a>	 Alignment		99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arabinose operon regulatory protein; <b>PDBTitle:</b> solution structure of dna binding domain of e. coli arac
9	<a href="#">c3lsgD_</a>	 Alignment		99.8	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> two-component response regulator yesn; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
10	<a href="#">d1d5ya2</a>	 Alignment		99.5	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
11	<a href="#">d1bl0a2</a>	 Alignment		99.5	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator

12	<a href="#">d2arca_</a>	Alignment		98.9	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Regulatory protein AraC <b>Family:</b> Regulatory protein AraC
13	<a href="#">d1bl0a1</a>	Alignment		98.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
14	<a href="#">d1d5ya1</a>	Alignment		98.8	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
15	<a href="#">c1zgwA_</a>	Alignment		98.7	20	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ada polyprotein; <b>PDBTitle:</b> nmr structure of e. coli ada protein in complex with dna
16	<a href="#">c3ibmB_</a>	Alignment		98.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of cupin 2 domain-containing protein hha1_0468 from2 halorhodospira halophila
17	<a href="#">c3kgzA_</a>	Alignment		98.6	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
18	<a href="#">d1yfua1</a>	Alignment		98.6	20	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like
19	<a href="#">c3jzvA_</a>	Alignment		98.5	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rru_a2000; <b>PDBTitle:</b> crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
20	<a href="#">d1vj2a_</a>	Alignment		98.5	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1459-like
21	<a href="#">c3h7yA_</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacilysin biosynthesis protein bacb; <b>PDBTitle:</b> crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
22	<a href="#">c3fjsC_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein with rmlc-like cupin fold; <b>PDBTitle:</b> crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
23	<a href="#">c2ozjB_</a>	Alignment	not modelled	98.4	11	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel; <b>PDBTitle:</b> crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
24	<a href="#">c3cewA_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized cupin protein; <b>PDBTitle:</b> crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
25	<a href="#">d1y3ta1</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Quercetin 2,3-dioxygenase-like
26	<a href="#">c2pfwB_</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
27	<a href="#">c2gu9B_</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> tetracenomycin polyketide synthesis protein; <b>PDBTitle:</b> crystal structure of xc5357 from xanthomonas

					campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
28	<a href="#">d1o4ta_</a>	Alignment	not modelled	98.3	25 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1287-like
29	<a href="#">c2d40C_</a>	Alignment	not modelled	98.3	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative gentisate 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of z3393 from escherichia coli o157:h7
30	<a href="#">c3bu7A_</a>	Alignment	not modelled	98.3	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gentisate 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure and biochemical characterization of gdosp,2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi
31	<a href="#">d3bu7a1</a>	Alignment	not modelled	98.3	15 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Gentisate 1,2-dioxygenase-like
32	<a href="#">c3d82A_</a>	Alignment	not modelled	98.3	16 <b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
33	<a href="#">d1y9qa2</a>	Alignment	not modelled	98.3	16 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Probable transcriptional regulator VC1968, C-terminal domain
34	<a href="#">d1lr5a_</a>	Alignment		98.3	17 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
35	<a href="#">d1sefa_</a>	Alignment	not modelled	98.2	12 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> YlbA-like
36	<a href="#">c1sefA_</a>	Alignment	not modelled	98.2	12 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
37	<a href="#">c2o8qA_</a>	Alignment	not modelled	98.2	23 <b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> 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
38	<a href="#">d2d40a1</a>	Alignment	not modelled	98.2	15 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Gentisate 1,2-dioxygenase-like
39	<a href="#">c3rnsA_</a>	Alignment	not modelled	98.2	17 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> cupin 2 conserved barrel domain protein from leptotrichia buccalis
40	<a href="#">d1sq4a_</a>	Alignment	not modelled	98.2	15 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> YlbA-like
41	<a href="#">d1zvfa1</a>	Alignment	not modelled	98.2	15 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like
42	<a href="#">d1yhfa1</a>	Alignment	not modelled	98.1	15 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1287-like
43	<a href="#">d2phda1</a>	Alignment	not modelled	98.1	16 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Gentisate 1,2-dioxygenase-like
44	<a href="#">d2b8ma1</a>	Alignment	not modelled	98.1	11 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> MJ0764-like
45	<a href="#">d1sfna_</a>	Alignment	not modelled	98.1	10 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> YlbA-like
46	<a href="#">d1v70a_</a>	Alignment	not modelled	98.1	21 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1287-like
47	<a href="#">d2f4pa1</a>	Alignment	not modelled	98.1	22 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1287-like
48	<a href="#">c3i7dB_</a>	Alignment	not modelled	98.1	21 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar phosphate isomerase; <b>PDBTitle:</b> 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
49	<a href="#">c3l2hD_</a>	Alignment	not modelled	98.1	23 <b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative sugar phosphate isomerase; <b>PDBTitle:</b> crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
50	<a href="#">d1uija1</a>	Alignment	not modelled	98.1	17 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
51	<a href="#">c2i45C_</a>	Alignment	not modelled	98.0	21 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of protein nmb1881 from neisseria

						meningitidis
52	<a href="#">c2oa2A_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2720 protein; <b>PDBTitle:</b> crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution
53	<a href="#">c3ht2A_</a>	Alignment	not modelled	98.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> remf protein; <b>PDBTitle:</b> zink containing polyketide cyclase remf from streptomyces2 resistomycificus
54	<a href="#">d1zrra1</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Acireductone dioxygenase
55	<a href="#">d1rc6a_</a>	Alignment	not modelled	98.0	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> YlbA-like
56	<a href="#">c2vpvA_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein mif2; <b>PDBTitle:</b> dimerization domain of mif2p
57	<a href="#">c3h8uA_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein with double-stranded <b>PDBTitle:</b> 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
58	<a href="#">c3bcwB_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
59	<a href="#">d1uika1</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
60	<a href="#">d1juha_</a>	Alignment	not modelled	97.9	22	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Quercetin 2,3-dioxygenase-like
61	<a href="#">d1dgwa_</a>	Alignment	not modelled	97.8	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
62	<a href="#">c2q30C_</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
63	<a href="#">d1x82a_</a>	Alignment	not modelled	97.8	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Glucose-6-phosphate isomerase, GPI
64	<a href="#">c3lwcA_</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
65	<a href="#">d1j3pa_</a>	Alignment	not modelled	97.7	20	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Glucose-6-phosphate isomerase, GPI
66	<a href="#">d1j58a_</a>	Alignment	not modelled	97.7	25	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
67	<a href="#">c3es1A_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> 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
68	<a href="#">c2fqpD_</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein bp2299; <b>PDBTitle:</b> crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
69	<a href="#">c2vqaC_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> metal-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> sll1358 protein; <b>PDBTitle:</b> protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.
70	<a href="#">c1y9qA_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
71	<a href="#">c2oziA_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rpa4178; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
72	<a href="#">c1uijA_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta subunit of beta conglycinin; <b>PDBTitle:</b> crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
73	<a href="#">c2eaaB_</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> 7s globulin-3; <b>PDBTitle:</b> crystal structure of adzuki bean 7s globulin-3
74	<a href="#">d1o5ua_</a>	Alignment	not modelled	97.4	22	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Hypothetical protein TM1112
75	<a href="#">d2et1a1</a>	Alignment	not modelled	97.4	22	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
76	<a href="#">d2bnma2</a>	Alignment	not modelled	97.3	19	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins

					<b>Family:</b> TM1459-like
77	<a href="#">dlfxza1</a>	Alignment	not modelled	97.3	12 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
78	<a href="#">d2phla2</a>	Alignment	not modelled	97.2	14 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
79	<a href="#">d2phla1</a>	Alignment	not modelled	97.2	16 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
80	<a href="#">c2cauA</a>	Alignment	not modelled	97.1	17 <b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (canavalin); <b>PDBTitle:</b> canavalin from jack bean
81	<a href="#">d2pyta1</a>	Alignment	not modelled	97.1	19 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> EutQ-like
82	<a href="#">c3s7eB</a>	Alignment	not modelled	97.0	16 <b>PDB header:</b> allergen <b>Chain:</b> B: <b>PDB Molecule:</b> allergen ara h 1, clone p41b; <b>PDBTitle:</b> crystal structure of ara h 1
83	<a href="#">d1od5a2</a>	Alignment	not modelled	96.9	13 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
84	<a href="#">c2opkC</a>	Alignment	not modelled	96.9	14 <b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
85	<a href="#">dlfxza2</a>	Alignment	not modelled	96.9	17 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
86	<a href="#">d1od5a1</a>	Alignment	not modelled	96.9	13 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
87	<a href="#">d1uika2</a>	Alignment	not modelled	96.9	14 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
88	<a href="#">c1cauB</a>	Alignment	not modelled	96.8	16 <b>PDB header:</b> seed storage protein <b>Chain:</b> B: <b>PDB Molecule:</b> canavalin; <b>PDBTitle:</b> determination of three crystal structures of canavalin by molecular2 replacement
89	<a href="#">d1vr3a1</a>	Alignment	not modelled	96.8	21 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Acireductone dioxygenase
90	<a href="#">c3ebrA</a>	Alignment	not modelled	96.8	8 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rmlc-like cupin; <b>PDBTitle:</b> crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
91	<a href="#">c1fxzC</a>	Alignment	not modelled	96.7	12 <b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycinin g1; <b>PDBTitle:</b> crystal structure of soybean proglycinin a1ab1b homotrimer
92	<a href="#">c3kglB</a>	Alignment	not modelled	96.7	10 <b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> cruciferin; <b>PDBTitle:</b> crystal structure of procruciferin, 11s globulin from2 brassica napus
93	<a href="#">d1uija2</a>	Alignment	not modelled	96.7	13 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
94	<a href="#">c2bnoA</a>	Alignment	not modelled	96.6	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
95	<a href="#">c3myxA</a>	Alignment	not modelled	96.5	16 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pspto_0244; <b>PDBTitle:</b> 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
96	<a href="#">c3kscD</a>	Alignment	not modelled	96.5	12 <b>PDB header:</b> plant protein <b>Chain:</b> D: <b>PDB Molecule:</b> lega class; <b>PDBTitle:</b> crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
97	<a href="#">c3o14B</a>	Alignment	not modelled	96.4	23 <b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> anti-ecfsigma factor, chrr; <b>PDBTitle:</b> crystal structure of an anti-ecfsigma factor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
98	<a href="#">c3qacA</a>	Alignment	not modelled	96.2	17 <b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> 11s globulin seed storage protein; <b>PDBTitle:</b> structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.
99	<a href="#">c2d5fB</a>	Alignment	not modelled	96.2	20 <b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycinin a3b4 subunit; <b>PDBTitle:</b> crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
100	<a href="#">c3es4B</a>	Alignment	not modelled	96.2	16 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein duf861 with a rmlc-like cupin fold; <b>PDBTitle:</b> 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
101	<a href="#">c2qnkA</a>	Alignment	not modelled	96.1	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyanthranilate 3,4-dioxygenase; <b>PDBTitle:</b> crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase



102	<a href="#">c2e9qA_</a>	Alignment	not modelled	96.1	18	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> 11s globulin subunit beta; <b>PDBTitle:</b> recombinant pro-11s globulin of pumpkin
103	<a href="#">c3balB_</a>	Alignment	not modelled	96.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylacetone-cleaving enzyme; <b>PDBTitle:</b> crystal structure of an acetylacetone dioxygenase from2 acinetobacter johnsonii
104	<a href="#">c3c3vA_</a>	Alignment	not modelled	95.9	12	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> arachin arah3 isoform; <b>PDBTitle:</b> crystal structure of peanut major allergen ara h 3
105	<a href="#">c3ehkC_</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> prunin; <b>PDBTitle:</b> crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
106	<a href="#">c3cjxE_</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> protein of unknown function with a cupin-like fold; <b>PDBTitle:</b> crystal structure of a protein of unknown function with a cupin-like2 fold (reut_b4571) from ralstonia eutropha jmp134 at 2.60 a resolution
107	<a href="#">d2hsga1</a>	Alignment	not modelled	95.3	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
108	<a href="#">c2xlfA_</a>	Alignment	not modelled	95.2	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sll1785 protein; <b>PDBTitle:</b> structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
109	<a href="#">d2o1qa1</a>	Alignment	not modelled	95.0	8	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Acetylacetone-cleaving enzyme-like
110	<a href="#">d2bjca1</a>	Alignment	not modelled	94.7	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
111	<a href="#">d1sgma1</a>	Alignment	not modelled	94.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
112	<a href="#">d1efaa1</a>	Alignment	not modelled	94.5	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
113	<a href="#">c1ey2A_</a>	Alignment	not modelled	94.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homogentisate 1,2-dioxygenase; <b>PDBTitle:</b> human homogentisate dioxygenase with fe(ii)
114	<a href="#">d1eyba_</a>	Alignment	not modelled	94.4	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Homogentisate dioxygenase
115	<a href="#">d1qpza1</a>	Alignment	not modelled	94.3	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
116	<a href="#">c2y0oA_</a>	Alignment	not modelled	94.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable d-lyxose ketol-isomerase; <b>PDBTitle:</b> the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
117	<a href="#">c3h5tA_</a>	Alignment	not modelled	94.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
118	<a href="#">c1sgmA_</a>	Alignment	not modelled	93.8	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator yxaf; <b>PDBTitle:</b> crystal structure of hypothetical protein yxaf
119	<a href="#">d1vrba1</a>	Alignment	not modelled	93.7	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminatase synthase-like <b>Family:</b> Asparaginyl hydroxylase-like
120	<a href="#">c3h1yA_</a>	Alignment	not modelled	93.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mannose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)