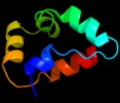
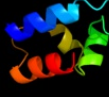
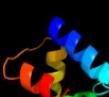
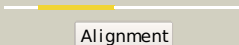
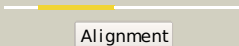
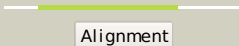
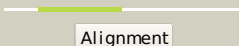
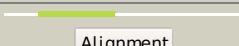
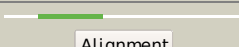
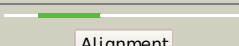
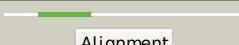
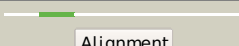
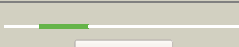
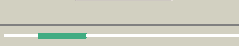
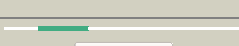
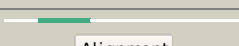
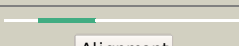


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bd1B_	 Alignment		96.5	28	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
2	c3bdnB_	 Alignment		96.1	13	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
3	c2fjrB_	 Alignment		95.8	24	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
4	c2kpiA_	 Alignment		95.1	22	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
5	c3op9A_	 Alignment		94.8	14	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
6	c3dnvB_	 Alignment		93.9	11	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
7	d1r69a_	 Alignment		93.7	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
8	d1sq8a_	 Alignment		93.6	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
9	c3clcC_	 Alignment		93.1	9	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp13961 tetramer in complex with its natural 35 base-pair operator
10	d2croa_	 Alignment		93.0	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
11	c3f52A_	 Alignment		92.9	21	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum

12	d1y9qa1	Alignment		92.9	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
13	d1l1ib_	Alignment		92.9	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
14	d1b0na2	Alignment		92.6	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
15	d2a6ca1	Alignment		92.4	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
16	c2ef8A_	Alignment		92.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
17	d2b5aa1	Alignment		91.7	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
18	d1adra_	Alignment		91.7	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
19	d1y7ya1	Alignment		91.6	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
20	c3ivpD_	Alignment		91.4	25	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
21	d1x57a1	Alignment	not modelled	91.2	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
22	c2o38A_	Alignment	not modelled	90.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
23	d2o38a1	Alignment	not modelled	90.5	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
24	d1lmb3_	Alignment	not modelled	90.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
25	c2elhA_	Alignment	not modelled	90.3	30	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
26	c3cecA_	Alignment	not modelled	90.0	22	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
27	d1rzsa_	Alignment	not modelled	89.8	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
28	c2ewtA_	Alignment	not modelled	89.3	17	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd

29	d2r1jl1	Alignment	not modelled	89.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
30	c3b7hA	Alignment	not modelled	89.2	7	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
31	c3omtA	Alignment	not modelled	88.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
32	c2xcjB	Alignment	not modelled	87.6	10	PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
33	c1b0nA	Alignment	not modelled	87.4	20	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
34	d1utxa	Alignment	not modelled	87.3	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
35	d1bw6a	Alignment	not modelled	86.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
36	c3f6wE	Alignment	not modelled	86.2	9	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
37	c3eusB	Alignment	not modelled	86.2	9	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
38	d2icta1	Alignment	not modelled	86.0	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
39	c3mlfC	Alignment	not modelled	85.3	19	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
40	d1rioa	Alignment	not modelled	85.1	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
41	c3bs3A	Alignment	not modelled	84.8	19	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
42	c1hlvA	Alignment	not modelled	83.9	24	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
43	c3t76A	Alignment	not modelled	82.9	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
44	d1hlva1	Alignment	not modelled	82.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
45	c3k2zA	Alignment	not modelled	81.9	24	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
46	c2jvlA	Alignment	not modelled	81.4	21	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
47	d1g3wa1	Alignment	not modelled	80.7	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
48	d1j9ia	Alignment	not modelled	79.8	26	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
49	d2jn6a1	Alignment	not modelled	79.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
50	d2isya1	Alignment	not modelled	78.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
51	c3fmyA	Alignment	not modelled	76.5	18	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygitb3021)
52	c3kxaD	Alignment	not modelled	76.2	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
53	d2ev0a1	Alignment	not modelled	76.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
54	c1y9qA	Alignment	not modelled	74.1	11	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
55	c3trbA	Alignment	not modelled	72.0	22	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addition module antidote protein of a higa (higa)2 family from coxiella burnetii

56	c2ppxA	 Alignment	not modelled	70.5	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
57	d2ppxA1	 Alignment	not modelled	70.5	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
58	c3lisB	 Alignment	not modelled	69.1	15	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
59	c2wusR	 Alignment	not modelled	68.8	9	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape2 protein rodZ
60	c2ebyA	 Alignment	not modelled	66.6	16	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
61	c2bnoA	 Alignment	not modelled	65.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenisi.
62	d2ofya1	 Alignment	not modelled	64.1	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
63	c6paxA	 Alignment	not modelled	61.4	19	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
64	c1u78A	 Alignment	not modelled	58.5	19	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
65	d1pdnc	 Alignment	not modelled	58.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
66	c3fymA	 Alignment	not modelled	58.1	11	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of ymfM, a putative dna-binding membrane2 protein from staphylococcus aureus
67	d3ctaa1	 Alignment	not modelled	57.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
68	c2rn7A	 Alignment	not modelled	55.6	14	PDB header: unknown function Chain: A: PDB Molecule: is629 orfA; PDBTitle: nmr solution structure of tnpE protein from shigella2 flexneri. northeast structural genomics target sfr125
69	c2hinA	 Alignment	not modelled	54.9	32	PDB header: transcription Chain: A: PDB Molecule: repressor protein; PDBTitle: structure of n15 cro at 1.05 a: an ortholog of lambda cro2 with a completely different but equally effective3 dimerization mechanism
70	d1jhfa1	 Alignment	not modelled	54.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
71	c1f5tA	 Alignment	not modelled	52.2	15	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
72	d2coba1	 Alignment	not modelled	51.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
73	c2h09A	 Alignment	not modelled	51.5	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
74	c3gn5B	 Alignment	not modelled	47.8	13	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
75	c1g3wA	 Alignment	not modelled	45.3	14	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
76	d1d1la	 Alignment	not modelled	44.2	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
77	d2cg4a1	 Alignment	not modelled	43.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
78	d6paxA1	 Alignment	not modelled	43.5	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
79	d2cfxA1	 Alignment	not modelled	42.1	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
80	c3ctaA	 Alignment	not modelled	41.7	19	PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma2 acidophilum
81	d1zs4a1	 Alignment	not modelled	38.3	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Bacteriophage CII protein
						Fold: lambda repressor-like DNA-binding domains

82	d4croa_	Alignment	not modelled	37.4	22	Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
83	d1nera_	Alignment	not modelled	37.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
84	c2x4hA_	Alignment	not modelled	36.4	20	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus
85	c2pijB_	Alignment	not modelled	36.3	17	PDB header: transcription Chain: B: PDB Molecule: prophage pfl 6 cro; PDBTitle: structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
86	c1fx7C_	Alignment	not modelled	34.1	14	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
87	d3orca_	Alignment	not modelled	32.5	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
88	c2ao9H_	Alignment	not modelled	31.8	19	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: phage protein; PDBTitle: structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
89	c2o8xA_	Alignment	not modelled	31.7	16	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
90	d1jkva_	Alignment	not modelled	30.9	17	Fold: Ferritin-like Superfamily: Ferritin-like Family: Manganese catalase (T-catalase)
91	d1k78a1	Alignment	not modelled	30.4	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
92	d1vz0a1	Alignment	not modelled	29.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
93	c2it0A_	Alignment	not modelled	27.9	14	PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii
94	d1or7a1	Alignment	not modelled	27.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
95	d1xsva_	Alignment	not modelled	27.0	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
96	d1ilga1	Alignment	not modelled	26.7	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
97	c3i4pA_	Alignment	not modelled	26.1	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
98	c3hefB_	Alignment	not modelled	25.8	18	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
99	c2l4aA_	Alignment	not modelled	25.6	14	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
100	c2ev5B_	Alignment	not modelled	25.6	23	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
101	d1qnta2	Alignment	not modelled	25.6	28	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
102	d1rp3a2	Alignment	not modelled	25.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
103	c2cg4B_	Alignment	not modelled	24.7	24	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
104	d2cyya1	Alignment	not modelled	24.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
105	d2g7ga1	Alignment	not modelled	23.5	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
106	c3tgnA_	Alignment	not modelled	22.5	26	PDB header: transcription Chain: A: PDB Molecule: adc operon repressor adcr; PDBTitle: crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
107	d1xrsb2	Alignment	not modelled	22.3	35	Fold: Dodecin subunit-like Superfamily: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain Family: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
108	c2k27A_	Alignment	not modelled	22.2	19	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8;

					PDBTitle: solution structure of human pax8 paired box domain
109	c3hugA	Alignment	not modelled	22.0	14 PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI
110	c2vbzA	Alignment	not modelled	21.2	11 PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
111	c3qsvD	Alignment	not modelled	20.8	11 PDB header: transcription/dna Chain: D: PDB Molecule: mothers against decapentaplegic homolog 4; PDBTitle: structural basis for dna recognition by constitutive smad4 mh1 dimers
112	c1z4hA	Alignment	not modelled	20.3	26 PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
113	d2vkea1	Alignment	not modelled	20.3	18 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
114	d3broa1	Alignment	not modelled	20.3	4 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators