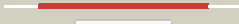



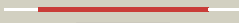

















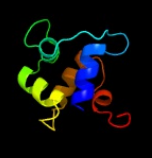



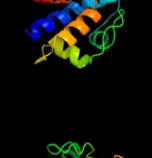
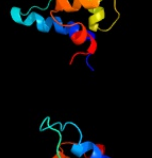
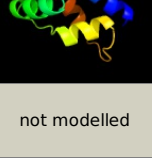


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3849_(espR)_4323677_4324075
 Date Sat Aug 10 22:05:03 BST 2019
 Unique Job ID b85b976f7b0e1383

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qyxD_	 Alignment		100.0	100	PDB header: transcription/dna Chain: D: PDB Molecule: esx-1 secretion-associated regulator espR; PDBTitle: crystal structure of mycobacterium tuberculosis espR in complex with a2 small dna fragment
2	c3r1fO_	 Alignment		99.9	98	PDB header: transcription Chain: O: PDB Molecule: esx-1 secretion-associated regulator espR; PDBTitle: crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
3	c3ivpD_	 Alignment		99.7	12	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.
4	c3op9A_	 Alignment		99.6	14	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
5	c1b0nA_	 Alignment		99.6	14	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
6	c4o8bA_	 Alignment		99.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr
7	c5d4zF_	 Alignment		99.6	15	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
8	c3lisB_	 Alignment		99.5	19	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
9	c2bnoA_	 Alignment		99.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
10	c3zhiA_	 Alignment		99.5	19	PDB header: transcription Chain: A: PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage tp901-1
11	c2kpiA_	 Alignment		99.4	23	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

12	d1b0na2	Alignment		99.4	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
13	c5woqA	Alignment		99.4	20	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
14	c1y9qA	Alignment		99.4	18	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
15	c5jubA	Alignment		99.4	15	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of comr from s.thermophilus in complex with dna and2 its signalling peptide coms.
16	d1y9qa1	Alignment		99.4	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
17	c3f52A	Alignment		99.4	20	PDB header: transcription activator Chain: A; PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
18	d2b5aa1	Alignment		99.3	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
19	d2r1jl1	Alignment		99.3	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
20	c2ewtA	Alignment		99.3	16	PDB header: dna binding protein Chain: A; PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bidd
21	d2ofya1	Alignment	not modelled	99.3	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
22	d1adra	Alignment	not modelled	99.3	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
23	c3clcC	Alignment	not modelled	99.3	10	PDB header: transcription regulator/dna Chain: C; PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
24	c2mezA	Alignment	not modelled	99.3	13	PDB header: rna binding protein Chain: A; PDB Molecule: multi-protein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaeal mbf1 on ribosomes suggests role as2 recruitment factor
25	d2croa	Alignment	not modelled	99.3	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
26	c3vk0B	Alignment	not modelled	99.3	10	PDB header: dna binding protein Chain: B; PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhf from2 neisseria
27	c3b7hA	Alignment	not modelled	99.3	17	PDB header: structural protein Chain: A; PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
28	d1y7ya1	Alignment	not modelled	99.3	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like

29	d1r69a_	Alignment	not modelled	99.3	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
30	c3m1fC_	Alignment	not modelled	99.3	13	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
31	c2xcjB_	Alignment	not modelled	99.3	15	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
32	c3pxpA_	Alignment	not modelled	99.3	9	PDB header: transcription regulator Chain: A: PDB Molecule: helix-turn-helix domain protein; PDBTitle: crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
33	d1x57a1	Alignment	not modelled	99.3	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
34	c3bs3A_	Alignment	not modelled	99.3	14	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
35	d1sq8a_	Alignment	not modelled	99.3	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
36	c2ebyA_	Alignment	not modelled	99.3	18	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
37	c3trbA_	Alignment	not modelled	99.2	14	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
38	c3omtA_	Alignment	not modelled	99.2	15	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.
39	c3f6wE_	Alignment	not modelled	99.2	11	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
40	d2icta1	Alignment	not modelled	99.2	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
41	c3cecA_	Alignment	not modelled	99.2	12	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
42	c6b9rD_	Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
43	d1utxa_	Alignment	not modelled	99.2	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
44	d1rioa_	Alignment	not modelled	99.2	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
45	c5fd4B_	Alignment	not modelled	99.2	12	PDB header: transcription regulator Chain: B: PDB Molecule: comr; PDBTitle: crystal structure of comr from streptococcus suis
46	c4mcxE_	Alignment	not modelled	99.2	10	PDB header: toxin Chain: E: PDB Molecule: antidote protein; PDBTitle: p. vulgaris higa structure, crystal form 2
47	c6b9tH_	Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: H: PDB Molecule: methylphosphonate synthase; PDBTitle: crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
48	c4yv9C_	Alignment	not modelled	99.2	12	PDB header: dna binding protein/inhibitor Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of streptococcus dysgalactiae shp pheromone2 receptor rgg2
49	c4rykA_	Alignment	not modelled	99.2	13	PDB header: dna binding protein Chain: A: PDB Molecule: lmo0325 protein; PDBTitle: crystal structure of a putative transcriptional regulator from2 listeria monocytogenes egd-e
50	c3kxaD_	Alignment	not modelled	99.2	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
51	c6f8sA_	Alignment	not modelled	99.2	11	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
52	d1lib_	Alignment	not modelled	99.2	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
53	c2jvIA_	Alignment	not modelled	99.2	13	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
54	d2o38a1	Alignment	not modelled	99.1	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354

55	c2o38A	Alignment	not modelled	99.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
56	d1lmb3	Alignment	not modelled	99.1	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
57	c3t76A	Alignment	not modelled	99.1	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
58	c5uk3J	Alignment	not modelled	99.1	10	PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
59	c3dnnB	Alignment	not modelled	99.1	12	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
60	c3eusB	Alignment	not modelled	99.0	13	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
61	d2a6ca1	Alignment	not modelled	99.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
62	c2grmB	Alignment	not modelled	99.0	7	PDB header: transcription Chain: B: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/icf10 complex
63	c2ef8A	Alignment	not modelled	99.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
64	c5d50L	Alignment	not modelled	99.0	17	PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
65	c4pu4C	Alignment	not modelled	99.0	9	PDB header: toxin/antitoxin/dna Chain: C: PDB Molecule: toxin-antitoxin system antidote transcriptional repressor PDBTitle: shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
66	c4ybaA	Alignment	not modelled	99.0	17	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
67	c3bdnB	Alignment	not modelled	99.0	18	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
68	c4ghjA	Alignment	not modelled	98.9	15	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
69	c2axzC	Alignment	not modelled	98.9	8	PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
70	c2qfcB	Alignment	not modelled	98.9	16	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
71	c2fjrB	Alignment	not modelled	98.8	12	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
72	c2wusR	Alignment	not modelled	98.8	6	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
73	c3fymA	Alignment	not modelled	98.8	16	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of yfm, a putative dna-binding membrane2 protein from staphylococcus aureus
74	c5j9iH	Alignment	not modelled	98.6	12	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
75	c4gqmA	Alignment	not modelled	98.6	13	PDB header: unknown function Chain: A: PDB Molecule: ct009; PDBTitle: crystal structure of a helix-turn-helix containing hypothetical2 protein (ct009) from chlamydia trachomatis in a sub-domain swap3 conformation
76	c2ppxA	Alignment	not modelled	98.5	16	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
77	d2ppxa1	Alignment	not modelled	98.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
78	c3fmyA	Alignment	not modelled	98.5	12	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)
79	c5jaaB	Alignment	not modelled	98.3	15	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
80	c6fkgC	Alignment	not modelled	98.1	17	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
						PDB header: dna binding protein

81	c3gn5B_	Alignment	not modelled	98.0	12	Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
82	c2mqkA_	Alignment	not modelled	97.9	13	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
83	c5u57B_	Alignment	not modelled	96.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
84	d2bnma1	Alignment	not modelled	96.2	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
85	d1nera_	Alignment	not modelled	96.1	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
86	c3bd1B_	Alignment	not modelled	95.9	11	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
87	d2bjca1	Alignment	not modelled	95.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
88	d1lcda_	Alignment	not modelled	95.1	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
89	c1efaA_	Alignment	not modelled	94.5	16	PDB header: transcription/dna Chain: A: PDB Molecule: lac repressor; PDBTitle: crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
90	c3kxD_	Alignment	not modelled	94.4	20	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
91	d1efaa1	Alignment	not modelled	94.3	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
92	d1dwka1	Alignment	not modelled	93.6	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
93	d1qpza1	Alignment	not modelled	93.5	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
94	d1s4ka_	Alignment	not modelled	93.4	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdiL-like
95	c5syszA_	Alignment	not modelled	93.2	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
96	d2hsqa1	Alignment	not modelled	93.2	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
97	c1lbgB_	Alignment	not modelled	93.0	20	PDB header: PDB COMPND:
98	c2lcva_	Alignment	not modelled	92.8	22	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
99	c4go1A_	Alignment	not modelled	92.1	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
100	c2l8nA_	Alignment	not modelled	92.1	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
101	c2iv1J_	Alignment	not modelled	91.8	5	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
102	c1bdhA_	Alignment	not modelled	91.8	22	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
103	d1luxca_	Alignment	not modelled	91.7	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
104	d1ic8a2	Alignment	not modelled	91.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
105	d1e3oc2	Alignment	not modelled	91.5	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
106	c3h5tA_	Alignment	not modelled	91.2	17	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
107	d1au7a2	Alignment	not modelled	91.0	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain

108	d1luxda_	Alignment	not modelled	90.7	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LacI-like bacterial regulator
109	c2auwB_	Alignment	not modelled	90.3	23	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
110	c2w48D_	Alignment	not modelled	89.8	17	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
111	c1zvvA_	Alignment	not modelled	89.6	21	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
112	c2ahqA_	Alignment	not modelled	89.0	15	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
113	c1r71B_	Alignment	not modelled	88.0	15	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in complex with2 the operator dna
114	c1b4aA_	Alignment	not modelled	88.0	14	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
115	d1bw6a_	Alignment	not modelled	87.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
116	c3mkyP_	Alignment	not modelled	87.0	12	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
117	d2p5ka1	Alignment	not modelled	86.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
118	c2o8kA_	Alignment	not modelled	86.8	14	PDB header: transcription/dna Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
119	d1hlva1	Alignment	not modelled	86.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
120	d2auwa1	Alignment	not modelled	86.2	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like