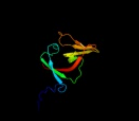
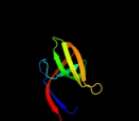
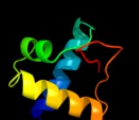
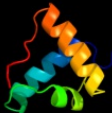


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k2zA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
2	d1jhfa2	 Alignment		100.0	99	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: LexA-related
3	c1jhhB_	 Alignment		99.9	99	PDB header: hydrolase Chain: B: PDB Molecule: lexa repressor; PDBTitle: lexa s119a mutant
4	c3bdnB_	 Alignment		99.9	24	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
5	d1umua_	 Alignment		99.9	32	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: LexA-related
6	c2hnfA_	 Alignment		99.9	28	PDB header: viral protein Chain: A: PDB Molecule: repressor protein ci101-229dm-k192a; PDBTitle: structure of a hyper-cleavable monomeric fragment of phage2 lambda repressor containing the cleavage site region
7	c2fjrB_	 Alignment		99.9	13	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
8	d1f39a_	 Alignment		99.8	32	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: LexA-related
9	d1jhfa1	 Alignment		99.5	100	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
10	c2fkdk_	 Alignment		98.9	21	PDB header: transcription regulator Chain: K: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of the c-terminal domain of bacteriophage2 186 repressor
11	d1stza1	 Alignment		98.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain

12	d1b12a_	Alignment		97.4	21	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: Type 1 signal peptidase
13	c3eusB_	Alignment		97.3	19	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroiy
14	c2x4hA_	Alignment		97.3	20	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
15	c1fx7C_	Alignment		97.2	25	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
16	c1y9qA_	Alignment		97.2	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
17	c2it0A_	Alignment		97.0	25	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
18	d1rioa_	Alignment		97.0	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
19	c1f5tA_	Alignment		97.0	24	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dbx consensus binding sequence
20	c3f6wE_	Alignment		96.9	36	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
21	d1l1ib_	Alignment	not modelled	96.9	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
22	c1stzB_	Alignment	not modelled	96.8	20	PDB header: transcription Chain: B: PDB Molecule: heat-inducible transcription repressor hrca homolog; PDBTitle: crystal structure of a hypothetical protein at 2.2 a resolution
23	d1lmb3_	Alignment	not modelled	96.8	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
24	c2vn2B_	Alignment	not modelled	96.7	25	PDB header: replication Chain: B: PDB Molecule: chromosome replication initiation protein; PDBTitle: crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
25	c3fmyA_	Alignment	not modelled	96.6	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 (ygit/b3021)
26	c3op9A_	Alignment	not modelled	96.6	13	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
27	c2bnoA_	Alignment	not modelled	96.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenisi.
28	d2ev0a1	Alignment	not modelled	96.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein

29	c2ef8A_	Alignment	not modelled	96.5	14	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
30	d2isya1	Alignment	not modelled	96.5	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
31	d2a6ca1	Alignment	not modelled	96.4	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
32	d1g3wa1	Alignment	not modelled	96.4	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
33	c2kpiA_	Alignment	not modelled	96.4	21	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
34	c3cecA_	Alignment	not modelled	96.4	20	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
35	c3ivpD_	Alignment	not modelled	96.3	13	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.
36	c2v79B_	Alignment	not modelled	96.3	18	PDB header: dna-binding protein Chain: B: PDB Molecule: dna replication protein dnad; PDBTitle: crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
37	d1y9qa1	Alignment	not modelled	96.2	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
38	d2b5aa1	Alignment	not modelled	96.2	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
39	d2croa_	Alignment	not modelled	96.1	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
40	c3f52A_	Alignment	not modelled	96.1	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
41	c3bs3A_	Alignment	not modelled	96.1	18	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	c2o38A_	Alignment	not modelled	96.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
43	d2o38a1	Alignment	not modelled	96.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
44	c2wteB_	Alignment	not modelled	96.1	12	PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
45	c2xcjB_	Alignment	not modelled	96.1	11	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
46	c3b7hA_	Alignment	not modelled	96.1	14	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
47	d1adra_	Alignment	not modelled	96.0	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
48	d2ppxa1	Alignment	not modelled	96.0	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
49	c2ppxA_	Alignment	not modelled	96.0	12	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
50	d1biaa1	Alignment	not modelled	96.0	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
51	d2icta1	Alignment	not modelled	95.9	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
52	d1sq8a_	Alignment	not modelled	95.9	31	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
53	c3sztB_	Alignment	not modelled	95.8	25	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
54	c3omtA_	Alignment	not modelled	95.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;

54	c30m1A_	Alignment	not modelled	95.8	9	PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
55	c3dnyB_	Alignment	not modelled	95.8	15	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
56	d1x57a1	Alignment	not modelled	95.8	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
57	d1y7ya1	Alignment	not modelled	95.8	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
58	c2ewtA_	Alignment	not modelled	95.7	9	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
59	c3clcC_	Alignment	not modelled	95.7	16	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
60	c2q0oA_	Alignment	not modelled	95.7	17	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
61	d1r69a_	Alignment	not modelled	95.7	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
62	d1ku9a_	Alignment	not modelled	95.6	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA-binding protein Mj223
63	c3gn5B_	Alignment	not modelled	95.5	21	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)
64	c1b0nA_	Alignment	not modelled	95.5	15	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
65	c3t76A_	Alignment	not modelled	95.5	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
66	c1g3wA_	Alignment	not modelled	95.4	25	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
67	d2cfxa1	Alignment	not modelled	95.4	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
68	d2r1j11	Alignment	not modelled	95.4	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
69	d1b0na2	Alignment	not modelled	95.4	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
70	c2wusR_	Alignment	not modelled	95.4	10	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape2 protein rodz
71	c1zljE_	Alignment	not modelled	95.3	22	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
72	d1l3la1	Alignment	not modelled	95.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
73	d2ofya1	Alignment	not modelled	95.3	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
74	c3mlfC_	Alignment	not modelled	95.3	13	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
75	c3qp5C_	Alignment	not modelled	95.3	25	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
76	c2h09A_	Alignment	not modelled	95.3	33	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
77	c3lisB_	Alignment	not modelled	95.2	11	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
78	c3nqoB_	Alignment	not modelled	95.2	20	PDB header: transcription Chain: B: PDB Molecule: marr-family transcriptional regulator; PDBTitle: crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
79	c1h0mD_	Alignment	not modelled	95.1	18	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
						PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator vanug;

80	c2ev5B_	Alignment	not modelled	95.1	14	Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
81	d1a04a1	Alignment	not modelled	95.0	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
82	d1aoya_	Alignment	not modelled	95.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
83	c3r0aB_	Alignment	not modelled	95.0	12	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
84	c3bwgA_	Alignment	not modelled	95.0	23	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator yydk; PDBTitle: the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
85	c2l4aA_	Alignment	not modelled	95.0	28	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
86	c2krfB_	Alignment	not modelled	95.0	24	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
87	d2cg4a1	Alignment	not modelled	94.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
88	c2w48D_	Alignment	not modelled	94.9	23	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
89	d1lutxa_	Alignment	not modelled	94.9	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
90	c3tgnA_	Alignment	not modelled	94.9	30	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
91	c1vi0B_	Alignment	not modelled	94.9	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator
92	d2d1ha1	Alignment	not modelled	94.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
93	c3iwfA_	Alignment	not modelled	94.8	19	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
94	d1mkma1	Alignment	not modelled	94.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lclR, N-terminal domain
95	d3broa1	Alignment	not modelled	94.7	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
96	d3bwga1	Alignment	not modelled	94.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
97	c3c2bA_	Alignment	not modelled	94.7	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens
98	d1p4wa_	Alignment	not modelled	94.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
99	c3eetA_	Alignment	not modelled	94.7	33	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntR-family transcriptional regulator; PDBTitle: crystal structure of putative gntR-family transcriptional2 regulator
100	c3edpB_	Alignment	not modelled	94.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin2111 protein; PDBTitle: the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
101	c2ebyA_	Alignment	not modelled	94.6	13	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
102	d2hs5a1	Alignment	not modelled	94.6	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
103	c2g3bB_	Alignment	not modelled	94.6	21	PDB header: transcription Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
104	d1fsea_	Alignment	not modelled	94.6	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
105	c3g3zA_	Alignment	not modelled	94.6	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis

106	d1ku3a_	Alignment	not modelled	94.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
107	c3trbA_	Alignment	not modelled	94.5	12	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
108	c2e1cA_	Alignment	not modelled	94.5	15	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
109	c3by6C_	Alignment	not modelled	94.5	21	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
110	d1rp3a1	Alignment	not modelled	94.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
111	c2qwwB_	Alignment	not modelled	94.5	22	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
112	c2vbzA_	Alignment	not modelled	94.4	24	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
113	c3neuA_	Alignment	not modelled	94.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
114	c3kxuD_	Alignment	not modelled	94.3	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
115	c1u78A_	Alignment	not modelled	94.3	20	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
116	c2du9A_	Alignment	not modelled	94.2	23	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
117	d1ilga1	Alignment	not modelled	94.2	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
118	d2p7vb1	Alignment	not modelled	94.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
119	d1sfxa_	Alignment	not modelled	94.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
120	c2nyxB_	Alignment	not modelled	94.1	17	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis