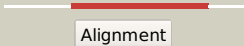

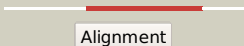

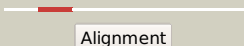

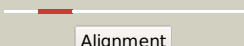

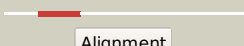

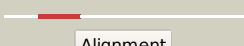

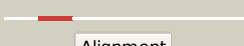




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1129c_(-)_1253079_1254539
Date	Wed Jul 31 22:05:21 BST 2019
Unique Job ID	5ae1ebfa125b665a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6cz6D_	 Alignment		100.0	98	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator prpr; PDBTitle: mycobacterium tuberculosis transcriptional regulator
2	c3dtkA_	 Alignment		99.9	13	PDB header: gene regulation Chain: A: PDB Molecule: irre protein; PDBTitle: crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
3	c1y9qA_	 Alignment		99.4	21	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
4	c2bnoA_	 Alignment		99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
5	c3ivpD_	 Alignment		99.3	18	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.
6	c1b0nA_	 Alignment		99.3	21	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
7	c3op9A_	 Alignment		99.3	23	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
8	c3lisB_	 Alignment		99.3	18	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
9	c2ewtA_	 Alignment		99.3	24	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bidd
10	c3vk0B_	 Alignment		99.3	20	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhf from2 neisseria
11	c3f52A_	 Alignment		99.3	24	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	c6b9rD	Alignment		99.3	26	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
13	c6b9tH	Alignment		99.2	14	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
14	c5woqA	Alignment		99.2	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
15	c2kpiA	Alignment		99.2	13	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
16	d1rioa	Alignment		99.2	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
17	d1y9qa1	Alignment		99.2	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
18	c2meza	Alignment		99.2	17	PDB header: rna binding protein Chain: A: PDB Molecule: multi-protein bridging factor (mbp-like); PDBTitle: flexible anchoring of archael mbf1 on ribosomes suggests role as2 recruitment factor
19	c3mlfC	Alignment		99.2	20	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
20	d2b5aa1	Alignment		99.2	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
21	d2r1j1	Alignment	not modelled	99.2	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
22	d2icta1	Alignment	not modelled	99.2	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
23	d1adra	Alignment	not modelled	99.2	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
24	d1b0na2	Alignment	not modelled	99.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
25	c4mcxE	Alignment	not modelled	99.2	12	PDB header: toxin Chain: E: PDB Molecule: antidote protein; PDBTitle: p. vulgaris higba structure, crystal form 2
26	c4o8bA	Alignment	not modelled	99.2	20	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr
27	d1y7ya1	Alignment	not modelled	99.2	35	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
28	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 PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein;

29	c3clcC	Alignment	not modelled	99.2	24	PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system;
30	c3cecA	Alignment	not modelled	99.2	18	PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq;
31	c2ebyA	Alignment	not modelled	99.2	23	PDBTitle: crystal structure of a hypothetical protein from e. coli PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein;
32	c3f6wE	Alignment	not modelled	99.2	22	PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator;
33	c5jubA	Alignment	not modelled	99.1	12	PDBTitle: crystal structure of comr from s.thermophilus in complex with dna and2 its signalling peptide coms. PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein;
34	c3bs3A	Alignment	not modelled	99.1	14	PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
36	c2o38A	Alignment	not modelled	99.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
37	c3omtA	Alignment	not modelled	99.1	17	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.
38	d2ofya1	Alignment	not modelled	99.1	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
39	d1x57a1	Alignment	not modelled	99.1	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
40	c3kxaD	Alignment	not modelled	99.1	24	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
41	d1r69a	Alignment	not modelled	99.1	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
42	c3qyxD	Alignment	not modelled	99.1	19	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
43	c3trbA	Alignment	not modelled	99.1	27	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
44	d1sq8a	Alignment	not modelled	99.1	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
45	c3b7hA	Alignment	not modelled	99.1	19	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
46	d2croa	Alignment	not modelled	99.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
47	d1lutxa	Alignment	not modelled	99.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
48	c6f8sA	Alignment	not modelled	99.1	27	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
49	c4ybaA	Alignment	not modelled	99.1	17	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
50	d1llib	Alignment	not modelled	99.1	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
51	c2jvIA	Alignment	not modelled	99.1	17	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
52	c5uk3J	Alignment	not modelled	99.1	14	PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
53	d1lmb3	Alignment	not modelled	99.1	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
54	c5d4zF	Alignment	not modelled	99.1	19	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
55	c4rykA	Alignment	not modelled	99.1	25	PDB header: dna binding protein Chain: A: PDB Molecule: lmo0325 protein; PDBTitle: crystal structure of a putative transcriptional regulator

						from2 listeria monocytogenes egd-e
56	c3eusB_	Alignment	not modelled	99.1	30	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
57	c5fd4B_	Alignment	not modelled	99.1	19	PDB header: transcription regulator Chain: B: PDB Molecule: comr; PDBTitle: crystal structure of comr from streptococcus suis
58	c4yv9C_	Alignment	not modelled	99.0	30	PDB header: dna binding protein/inhibitor Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of streptococcus dysgalactiae shp pheromone2 receptor rgg2
59	c3pxpA_	Alignment	not modelled	99.0	29	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
60	c4pu4C_	Alignment	not modelled	99.0	12	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)
61	c2xcjB_	Alignment	not modelled	99.0	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	c2ef8A_	Alignment	not modelled	99.0	30	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
63	c3dnvB_	Alignment	not modelled	99.0	25	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
64	c3bdnB_	Alignment	not modelled	99.0	19	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
65	c4ghjA_	Alignment	not modelled	98.9	22	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
66	d2a6ca1	Alignment	not modelled	98.9	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
67	c2grmB_	Alignment	not modelled	98.9	31	PDB header: transcription Chain: B: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/icf10 complex
68	c3t76A_	Alignment	not modelled	98.9	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
69	c2wusR_	Alignment	not modelled	98.9	20	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
70	c2axzC_	Alignment	not modelled	98.9	31	PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
71	c3fymA_	Alignment	not modelled	98.8	15	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
72	c2qfcB_	Alignment	not modelled	98.8	22	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
73	c5j9iH_	Alignment	not modelled	98.8	12	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
74	c4gqmA_	Alignment	not modelled	98.8	15	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
75	c2fjrB_	Alignment	not modelled	98.8	13	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
76	c3fmyA_	Alignment	not modelled	98.7	16	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)
77	c5d50I_	Alignment	not modelled	98.7	14	PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
78	d2ppxa1	Alignment	not modelled	98.7	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
79	c2ppxA_	Alignment	not modelled	98.7	14	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
80	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
81	c3gn5B_	Alignment	not modelled	98.7	17	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa

81	c3gnB	Alignment	not modelled	98.4	17	(ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
82	c6fkqC	Alignment	not modelled	98.2	17	PDB header: toxin Chain: C; PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
83	c3r1fO	Alignment	not modelled	97.9	25	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
84	c2mqkA	Alignment	not modelled	97.6	23	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
85	d1dwka1	Alignment	not modelled	96.9	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
86	c3bd1B	Alignment	not modelled	96.7	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	c2lv1J	Alignment	not modelled	96.6	14	PDB header: lyase Chain: J; PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
88	d2bnma1	Alignment	not modelled	96.6	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
89	d1nera	Alignment	not modelled	96.6	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
90	c2auwB	Alignment	not modelled	96.1	18	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
91	c5u57B	Alignment	not modelled	95.4	10	PDB header: oxidoreductase Chain: B; PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
92	d1lcda	Alignment	not modelled	95.4	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
93	d2hsga1	Alignment	not modelled	95.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
94	d1lc8a2	Alignment	not modelled	95.1	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
95	c5j2yA	Alignment	not modelled	95.0	20	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
96	d2bjca1	Alignment	not modelled	95.0	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
97	d2awia1	Alignment	not modelled	95.0	33	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: PrgX N-terminal domain-like
98	c3kxD	Alignment	not modelled	94.9	17	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
99	c5sysA	Alignment	not modelled	94.7	10	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
100	c1efaA	Alignment	not modelled	94.7	13	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
101	d1efaa1	Alignment	not modelled	94.6	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
102	c2lcvA	Alignment	not modelled	94.3	14	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
103	d1qpza1	Alignment	not modelled	94.0	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
104	c1bdhA	Alignment	not modelled	93.9	22	PDB header: transcription/dna Chain: A; PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
105	c2l8nA	Alignment	not modelled	93.9	13	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
106	c1lbgB	Alignment	not modelled	93.9	13	PDB header: PDB COMPND:
107	c2k9qB	Alignment	not modelled	93.8	13	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.

108	c4la3B_	Alignment	not modelled	93.7	13	PDB header: lyase Chain: B: PDB Molecule: dimethylsulphoniopropionate (dmsp) lyase dddq; PDBTitle: crystal structure of dimethylsulphoniopropionate (dmsp) lyase dddq2 y131a in complex with dmsp
109	d2auwa1	Alignment	not modelled	93.7	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
110	d1uxca_	Alignment	not modelled	93.6	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LacI-like bacterial regulator
111	c1ic8B_	Alignment	not modelled	93.6	16	PDB header: transcription/dna Chain: B: PDB Molecule: hepatocyte nuclear factor 1-alpha; PDBTitle: hepatocyte nuclear factor 1a bound to dna : mody3 gene product
112	d1uxda_	Alignment	not modelled	93.6	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LacI-like bacterial regulator
113	c3h5tA_	Alignment	not modelled	93.1	15	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
114	c1zvva_	Alignment	not modelled	93.0	16	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
115	d1au7a2	Alignment	not modelled	92.5	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
116	c3vwbA_	Alignment	not modelled	92.4	29	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 icsb promoter
117	c3l1pA_	Alignment	not modelled	92.3	20	PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex
118	d1e3oc2	Alignment	not modelled	92.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
119	c2h8rA_	Alignment	not modelled	92.0	16	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
120	c4go1A_	Alignment	not modelled	91.9	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.