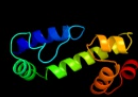
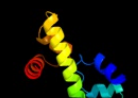
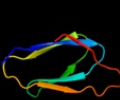


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	 Alignment		100.0	21	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxT from vibrio cholerae o395
2	c1d5yD_	 Alignment		99.9	17	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	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
4	c3mklB_	 Alignment		99.9	35	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
5	c1bl0A_	 Alignment		99.9	17	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
6	c3oouA_	 Alignment		99.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unkown function from listeria innocua
7	c2k9sA_	 Alignment		99.9	18	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
8	c3mn2B_	 Alignment		99.9	20	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
9	c3lsgD_	 Alignment		99.8	24	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	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
11	d1d5ya2	 Alignment		99.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator

12	d1d5ya1	Alignment		98.8	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
13	d1bl0a1	Alignment		98.8	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
14	c1zgwA	Alignment		98.6	10	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polypeptide; PDBTitle: nmr structure of e. coli ada protein in complex with dna
15	d2arca	Alignment		97.7	15	Fold: Double-stranded beta-helix Superfamily: Regulatory protein AraC Family: Regulatory protein AraC
16	c3ibmB	Alignment		96.0	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 hha_0468 from2 halorhodospira halophila
17	c3fjsC	Alignment		95.8	13	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
18	c3kgzA	Alignment		95.5	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
19	c3cewA	Alignment		95.5	13	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
20	c3h7yA	Alignment		95.4	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: bacilysin biosynthesis protein bacb; PDBTitle: crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
21	c2pfwB	Alignment	not modelled	95.4	6	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
22	c3jzvA	Alignment	not modelled	95.4	6	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.
23	d1y3ta1	Alignment	not modelled	95.3	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
24	c2opkC	Alignment	not modelled	95.3	17	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
25	c2vpvA	Alignment	not modelled	95.2	10	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
26	d1y9qa2	Alignment	not modelled	95.2	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
27	c3iwfA	Alignment	not modelled	95.0	16	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
28	d1yhfa1	Alignment	not modelled	94.9	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like

29	c2gu9B_	Alignment	not modelled	94.9	8	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
30	d1o4ta_	Alignment	not modelled	94.8	0	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
31	c2o8qA_	Alignment	not modelled	94.8	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
32	d1vj2a_	Alignment	not modelled	94.8	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
33	d2d40a1	Alignment	not modelled	94.7	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
34	c3lwcA_	Alignment	not modelled	94.5	6	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
35	d1v70a_	Alignment	not modelled	94.5	6	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
36	c2d40C_	Alignment	not modelled	94.4	10	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
37	d1efaa1	Alignment	not modelled	94.1	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
38	d2b8ma1	Alignment	not modelled	94.1	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
39	d3bu7a1	Alignment	not modelled	94.0	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
40	c3bu7A_	Alignment	not modelled	94.0	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
41	d2hsqa1	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
42	c2ozjB_	Alignment	not modelled	93.9	15	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	c2q30C_	Alignment	not modelled	93.8	6	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
44	d2bjca1	Alignment	not modelled	93.7	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
45	d1juha_	Alignment	not modelled	93.6	6	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
46	d1sfna_	Alignment	not modelled	93.6	4	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
47	c3d82A_	Alignment	not modelled	93.6	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
48	d2phda1	Alignment	not modelled	93.4	3	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
49	d1rc6a_	Alignment	not modelled	93.4	2	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
50	d1sq4a_	Alignment	not modelled	93.2	9	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
51	c3l2hD_	Alignment	not modelled	93.0	8	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
52	c3ht2A_	Alignment	not modelled	93.0	8	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
53	c2i45C_	Alignment	not modelled	92.5	4	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria

						meningitidis
54	c1u78A_	Alignment	not modelled	92.4	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
55	c3h8uA_	Alignment	not modelled	92.4	8	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
56	c3kxD_	Alignment	not modelled	92.4	28	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
57	d2pyta1	Alignment	not modelled	92.3	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: EutQ-like
58	d1qpza1	Alignment	not modelled	92.3	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
59	c3i7dB_	Alignment	not modelled	91.5	6	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
60	d1o5ua_	Alignment	not modelled	90.8	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
61	d2o3fa1	Alignment	not modelled	90.7	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
62	c2o3fC_	Alignment	not modelled	90.7	9	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.
63	c3h5tA_	Alignment	not modelled	90.7	28	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
64	d1j5ya1	Alignment	not modelled	90.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
65	d2f4pa1	Alignment	not modelled	90.6	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
66	c3myxA_	Alignment	not modelled	90.4	6	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
67	d1sefa_	Alignment	not modelled	90.3	4	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
68	c1sefA_	Alignment	not modelled	90.3	4	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
69	d1lr5a_	Alignment	not modelled	90.3	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
70	d1lcda_	Alignment	not modelled	90.0	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
71	c3rnsA_	Alignment	not modelled	89.7	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
72	d1biaa1	Alignment	not modelled	89.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
73	c3bcwB_	Alignment	not modelled	89.4	2	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
74	c2oa2A_	Alignment	not modelled	89.0	4	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
75	d1yfua1	Alignment	not modelled	88.8	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
76	d1t56a1	Alignment	not modelled	88.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
77	c1bdhA_	Alignment	not modelled	87.8	15	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex

78	d2cg4a1	Alignment	not modelled	87.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
79	c3on4D_	Alignment	not modelled	87.7	14	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from legionella2 pneumophila
80	c3gevC_	Alignment	not modelled	87.6	9	PDB header: cell adhesion Chain: C: PDB Molecule: intercellular adhesion protein r; PDBTitle: crystal structure of icar from staphylococcus aureus, a member of the2 tetracycline repressor protein family
81	d1jt6a1	Alignment	not modelled	87.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
82	d2fq4a1	Alignment	not modelled	87.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
83	c1jumB_	Alignment	not modelled	86.8	12	PDB header: transcription Chain: B: PDB Molecule: hypothetical transcriptional regulator in qaca PDBTitle: crystal structure of the multidrug binding transcriptional2 repressor qacr bound to the natural drug berberine
84	d2i10a1	Alignment	not modelled	86.3	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
85	d1ui5a1	Alignment	not modelled	86.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
86	c3e7lD_	Alignment	not modelled	86.1	13	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
87	c2r0qF_	Alignment	not modelled	86.0	7	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
88	d2gfna1	Alignment	not modelled	85.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
89	c2g7sA_	Alignment	not modelled	85.8	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens
90	c1zvva_	Alignment	not modelled	85.8	14	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
91	c2gfnA_	Alignment	not modelled	85.7	11	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator pksa related protein; PDBTitle: crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1
92	d1g2ha_	Alignment	not modelled	85.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
93	d1sgma1	Alignment	not modelled	85.5	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
94	d1mkma1	Alignment	not modelled	85.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lcr, N-terminal domain
95	c2l4aA_	Alignment	not modelled	85.3	9	PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
96	d2g7sa1	Alignment	not modelled	85.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
97	d2cyya1	Alignment	not modelled	85.3	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
98	d2fd5a1	Alignment	not modelled	85.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
99	d2vkea1	Alignment	not modelled	85.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
100	c2eh3A_	Alignment	not modelled	85.1	9	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
101	d1fipa_	Alignment	not modelled	85.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
102	d1v7ba1	Alignment	not modelled	85.0	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
103	d1etxa_	Alignment	not modelled	84.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
						Fold: DNA/RNA-binding 3-helical bundle

104	d3c07a1	Alignment	not modelled	84.8	18	Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
105	c3r0aB_	Alignment	not modelled	84.8	6	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
106	d1uika1	Alignment	not modelled	84.8	6	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
107	d1dgwa_	Alignment	not modelled	84.8	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
108	c2f07A_	Alignment	not modelled	84.6	11	PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
109	d2fbqa1	Alignment	not modelled	84.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
110	d1yifa1	Alignment	not modelled	84.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
111	d2cfxa1	Alignment	not modelled	84.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
112	d1pb6a1	Alignment	not modelled	84.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
113	c2dg7A_	Alignment	not modelled	84.2	15	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)
114	d2g3ba1	Alignment	not modelled	84.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
115	d2fx0a1	Alignment	not modelled	84.0	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
116	c3ppbB_	Alignment	not modelled	84.0	7	PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr family transcription regulator; PDBTitle: crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
117	d2id3a1	Alignment	not modelled	84.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
118	d2gena1	Alignment	not modelled	83.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
119	c1vi0B_	Alignment	not modelled	83.7	9	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator
120	d1ilga1	Alignment	not modelled	83.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain