










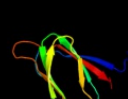


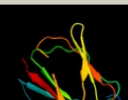


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	 Alignment		100.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxT from vibrio cholerae o395
2	c1d5yD_	 Alignment		99.9	22	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	c3oiqA_	 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	20	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
6	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
7	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
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	d1d5ya2	 Alignment		99.5	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
11	d1bl0a2	 Alignment		99.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator

12	d2arca_	Alignment		98.9	14	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	15	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	20	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		98.7	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 rhodospseudomonas palustris
18	c3jzva_	Alignment		98.7	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	d1vj2a_	Alignment		98.6	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
20	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
21	d1yfua1	Alignment	not modelled	98.6	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
22	c3fjsC_	Alignment	not modelled	98.5	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
23	c2ozjB_	Alignment		98.4	14	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	d1y9qa2	Alignment	not modelled	98.4	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
25	c2gu9B_	Alignment	not modelled	98.4	14	PDB header: immune system Chain: B: PDB Molecule: tetracenomycin polyketide synthesis protein; PDBTitle: crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
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

27	d1lr5a_	Alignment	not modelled	98.3	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
28	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
29	d1o4ta_	Alignment	not modelled	98.3	23	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
30	c2d40C_	Alignment	not modelled	98.3	17	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
31	d1y3ta1	Alignment	not modelled	98.3	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
32	d1uika1	Alignment	not modelled	98.3	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
33	d1v70a_	Alignment	not modelled	98.3	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
34	c2pfwB_	Alignment	not modelled	98.3	19	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
35	c3d82A_	Alignment	not modelled	98.3	21	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
36	c3bu7A_	Alignment	not modelled	98.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: gentisate 1,2-dioxygenase; PDBTitle: crystal structure and biochemical characterization of gdsop,2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi
37	d3bu7a1	Alignment	not modelled	98.2	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
38	d1sq4a_	Alignment	not modelled	98.2	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
39	d2b8ma1	Alignment	not modelled	98.2	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
40	d1sefa_	Alignment	not modelled	98.2	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
41	c1sefA_	Alignment	not modelled	98.2	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
42	d2d40a1	Alignment	not modelled	98.2	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
43	d1uija1	Alignment	not modelled	98.2	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
44	d1sfna_	Alignment	not modelled	98.2	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
45	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 (bx_e_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
46	c2oa2A_	Alignment	not modelled	98.2	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
47	d1yhfa1	Alignment	not modelled	98.2	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
48	d2f4pa1	Alignment	not modelled	98.1	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
49	c3i7dB_	Alignment	not modelled	98.1	22	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
50	c3l2hD_	Alignment	not modelled	98.1	20	PDB header: isomerase Chain: D: PDB Molecule: putative sugar phosphate isomerase; PDBTitle: crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
51	c3h8uA_	Alignment	not modelled	98.1	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
52	c2i45C	Alignment	not modelled	98.1	21	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
53	c3ht2A	Alignment	not modelled	98.1	25	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
54	d2phda1	Alignment	not modelled	98.1	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
55	c3bcwB	Alignment	not modelled	98.1	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
56	dlzvfa1	Alignment	not modelled	98.0	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
57	c2vpvA	Alignment	not modelled	98.0	13	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
58	dlrc6a	Alignment	not modelled	98.0	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
59	dlzrra1	Alignment	not modelled	98.0	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
60	dlgdwa	Alignment	not modelled	98.0	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
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	dljuha	Alignment	not modelled	97.9	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
63	c2q30C	Alignment	not modelled	97.9	15	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	dlx82a	Alignment	not modelled	97.8	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
65	c2fqpD	Alignment	not modelled	97.8	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
66	clv9qA	Alignment	not modelled	97.7	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
67	dlj58a	Alignment	not modelled	97.7	23	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
68	dlj3pa	Alignment	not modelled	97.7	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
69	dlfxza1	Alignment	not modelled	97.7	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
70	c2vqaC	Alignment	not modelled	97.7	19	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.
71	c2eaaB	Alignment	not modelled	97.7	18	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
72	cluijA	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)
73	c3es1A	Alignment	not modelled	97.6	15	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
74	c2oziA	Alignment	not modelled	97.6	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
75	d2phla1	Alignment	not modelled	97.5	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
76	d2etla1	Alignment	not modelled	97.5	23	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
						Fold: Double-stranded beta-helix

77	d1o5ua_	Alignment	not modelled	97.5	24	Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
78	d2bnma2	Alignment	not modelled	97.5	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
79	c2cauA_	Alignment	not modelled	97.4	16	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
80	c3s7eB_	Alignment	not modelled	97.4	17	PDB header: allergen Chain: B: PDB Molecule: allergen ara h 1, clone p41b; PDBTitle: crystal structure of ara h 1
81	d2phla2	Alignment	not modelled	97.2	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
82	d2pyta1	Alignment	not modelled	97.2	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: EutQ-like
83	c1cauB_	Alignment	not modelled	97.0	13	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
84	d1uika2	Alignment	not modelled	97.0	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
85	d1od5a1	Alignment	not modelled	97.0	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
86	d1fxza2	Alignment	not modelled	96.9	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
87	c1fxzC_	Alignment	not modelled	96.9	12	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
88	c3kglB_	Alignment	not modelled	96.9	9	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from2 brassica napus
89	d1od5a2	Alignment	not modelled	96.9	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
90	c2opkC_	Alignment	not modelled	96.9	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
91	d1vr3a1	Alignment	not modelled	96.8	23	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
92	c2bnoA_	Alignment	not modelled	96.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenisi.
93	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.
94	d1uija2	Alignment	not modelled	96.7	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
95	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
96	c3es4B_	Alignment	not modelled	96.5	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
97	c2d5fB_	Alignment	not modelled	96.5	18	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
98	c3myxA_	Alignment	not modelled	96.5	16	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
99	c2e9qA_	Alignment	not modelled	96.3	21	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin subunit beta; PDBTitle: recombinant pro-11s globulin of pumpkin
100	c3c3vA_	Alignment	not modelled	96.2	9	PDB header: allergen Chain: A: PDB Molecule: arachin arah3 isoform; PDBTitle: crystal structure of peanut major allergen ara h 3
101	c3ehkC_	Alignment	not modelled	95.9	13	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
102	c3o14B_	Alignment	not modelled	95.7	23	PDB header: gene regulation Chain: B: PDB Molecule: anti-ecfsigma factor, chrr; PDBTitle: crystal structure of an anti-ecfsigma factor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution

103	d2hsga1	Alignment	not modelled	95.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
104	c2xlfA	Alignment	not modelled	95.3	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)
105	d2bjca1	Alignment	not modelled	95.1	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
106	c3balB	Alignment	not modelled	95.0	10	PDB header: oxidoreductase Chain: B: PDB Molecule: acetylacetone-cleaving enzyme; PDBTitle: crystal structure of an acetylacetone dioxygenase from2 acinetobacter johnsonii
107	d1efaa1	Alignment	not modelled	95.0	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
108	c2qnkA	Alignment	not modelled	95.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyanthranilate 3,4-dioxygenase; PDBTitle: crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
109	c3cxE	Alignment	not modelled	94.7	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
110	d1qpza1	Alignment	not modelled	94.6	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
111	c3h5tA	Alignment	not modelled	94.1	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
112	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)
113	d2o1qa1	Alignment	not modelled	93.9	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acetylacetone-cleaving enzyme-like
114	c3fx3A	Alignment	not modelled	93.8	13	PDB header: camp-binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: structure of a putative camp-binding regulatory protein from2 silicibacter pomeroyi dss-3
115	c2y0oA	Alignment	not modelled	93.7	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
116	d2pa7a1	Alignment	not modelled	93.5	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
117	c1ey2A	Alignment	not modelled	93.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: human homogentisate dioxygenase with fe(ii)
118	d1eyba	Alignment	not modelled	93.4	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Homogentisate dioxygenase
119	c3kxD	Alignment	not modelled	93.4	21	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
120	c3eqeB	Alignment	not modelled	93.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative cystein deoxygenase; PDBTitle: crystal structure of the yubc protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr112.