





























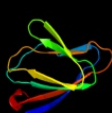


Phyre2

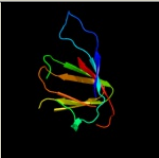
Email	I.a.kelley@imperial.ac.uk
Description	P76241
Date	Thu Jan 5 12:21:05 GMT 2012
Unique Job ID	132bf09bb0e326cb

Detailed template information



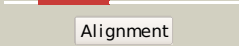
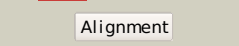

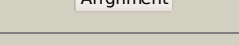


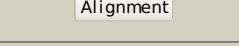


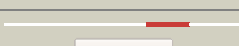

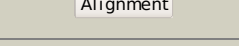




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	 Alignment		100.0	11	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxT from vibrio cholerae o395
2	c1d5yD_	 Alignment		99.9	21	PDB header: transcription/dna Chain: D: PDB Molecule: rob transcription factor; PDBTitle: crystal structure of the e. coli rob transcription factor2 in complex with dna
3	c3oi0A_	 Alignment		99.9	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (arac-type dna-binding domain- PDBTitle: crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
4	c1bl0A_	 Alignment		99.9	19	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
5	c3oo0A_	 Alignment		99.9	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unkown function from listeria innocua
6	c2k9sA_	 Alignment		99.9	20	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
7	c3mn2B_	 Alignment		99.9	16	PDB header: transcription regulator Chain: B: PDB Molecule: probable arac family transcriptional regulator; PDBTitle: the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
8	c3mk1B_	 Alignment		99.9	22	PDB header: transcription regulator Chain: B: PDB Molecule: hth-type transcriptional regulator gadx; PDBTitle: crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
9	c3lsgD_	 Alignment		99.8	20	PDB header: transcription regulator Chain: D: PDB Molecule: two-component response regulator yesn; PDBTitle: the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
10	d1bl0a2	 Alignment		99.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
11	d1d5ya2	 Alignment		99.4	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator

12	d1d5ya1	Alignment		99.1	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
13	d1bl0a1	Alignment		99.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
14	c1zgwA_	Alignment		98.9	25	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polypeptide; PDBTitle: nmr structure of e. coli ada protein in complex with dna
15	c3ibmB_	Alignment		98.9	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 hha1_0468 from2 halorhodospira halophila
16	c3jzvA_	Alignment		98.7	21	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.
17	d1o4ta_	Alignment		98.7	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
18	c3kgzA_	Alignment		98.7	18	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
19	c2pfwB_	Alignment		98.7	15	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
20	d1vj2a_	Alignment		98.6	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
21	c3fjsC_	Alignment	not modelled	98.6	14	PDB header: biosynthetic protein Chain: C: PDB Molecule: uncharacterized protein with rmlc-like cupin fold; PDBTitle: crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
22	c3h7yA_	Alignment	not modelled	98.6	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
23	c2ozjB_	Alignment	not modelled	98.6	13	PDB header: unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel; PDBTitle: crystal structure of a cupin superfamily protein (dsy2733) from2 desulfotobacterium hafniense dcb-2 at 1.60 a resolution
24	d2arca_	Alignment	not modelled	98.6	13	Fold: Double-stranded beta-helix Superfamily: Regulatory protein AraC Family: Regulatory protein AraC
25	c3rnsA_	Alignment	not modelled	98.5	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
26	d1yhfa1	Alignment	not modelled	98.5	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
27	d2f4pa1	Alignment	not modelled	98.5	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
28	d1y3ta1	Alignment	not modelled	98.5	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins

						Family: Quercetin 2,3-dioxygenase-like
29	c3cewA	Alignment	not modelled	98.5	16	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
30	d1sfna	Alignment	not modelled	98.5	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
31	c3bu7A	Alignment	not modelled	98.5	11	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
32	d3bu7a1	Alignment	not modelled	98.5	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
33	c2d40C	Alignment	not modelled	98.4	12	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
34	d1sq4a	Alignment	not modelled	98.4	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
35	d1sefa	Alignment	not modelled	98.4	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
36	clsefA	Alignment	not modelled	98.4	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
37	d2d40a1	Alignment	not modelled	98.4	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
38	c2gu9B	Alignment	not modelled	98.4	18	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
39	d2phda1	Alignment	not modelled	98.4	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
40	d1y9qa2	Alignment	not modelled	98.4	9	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
41	d1yfua1	Alignment	not modelled	98.4	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
42	d1rc6a	Alignment	not modelled	98.4	9	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
43	d1uika1	Alignment	not modelled	98.4	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
44	d1lr5a	Alignment	not modelled	98.4	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
45	c3d82A	Alignment	not modelled	98.4	16	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
46	d1v70a	Alignment	not modelled	98.3	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
47	c2i45C	Alignment	not modelled	98.3	13	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
48	c2vpvA	Alignment	not modelled	98.3	17	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
49	d2b8ma1	Alignment	not modelled	98.3	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
50	c3ht2A	Alignment	not modelled	98.3	20	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
51	c3i7dB	Alignment	not modelled	98.2	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
52	c3l2hD	Alignment	not modelled	98.2	22	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
53	c3a30C	Alignment	not modelled	98.2	16	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein;

53	c2q3vc	Alignment	not modelled	98.2	10	PDBTitle: crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution 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
54	c2oa2A	Alignment	not modelled	98.2	18	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
55	c2o8qA	Alignment	not modelled	98.2	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
56	c3es1A	Alignment	not modelled	98.1	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
57	dlzvfal	Alignment	not modelled	98.1	15	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
58	c3h8uA	Alignment	not modelled	98.1	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
59	dluiika2	Alignment	not modelled	98.1	14	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
60	clcauB	Alignment	not modelled	98.0	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
61	dlldgwa	Alignment	not modelled	98.0	15	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
62	c2fqpd	Alignment	not modelled	98.0	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
63	dlfxza2	Alignment	not modelled	98.0	12	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
64	c2ozia	Alignment	not modelled	98.0	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
65	dluija1	Alignment	not modelled	98.0	16	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.
66	c2vqaC	Alignment	not modelled	97.9	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
67	dljuha	Alignment	not modelled	97.9	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
68	c3lwcA	Alignment	not modelled	97.9	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
69	dluija2	Alignment	not modelled	97.9	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
70	d2etla1	Alignment	not modelled	97.9	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
71	dlj58a	Alignment	not modelled	97.9	17	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
72	c3bcwB	Alignment	not modelled	97.9	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
73	d2phla2	Alignment	not modelled	97.8	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
74	dlzrra1	Alignment	not modelled	97.8	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
75	d2bnma2	Alignment		97.8	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
76	dlj3pa	Alignment	not modelled	97.8	20	

77	dlfxza1	Alignment	not modelled	97.8	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
78	c1y9qA	Alignment	not modelled	97.8	8	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	dlx82a	Alignment	not modelled	97.7	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
80	dlod5a2	Alignment	not modelled	97.6	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
81	cluijA	Alignment	not modelled	97.6	19	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)
82	dlod5a1	Alignment	not modelled	97.6	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
83	dlo5ua	Alignment	not modelled	97.5	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
84	clfxzC	Alignment	not modelled	97.5	14	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
85	d2phla1	Alignment	not modelled	97.4	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
86	c2cauA	Alignment	not modelled	97.4	17	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
87	c2e9qA	Alignment	not modelled	97.4	13	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin subunit beta; PDBTitle: recombinant pro-11s globulin of pumpkin
88	c3kglB	Alignment	not modelled	97.4	13	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from2 brassica napus
89	c3s7eB	Alignment	not modelled	97.4	12	PDB header: allergen Chain: B: PDB Molecule: allergen ara h 1, clone p41b; PDBTitle: crystal structure of ara h 1
90	c3kscD	Alignment	not modelled	97.3	12	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
91	c2eaaB	Alignment	not modelled	97.2	16	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
92	c2bnoA	Alignment	not modelled	97.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorensis.
93	d2pyta1	Alignment	not modelled	97.2	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: EutQ-like
94	c2opkC	Alignment	not modelled	97.1	15	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
95	c3c3vA	Alignment	not modelled	97.1	12	PDB header: allergen Chain: A: PDB Molecule: arachin arah3 isoform; PDBTitle: crystal structure of peanut major allergen ara h 3
96	c2d5fB	Alignment	not modelled	97.1	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
97	c3ebrA	Alignment	not modelled	97.0	11	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
98	c3o14B	Alignment	not modelled	96.9	20	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
99	c3ehkC	Alignment	not modelled	96.9	19	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
100	dlvr3a1	Alignment	not modelled	96.8	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
101	c3myxA	Alignment	not modelled	96.7	12	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
102	c2xlfA	Alignment	not modelled	96.7	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)

103	c3balB	 Alignment	not modelled	96.6	8	PDB header: oxidoreductase Chain: B: PDB Molecule: acetylacetone-cleaving enzyme; PDBTitle: crystal structure of an acetylacetone dioxygenase from2 acinetobacter johnsonii
104	c3cjxE	 Alignment	not modelled	96.1	18	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 like cupin fold (reut_b4571) from ralstonia eutropha jmp134 at 2.60 a resolution
105	d2o1qa1	 Alignment	not modelled	95.8	9	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acetylacetone-cleaving enzyme-like
106	c3es4B	 Alignment	not modelled	95.7	12	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
107	c1ey2A	 Alignment	not modelled	95.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: human homogentisate dioxygenase with fe(ii)
108	d1eyba	 Alignment	not modelled	95.5	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Homogentisate dioxygenase
109	c2y0oA	 Alignment	not modelled	95.4	17	PDB header: isomerase Chain: A: PDB Molecule: probable d-lyxose ketol-isomerase; PDBTitle: the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
110	c2qnkA	 Alignment	not modelled	95.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyanthranilate 3,4-dioxygenase; PDBTitle: crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
111	d1vrba1	 Alignment	not modelled	94.8	19	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Asparaginyl hydroxylase-like
112	d2hsqa1	 Alignment	not modelled	94.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
113	d2o3fa1	 Alignment	not modelled	94.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
114	d2pa7a1	 Alignment	not modelled	94.4	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
115	c2o3fC	 Alignment	not modelled	94.4	18	PDB header: transcription Chain: C: PDB Molecule: putative hth-type transcriptional regulator ybbh; PDBTitle: structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
116	c3iwfA	 Alignment	not modelled	94.3	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
117	c3mpbA	 Alignment	not modelled	94.1	24	PDB header: isomerase Chain: A: PDB Molecule: sugar isomerase; PDBTitle: z5688 from e. coli o157:h7 bound to fructose
118	d1efaa1	 Alignment	not modelled	94.0	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
119	d1sgma1	 Alignment	not modelled	93.5	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
120	d1tq5a1	 Alignment	not modelled	93.4	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Pirin-like