
















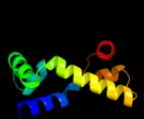






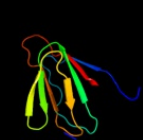

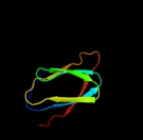
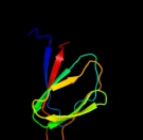
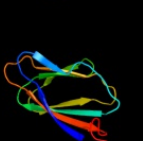
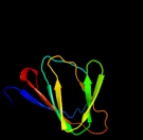



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A4UR86
Date	Thu Jan 5 10:55:12 GMT 2012
Unique Job ID	9200d69b0bbc61c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	 Alignment		100.0	13	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	22	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	c3oouA_	 Alignment		99.9	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unkown function from listeria innocua
4	c3oioA_	 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
5	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
6	c3mn2B_	 Alignment		99.9	21	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
7	c3mklB_	 Alignment		99.9	19	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
8	c2k9sA_	 Alignment		99.9	17	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
9	c3lsgD_	 Alignment		99.8	21	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	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
11	d1d5ya2	 Alignment		99.5	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator

12	d2arca_	Alignment		98.9	15	Fold: Double-stranded beta-helix Superfamily: Regulatory protein AraC Family: Regulatory protein AraC
13	d1bl0a1	Alignment		98.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
14	d1d5ya1	Alignment		98.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
15	c3ibmB_	Alignment		98.8	16	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	c1zgwa_	Alignment		98.7	19	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polypeptide; PDBTitle: nmr structure of e. coli ada protein in complex with dna
17	c3kgza_	Alignment		98.6	21	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
18	c3jzva_	Alignment		98.6	19	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.
19	c3h7ya_	Alignment		98.6	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
20	d1vj2a_	Alignment		98.6	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
21	d1yfua1	Alignment	not modelled	98.6	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
22	c2ozjB_	Alignment		98.5	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
23	c3fjsC_	Alignment	not modelled	98.4	16	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
24	d1y3ta1	Alignment	not modelled	98.4	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
25	d1y9qa2	Alignment	not modelled	98.4	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
26	c3cewa_	Alignment	not modelled	98.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized cupin protein; PDBTitle: crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
						PDB header: immune system Chain: B: PDB Molecule: tetracenomycin polyketide synthesis

27	c2gu9B_	Alignment	not modelled	98.3	14	protein; PDBTitle: crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
28	c2pfbB_	Alignment	not modelled	98.3	21	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
29	dlsq4a_	Alignment	not modelled	98.3	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
30	dlsefa_	Alignment	not modelled	98.3	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
31	clsefA_	Alignment	not modelled	98.3	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
32	dl1r5a_	Alignment	not modelled	98.3	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
33	c3rnsA_	Alignment	not modelled	98.3	18	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
34	dluika1	Alignment	not modelled	98.3	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
35	c3bu7A_	Alignment	not modelled	98.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: gentisate 1,2-dioxygenase; PDBTitle: crystal structure and biochemical characterization of gdisp_2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi
36	d3bu7a1	Alignment	not modelled	98.3	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
37	dl04ta_	Alignment	not modelled	98.2	28	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
38	c3d82A_	Alignment	not modelled	98.2	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
39	dlsfna_	Alignment	not modelled	98.2	9	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
40	dl1yha1	Alignment	not modelled	98.2	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
41	c2d40C_	Alignment	not modelled	98.2	10	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
42	c2o8qA_	Alignment	not modelled	98.2	23	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 (bxo_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
43	dluija1	Alignment	not modelled	98.2	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
44	d2b8ma1	Alignment	not modelled	98.2	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
45	c3i7dB_	Alignment	not modelled	98.2	21	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
46	dlv70a_	Alignment	not modelled	98.2	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
47	d2phda1	Alignment	not modelled	98.2	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
48	d2d40a1	Alignment	not modelled	98.2	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
49	c3i2hD_	Alignment	not modelled	98.1	21	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
50	c3ht2A_	Alignment	not modelled	98.1	21	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
51	c2oa2A_	Alignment	not modelled	98.1	19	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

52	d2f4pa1	Alignment	not modelled	98.1	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
53	d1zvfa1	Alignment	not modelled	98.1	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
54	d1rc6a_	Alignment	not modelled	98.0	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
55	c2i45C_	Alignment	not modelled	98.0	21	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
56	c3bcwB_	Alignment	not modelled	98.0	15	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
57	d1zrra1	Alignment	not modelled	98.0	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
58	c3h8uA_	Alignment	not modelled	98.0	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
59	d1dgwa_	Alignment	not modelled	98.0	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
60	c2vpvA_	Alignment	not modelled	97.9	13	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
61	c3lwcA_	Alignment	not modelled	97.9	16	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
62	d1juha_	Alignment	not modelled	97.8	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
63	c2q30C_	Alignment	not modelled	97.8	14	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
64	d1x82a_	Alignment	not modelled	97.8	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
65	d1j3pa_	Alignment	not modelled	97.8	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
66	d1j58a_	Alignment	not modelled	97.7	25	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
67	c3es1A_	Alignment	not modelled	97.7	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
68	c2vqaC_	Alignment	not modelled	97.7	21	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.
69	c2fqpD_	Alignment	not modelled	97.6	18	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
70	c1y9qa_	Alignment	not modelled	97.6	16	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
71	c1uijA_	Alignment	not modelled	97.6	17	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)
72	c2eaaB_	Alignment	not modelled	97.6	18	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
73	d1o5ua_	Alignment	not modelled	97.5	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
74	d2et1a1	Alignment	not modelled	97.5	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
75	d1fxza1	Alignment	not modelled	97.5	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
76	c2oziA_	Alignment	not modelled	97.4	18	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

77	d2phla1	Alignment	not modelled	97.4	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
78	d2bnma2	Alignment	not modelled	97.3	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
79	c3s7eB	Alignment	not modelled	97.3	16	PDB header: allergen Chain: B: PDB Molecule: allergen ara h 1, clone p41b; PDBTitle: crystal structure of ara h 1
80	d2pyta1	Alignment	not modelled	97.3	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: EutQ-like
81	d2phla2	Alignment	not modelled	97.3	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
82	c2cauA	Alignment	not modelled	97.2	16	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
83	c2opkC	Alignment	not modelled	97.1	14	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
84	d1fxza2	Alignment	not modelled	97.1	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
85	d1od5a1	Alignment	not modelled	97.1	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
86	c1cauB	Alignment	not modelled	97.0	15	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
87	d1od5a2	Alignment	not modelled	97.0	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
88	d1uika2	Alignment	not modelled	97.0	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
89	c1fxzC	Alignment	not modelled	97.0	10	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
90	c3kglB	Alignment	not modelled	96.8	10	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from2 brassica napus
91	d1vr3a1	Alignment	not modelled	96.8	23	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
92	c3kscD	Alignment	not modelled	96.7	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.
93	c2bnoA	Alignment	not modelled	96.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
94	d1uija2	Alignment	not modelled	96.7	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
95	c3qacA	Alignment	not modelled	96.6	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.
96	c3myxA	Alignment	not modelled	96.6	15	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
97	c3ebrA	Alignment	not modelled	96.5	8	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	c2d5fB	Alignment	not modelled	96.5	20	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
99	c3es4B	Alignment	not modelled	96.4	16	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
100	c2e9gA	Alignment	not modelled	96.3	20	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin subunit beta; PDBTitle: recombinant pro-11s globulin of pumpkin
101	c3c3vA	Alignment	not modelled	96.2	10	PDB header: allergen Chain: A: PDB Molecule: arachin arah3 isoform; PDBTitle: crystal structure of peanut major allergen ara h 3
102	c2qnkA	Alignment	not modelled	96.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyanthranilate 3,4-dioxygenase; PDBTitle: crystal structure of human 3-hydroxyanthranilate 3,4-

						dioxygenase
103	c3o14B_	Alignment	not modelled	96.0	23	PDB header: gene regulation Chain: B: PDB Molecule: anti-ecfsigma factor, chrr; PDBTitle: crystal structure of an anti-ecfsigma factor, chrr (magu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
104	c3ehkC_	Alignment	not modelled	96.0	15	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
105	c3balB_	Alignment	not modelled	95.7	10	PDB header: oxidoreductase Chain: B: PDB Molecule: acetylacetone-cleaving enzyme; PDBTitle: crystal structure of an acetylacetone dioxygenase from2 acinetobacter johnsonii
106	c2xlfA_	Alignment	not modelled	95.4	16	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)
107	d2hsga1	Alignment	not modelled	95.2	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
108	d1sgma1	Alignment	not modelled	95.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
109	d2o1qa1	Alignment	not modelled	94.9	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acetylacetone-cleaving enzyme-like
110	c3on4D_	Alignment	not modelled	94.7	6	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from legionella2 pneumophila
111	c1sgmA_	Alignment	not modelled	94.6	11	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator yxaf; PDBTitle: crystal structure of hypothetical protein yxaf
112	c3cxE_	Alignment	not modelled	94.5	15	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
113	c2y0oA_	Alignment	not modelled	94.4	15	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
114	d1vrba1	Alignment	not modelled	94.3	14	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: Asparaginyl hydroxylase-like
115	d2bjca1	Alignment	not modelled	94.2	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
116	d1efaa1	Alignment	not modelled	94.1	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
117	c3h1yA_	Alignment	not modelled	94.0	13	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)
118	d1jt6a1	Alignment	not modelled	94.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
119	d2fbqa1	Alignment	not modelled	93.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
120	c2dg7A_	Alignment	not modelled	93.6	8	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)