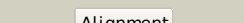
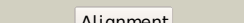
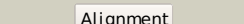
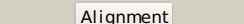
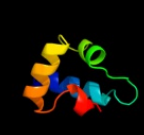
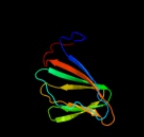
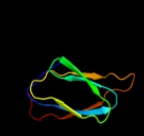
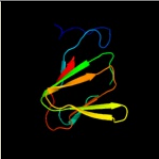


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	 Alignment		100.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxT from vibrio cholerae o395
2	c3oioA_	 Alignment		99.9	23	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
3	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
4	c3oouA_	 Alignment		99.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unkown function from listeria innocua
5	c1bl0A_	 Alignment		99.9	16	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
6	c2k9sA_	 Alignment		99.9	21	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	24	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	c3mklB_	 Alignment		99.9	29	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	19	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	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
11	d1d5ya2	 Alignment		99.5	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator

12	d1d5ya1	Alignment		99.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
13	d1bl0a1	Alignment		99.0	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
14	c1zgwa_	Alignment		98.9	24	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna
15	d2arca_	Alignment		98.5	9	Fold: Double-stranded beta-helix Superfamily: Regulatory protein AraC Family: Regulatory protein AraC
16	c3cewa_	Alignment		97.7	14	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
17	c3kgza_	Alignment		97.3	12	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		97.2	14	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	d1sq4a_	Alignment		97.1	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
20	c3ibmB_	Alignment		97.0	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
21	d2f4pa1	Alignment	not modelled	97.0	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
22	d1y9qa2	Alignment	not modelled	97.0	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
23	c3h7ya_	Alignment	not modelled	97.0	7	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
24	d1sfna_	Alignment	not modelled	97.0	4	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
25	d1o4ta_	Alignment	not modelled	96.9	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
26	c2vpva_	Alignment	not modelled	96.8	9	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
27	d1sefa_	Alignment	not modelled	96.8	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
28	c1sefa_	Alignment	not modelled	96.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
						Fold: Double-stranded beta-helix

29	d1rc6a_	Alignment	not modelled	96.8	18	Superfamily: RmlC-like cupins Family: YlbA-like
30	d1vj2a_	Alignment	not modelled	96.8	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
31	c2i45C_	Alignment	not modelled	96.8	16	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
32	d1uika1	Alignment	not modelled	96.8	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
33	c3es1A_	Alignment		96.8	17	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
34	c2q30C_	Alignment	not modelled	96.7	11	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
35	c2gu9B_	Alignment	not modelled	96.7	15	PDB header: immune system Chain: B: PDB Molecule: tetracenomycin polyketide synthesis protein; PDBTitle: crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
36	c2o8qA_	Alignment	not modelled	96.7	12	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
37	c3bcwB_	Alignment	not modelled	96.7	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
38	c3h8uA_	Alignment	not modelled	96.6	14	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 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
39	c2pfwB_	Alignment	not modelled	96.6	13	PDB header: unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
40	d1v70a_	Alignment	not modelled	96.5	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
41	c3fjsC_	Alignment	not modelled	96.5	15	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
42	c2ozjB_	Alignment	not modelled	96.5	16	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
43	d1uija1	Alignment	not modelled	96.5	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
44	c3i7dB_	Alignment	not modelled	96.5	11	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
45	c3d82A_	Alignment	not modelled	96.5	13	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	d2b8ma1	Alignment	not modelled	96.4	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
47	d1j3pa_	Alignment	not modelled	96.4	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
48	d1yhfa1	Alignment	not modelled	96.3	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
49	c3l2hD_	Alignment	not modelled	96.3	16	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	d1x82a_	Alignment	not modelled	96.3	23	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI

51	c3ht2A	Alignment	not modelled	96.3	12	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
52	c3rnsA	Alignment	not modelled	96.3	16	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
53	d1yfua1	Alignment	not modelled	96.2	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
54	d1lr5a	Alignment	not modelled	96.1	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
55	d1y3ta1	Alignment	not modelled	96.0	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
56	d2bnma2	Alignment	not modelled	95.9	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
57	c1uijA	Alignment	not modelled	95.9	15	PDB header: sugar binding protein Chain: A: PDB Molecule: beta subunit of beta conglycinin; PDBTitle: crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
58	c2oa2A	Alignment	not modelled	95.9	11	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
59	d1dgwa	Alignment	not modelled	95.8	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
60	d3bu7a1	Alignment	not modelled	95.8	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
61	c3bu7A	Alignment	not modelled	95.8	10	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
62	c2d40C	Alignment	not modelled	95.8	16	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
63	c2opkC	Alignment	not modelled	95.7	21	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
64	d1o5ua	Alignment	not modelled	95.7	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
65	c3lwcA	Alignment	not modelled	95.7	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
66	d2d40a1	Alignment	not modelled	95.5	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
67	c1y9qA	Alignment	not modelled	95.5	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
68	d2phda1	Alignment	not modelled	95.4	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
69	d1juha	Alignment	not modelled	95.4	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
70	c2fqpD	Alignment	not modelled	95.1	19	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
71	d1zrra1	Alignment	not modelled	95.1	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
72	c3iwfA	Alignment	not modelled	95.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpri family; PDBTitle: the crystal structure of the n-terminal domain of a rpri2 transcriptional regulator from staphylococcus epidermidis to 1.4a
73	d2hsga1	Alignment	not modelled	95.0	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
74	d1od5a1	Alignment	not modelled	94.9	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
75	d2pyta1	Alignment	not modelled	94.9	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: EutQ-like
76	d1zvfa1	Alignment	not modelled	94.9	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
						PDB header: plant protein

77	c2eaaB_	Alignment	not modelled	94.9	17	Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
78	d2phla1	Alignment	not modelled	94.9	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
79	c3s7eB_	Alignment	not modelled	94.8	15	PDB header: allergen Chain: B: PDB Molecule: allergen ara h 1, clone p41b; PDBTitle: crystal structure of ara h 1
80	d1fxza1	Alignment	not modelled	94.8	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
81	d1sgma1	Alignment	not modelled	94.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
82	c3es4B_	Alignment	not modelled	94.5	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
83	c2o3fC_	Alignment	not modelled	94.5	23	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.
84	d2o3fa1	Alignment	not modelled	94.4	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
85	c2vqaC_	Alignment	not modelled	94.4	12	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.
86	c3kglB_	Alignment	not modelled	94.2	14	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from2 brassica napus
87	d1efaa1	Alignment	not modelled	94.2	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
88	c2cauA_	Alignment	not modelled	94.2	14	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
89	d2bjca1	Alignment	not modelled	94.2	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
90	c1cauB_	Alignment	not modelled	94.1	16	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
91	d1j58a_	Alignment	not modelled	94.1	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
92	c3kscD_	Alignment	not modelled	94.0	16	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	d1qpza1	Alignment	not modelled	94.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
94	c2oziA_	Alignment	not modelled	93.9	11	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
95	c1fxzC_	Alignment	not modelled	93.8	19	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
96	d1j5ya1	Alignment	not modelled	93.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
97	c2d5fB_	Alignment	not modelled	93.8	17	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	c1sgmA_	Alignment	not modelled	93.7	12	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator yxaf; PDBTitle: crystal structure of hypothetical protein yxaf
99	c3kjd_	Alignment	not modelled	93.6	15	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
100	c3myxA_	Alignment	not modelled	93.4	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
101	c2eh3A_	Alignment	not modelled	93.4	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5
						PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family;

102	c3gziA_	Alignment	not modelled	93.4	11	PDBTitle: crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
103	d2i10a1	Alignment	not modelled	93.4	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
104	d1uija2	Alignment	not modelled	93.3	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
105	c1vi0B_	Alignment	not modelled	93.3	16	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator
106	d1od5a2	Alignment	not modelled	93.3	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
107	d2fbqa1	Alignment	not modelled	93.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
108	c3h5ta_	Alignment	not modelled	93.1	24	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
109	c3on4D_	Alignment	not modelled	93.0	11	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from legionella2 pneumophila
110	c2d6yA_	Alignment	not modelled	92.9	7	PDB header: gene regulation Chain: A: PDB Molecule: putative tetr family regulatory protein; PDBTitle: crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)
111	d1fxza2	Alignment	not modelled	92.9	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
112	d2g3ba1	Alignment	not modelled	92.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
113	c1bdhA_	Alignment	not modelled	92.8	15	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
114	d2et1a1	Alignment	not modelled	92.8	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
115	d1ui5a1	Alignment	not modelled	92.8	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
116	c2f07A_	Alignment	not modelled	92.8	13	PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
117	c3o60A_	Alignment	not modelled	92.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0861 protein; PDBTitle: the crystal structure of lin0861 from listeria innocua to 2.8a
118	d3c07a1	Alignment	not modelled	92.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
119	d1v7ba1	Alignment	not modelled	92.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
120	c3iuvA_	Alignment	not modelled	92.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized tetr family protein; PDBTitle: the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3