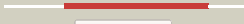



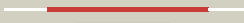




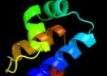









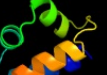




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2021c (-)_2266813_2267118
Date	Mon Aug 5 13:25:13 BST 2019
Unique Job ID	995d9312f8fbb400

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a6ca1	 Alignment		99.5	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
2	d2o38a1	 Alignment		99.5	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
3	c2o38A_	 Alignment		99.5	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
4	c2bnoA_	 Alignment		99.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
5	c1y9qA_	 Alignment		99.4	22	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
6	d1b0na2	 Alignment		99.4	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
7	c2mezA_	 Alignment		99.4	18	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
8	c3ivpD_	 Alignment		99.4	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.
9	d1rioA_	 Alignment		99.4	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
10	c3b7hA_	 Alignment		99.4	29	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
11	c1b0nA_	 Alignment		99.4	21	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex

12	c3vk0B_	Alignment		99.4	21	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhft from2 neisseria
13	c4pu4C_	Alignment		99.3	23	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)
14	c3op9A_	Alignment		99.3	20	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
15	c5woqA_	Alignment		99.3	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
16	c3f52A_	Alignment		99.3	23	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
17	d1utxa_	Alignment		99.3	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
18	c6b9rD_	Alignment		99.3	21	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
19	d1y9qa1	Alignment		99.3	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
20	c2kpiA_	Alignment		99.3	9	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
21	d1x57a1	Alignment	not modelled	99.3	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
22	c2ewtA_	Alignment	not modelled	99.3	22	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
23	c3dnvB_	Alignment	not modelled	99.3	21	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
24	c3clcC_	Alignment	not modelled	99.3	17	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
25	d2ofya1	Alignment	not modelled	99.3	30	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
26	d2b5aa1	Alignment	not modelled	99.3	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
27	c3eusB_	Alignment	not modelled	99.3	28	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
28	d1lmb3_	Alignment	not modelled	99.3	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
						PDB header: transcription

29	c3lisB_	Alignment	not modelled	99.3	18	Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
30	c5d4zF_	Alignment	not modelled	99.3	19	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
31	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
32	c6b9tH_	Alignment	not modelled	99.3	10	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
33	c4ghjA_	Alignment	not modelled	99.3	28	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
34	c3kxaD_	Alignment	not modelled	99.3	33	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
35	c3mfc_	Alignment	not modelled	99.3	26	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
36	d1lib_	Alignment	not modelled	99.2	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
37	c2jvIA_	Alignment	not modelled	99.2	18	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
38	c3f6wE_	Alignment	not modelled	99.2	26	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
39	d1y7ya1	Alignment	not modelled	99.2	33	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
40	c3t76A_	Alignment	not modelled	99.2	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
41	d2r1jl1	Alignment	not modelled	99.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
42	c3omtA_	Alignment	not modelled	99.2	19	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.
43	c3zhiA_	Alignment	not modelled	99.2	22	PDB header: transcription Chain: A: PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage tp901-1
44	d1adra_	Alignment	not modelled	99.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
45	c3pxpA_	Alignment	not modelled	99.2	20	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
46	c4ybaA_	Alignment	not modelled	99.2	25	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
47	c5uk3J_	Alignment	not modelled	99.2	17	PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
48	c5jubA_	Alignment	not modelled	99.2	16	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.
49	d2icta1	Alignment	not modelled	99.2	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
50	c2ef8A_	Alignment	not modelled	99.2	24	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
51	c2ebyA_	Alignment	not modelled	99.2	19	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
52	c4o8bA_	Alignment	not modelled	99.1	20	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr
53	d1r69a_	Alignment	not modelled	99.1	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
54	d2croa_	Alignment	not modelled	99.1	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
55	c4mcxE_	Alianment	not modelled	99.1	12	PDB header: toxin Chain: E: PDB Molecule: antidote protein;

						PDBTitle: p. vulgaris higa structure, crystal form 2
56	d1sq8a_	Alignment	not modelled	99.1	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
57	c5fd4B_	Alignment	not modelled	99.1	23	PDB header: transcription regulator Chain: B: PDB Molecule: comr; PDBTitle: crystal structure of comr from streptococcus suis
58	c3cecA_	Alignment	not modelled	99.1	15	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
59	c3bdnB_	Alignment	not modelled	99.1	19	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
60	c4rykA_	Alignment	not modelled	99.1	23	PDB header: dna binding protein Chain: A: PDB Molecule: lmo0325 protein; PDBTitle: crystal structure of a putative transcriptional regulator from2 listeria monocytogenes egd-e
61	c2xcjB_	Alignment	not modelled	99.1	12	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
62	c4yv9C_	Alignment	not modelled	99.0	23	PDB header: dna binding protein/inhibitor Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of streptococcus dysgalactiae shp pheromone2 receptor rgg2
63	c3trbA_	Alignment	not modelled	99.0	28	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
64	c6f8sA_	Alignment	not modelled	99.0	15	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
65	c3qyxD_	Alignment	not modelled	99.0	17	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
66	c2grmB_	Alignment	not modelled	98.9	18	PDB header: transcription Chain: B: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/icf10 complex
67	c2wusR_	Alignment	not modelled	98.9	19	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
68	c3fmyA_	Alignment	not modelled	98.9	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)
69	c3fymA_	Alignment	not modelled	98.9	21	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of yfym, a putative dna-binding membrane2 protein from staphylococcus aureus
70	c2axzC_	Alignment	not modelled	98.8	18	PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
71	c2qfcB_	Alignment	not modelled	98.8	26	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
72	c5j9iH_	Alignment	not modelled	98.8	13	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
73	d2ppxa1	Alignment	not modelled	98.8	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
74	c2ppxA_	Alignment	not modelled	98.8	23	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
75	c3gn5B_	Alignment	not modelled	98.7	18	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)
76	c5jaaB_	Alignment	not modelled	98.7	13	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
77	c4gqmA_	Alignment	not modelled	98.7	22	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
78	c2fjrB_	Alignment	not modelled	98.6	17	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
79	c5d50I_	Alignment	not modelled	98.6	20	PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
80	c6fkgC_	Alignment	not modelled	98.5	15	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
						PDB header: hydrolase

81	c2mqkA_	Alignment	not modelled	98.1	19	Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the nub aaa+ atpase
82	c3r1fO_	Alignment	not modelled	97.4	20	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
83	d2bnma1	Alignment	not modelled	96.8	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
84	d1nera_	Alignment	not modelled	96.5	5	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
85	c5j2yA_	Alignment	not modelled	96.4	29	PDB header: gene regulation/dna Chain: A: PDB Molecule: regulatory protein; PDBTitle: molecular insight into the regulatory mechanism of the quorum-sensing2 repressor rsal in pseudomonas aeruginosa
86	d1lcda_	Alignment	not modelled	96.3	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
87	c3bd1B_	Alignment	not modelled	96.3	14	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
88	d1dwka1	Alignment	not modelled	96.3	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
89	d2hsga1	Alignment	not modelled	96.3	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
90	d1luxca_	Alignment	not modelled	96.3	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
91	c1efaA_	Alignment	not modelled	96.3	18	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
92	d1e3oc2	Alignment	not modelled	96.2	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
93	d2bjca1	Alignment	not modelled	96.1	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
94	d1ic8a2	Alignment	not modelled	96.1	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
95	d1au7a2	Alignment	not modelled	96.1	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
96	c3kxD_	Alignment	not modelled	96.1	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
97	c2lv1J_	Alignment	not modelled	96.0	15	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
98	d1luxda_	Alignment	not modelled	96.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
99	c3l1pA_	Alignment	not modelled	96.0	23	PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex
100	c1ic8B_	Alignment	not modelled	95.8	15	PDB header: transcription/dna Chain: B: PDB Molecule: hepatocyte nuclear factor 1-alpha; PDBTitle: hepatocyte nuclear factor 1a bound to dna : mody3 gene product
101	c3h5tA_	Alignment	not modelled	95.8	20	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
102	d1efaa1	Alignment	not modelled	95.8	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
103	c2auwB_	Alignment	not modelled	95.7	15	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
104	c1lbgB_	Alignment	not modelled	95.6	25	PDB header: PDB COMPND:
105	d1qpza1	Alignment	not modelled	95.5	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
106	c2h8rA_	Alignment	not modelled	95.5	18	PDB header: transcription activator/dna Chain: A: PDB Molecule: hepatocyte nuclear factor 1-beta; PDBTitle: hepatocyte nuclear factor 1b bound to dna: mody5 gene2 product
107	c2l8nA_	Alignment	not modelled	95.4	21	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 PDB header: transcription/dna

108	c1bdhA_	Alignment	not modelled	95.3	24	Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
109	c3d1nK_	Alignment	not modelled	95.2	25	PDB header: transcription regulator/dna Chain: K: PDB Molecule: pou domain, class 6, transcription factor 1; PDBTitle: structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
110	c2lcvA_	Alignment	not modelled	95.2	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
111	c5u57B_	Alignment	not modelled	95.1	8	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
112	c5yszA_	Alignment	not modelled	95.0	32	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
113	c1zvvA_	Alignment	not modelled	94.9	25	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
114	c4go1A_	Alignment	not modelled	94.7	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
115	c3k2zA_	Alignment	not modelled	94.3	10	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
116	c3vwbA_	Alignment	not modelled	94.2	10	PDB header: transcription/dna Chain: A: PDB Molecule: virulence regulon transcriptional activator virb; PDBTitle: crystal structure of virb core domain (se-met derivative) complexed2 with the cis-acting site (5-bru modifications) upstream ic sb promoter
117	c2w48D_	Alignment	not modelled	93.9	24	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
118	d1r71a_	Alignment	not modelled	93.7	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
119	c1hf0A_	Alignment	not modelled	93.2	21	PDB header: transcription Chain: A: PDB Molecule: octamer-binding transcription factor 1; PDBTitle: crystal structure of the dna-binding domain of oct-1 bound to dna as a2 dimer
120	c2xsdC_	Alignment	not modelled	93.1	19	PDB header: transcription/dna Chain: C: PDB Molecule: pou domain, class 3, transcription factor 1; PDBTitle: crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna