



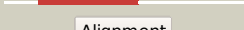











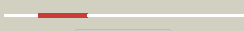





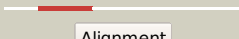
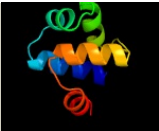
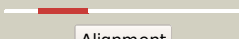











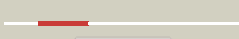



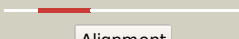



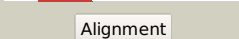
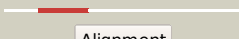
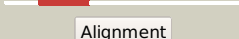



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0023 (-) _27595_28365
Date	Tue Jul 23 14:50:05 BST 2019
Unique Job ID	d22fb7ff9cf8fcf4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y9qA_	 Alignment		99.7	32	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
2	c2bnoA_	 Alignment		99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
3	c3pxpA_	 Alignment		99.6	19	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
4	c3ivpD_	 Alignment		99.6	14	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.
5	c3f52A_	 Alignment		99.6	34	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
6	c5woqA_	 Alignment		99.6	25	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
7	d1rioA_	 Alignment		99.6	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
8	c3f6wE_	 Alignment		99.6	20	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
9	c3op9A_	 Alignment		99.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
10	c3eusB_	 Alignment		99.6	15	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
11	c6b9tH_	 Alignment		99.6	11	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

12	c3clcC	 Alignment		99.6	18	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.espl396i tetramer in complex with its natural 35 base-pair operator
13	c2ewtA	 Alignment		99.6	23	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
14	c3vk0B	 Alignment		99.6	24	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhft from2 heisseria
15	c2mezA	 Alignment		99.5	28	PDB header: rna binding protein Chain: A: PDB Molecule: multiprotein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaean mbf1 on ribosomes suggests role as2 recruitment factor
16	c5fd4B	 Alignment		99.5	27	PDB header: transcription regulator Chain: B: PDB Molecule: comr; PDBTitle: crystal structure of comr from streptococcus suis
17	c6b9rD	 Alignment		99.5	20	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
18	c4pu4C	 Alignment		99.5	31	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)
19	d2b5aa1	 Alignment		99.5	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
20	c1b0nA	 Alignment		99.5	31	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
21	c5jubA	 Alignment	not modelled	99.5	21	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.
22	c2kpiA	 Alignment	not modelled	99.5	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
23	d1adra	 Alignment	not modelled	99.5	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
24	d2icta1	 Alignment	not modelled	99.5	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
25	c3kxaD	 Alignment	not modelled	99.5	27	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
26	d1y9qa1	 Alignment	not modelled	99.5	32	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
27	c2ebyA	 Alignment	not modelled	99.5	18	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
28	c4mcxE	 Alignment	not modelled	99.5	26	PDB header: toxin Chain: E: PDB Molecule: antidote protein; PDBTitle: p. vulgaris higba structure, crystal form 2
						Fold: lambda repressor-like DNA-binding domains

29	d1y7ya1	Alignment	not modelled	99.5	25	Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
30	d2r1jl1	Alignment	not modelled	99.5	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
31	d2ofya1	Alignment	not modelled	99.5	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
32	d1x57a1	Alignment	not modelled	99.5	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
33	d1lmb3_	Alignment	not modelled	99.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
34	c3cecA_	Alignment	not modelled	99.5	22	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
35	c3dnvB_	Alignment	not modelled	99.5	22	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
36	c3lisB_	Alignment	not modelled	99.5	15	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
37	d1llib_	Alignment	not modelled	99.5	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
38	c5uk3J_	Alignment	not modelled	99.5	15	PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
39	c3bs3A_	Alignment	not modelled	99.5	20	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
40	c3mIfC_	Alignment	not modelled	99.5	15	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
41	c3trbA_	Alignment	not modelled	99.5	21	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
42	c3zhiA_	Alignment	not modelled	99.5	13	PDB header: transcription Chain: A: PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage tp901-1
43	c3omtA_	Alignment	not modelled	99.5	8	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.
44	c4rykA_	Alignment	not modelled	99.5	19	PDB header: dna binding protein Chain: A: PDB Molecule: lmo0325 protein; PDBTitle: crystal structure of a putative transcriptional regulator from2 listeria monocytogenes egd-e
45	c6f8sA_	Alignment	not modelled	99.5	21	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
46	d1b0na2	Alignment	not modelled	99.5	31	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
47	d2o38a1	Alignment	not modelled	99.4	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
48	c2o38A_	Alignment	not modelled	99.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
49	d2a6ca1	Alignment	not modelled	99.4	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
50	d1r69a_	Alignment	not modelled	99.4	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
51	c2jvIA_	Alignment	not modelled	99.4	25	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
52	c3b7hA_	Alignment	not modelled	99.4	18	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
53	c5d4zF_	Alignment	not modelled	99.4	13	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
54	c4yv9C_	Alignment	not modelled	99.4	24	PDB header: dna binding protein/inhibitor Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of streptococcus dysgalactiae shp pheromone2 receptor rgg2
55	d1sq8a_	Alignment	not modelled	99.4	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains

					Family: Phage repressors
56	d2croa_	Alignment	not modelled	99.4	16 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
57	c4o8bA_	Alignment	not modelled	99.4	20 PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr
58	c2ef8A_	Alignment	not modelled	99.4	19 PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
59	c4ghjA_	Alignment	not modelled	99.4	21 PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
60	c2xcjB_	Alignment	not modelled	99.4	24 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
61	d1lutx_	Alignment	not modelled	99.4	24 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
62	c4ybaA_	Alignment	not modelled	99.4	25 PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
63	c2grmB_	Alignment	not modelled	99.4	17 PDB header: transcription Chain: B: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/icf10 complex
64	c2wusR_	Alignment	not modelled	99.3	25 PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
65	c3bdnB_	Alignment	not modelled	99.3	13 PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
66	c2axzC_	Alignment	not modelled	99.3	17 PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
67	c3t76A_	Alignment	not modelled	99.3	20 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
68	c3fymA_	Alignment	not modelled	99.3	17 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
69	c3qyxD_	Alignment	not modelled	99.3	25 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
70	c2qfcB_	Alignment	not modelled	99.3	23 PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
71	c5j9iH_	Alignment	not modelled	99.2	23 PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
72	d2ppxa1	Alignment	not modelled	99.2	15 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
73	c2ppxA_	Alignment	not modelled	99.2	15 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
74	c4gqmA_	Alignment	not modelled	99.2	27 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	c3fmyA_	Alignment	not modelled	99.2	17 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)
76	c5jaaB_	Alignment	not modelled	99.2	23 PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
77	c5d50I_	Alignment	not modelled	99.1	9 PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
78	c2fjrB_	Alignment	not modelled	99.0	11 PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
79	c3gn5B_	Alignment	not modelled	98.9	17 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)
80	c6fkqC_	Alignment	not modelled	98.7	9 PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
81	c2mqkA_	Alignment	not modelled	98.4	18 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

82	c3r1fO	Alignment	not modelled	98.1	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
83	d1dwka1	Alignment	not modelled	97.8	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
84	c2iv1J	Alignment	not modelled	97.7	20	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
85	d2hsga1	Alignment	not modelled	97.4	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
86	d1nera	Alignment	not modelled	97.3	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
87	c3bd1B	Alignment	not modelled	97.3	21	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	d1lcda	Alignment	not modelled	97.3	30	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	97.2	30	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	d2bjca1	Alignment	not modelled	97.2	30	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
91	d2bnma1	Alignment	not modelled	97.2	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
92	c5j2yA	Alignment	not modelled	97.1	19	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
93	c1lbgB	Alignment	not modelled	97.1	30	PDB header: PDB COMPND:
94	d1ic8a2	Alignment	not modelled	97.1	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
95	c3kxD	Alignment	not modelled	97.1	27	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
96	d1efaa1	Alignment	not modelled	97.0	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
97	c2auwB	Alignment	not modelled	97.0	17	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
98	c5sysA	Alignment	not modelled	97.0	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
99	d1qpza1	Alignment	not modelled	96.9	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
100	c1bdhA	Alignment	not modelled	96.9	24	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
101	c2lcvA	Alignment	not modelled	96.9	27	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
102	c2l8nA	Alignment	not modelled	96.8	26	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
103	c1zvva	Alignment	not modelled	96.7	25	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
104	c3h5tA	Alignment	not modelled	96.7	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
105	d1luxca	Alignment	not modelled	96.7	34	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
106	c4la3B	Alignment	not modelled	96.6	15	PDB header: lyase Chain: B: PDB Molecule: dimethylsulphoniopropionate (dmsp) lyase dddq; PDBTitle: crystal structure of dimethylsulphoniopropionate (dmsp) lyase dddq2 y131a in complex with dmsp
107	d1luxda	Alignment	not modelled	96.5	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
108	d2awia1	Alignment	not modelled	96.4	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains

						Family: PrgX N-terminal domain-like
109	c4go1A	Alignment	not modelled	96.3	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator Isrr; PDBTitle: crystal structure of full length transcription repressor Isrr from e.2 coli.
110	d1au7a2	Alignment	not modelled	96.2	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
111	c5u57B	Alignment	not modelled	96.2	20	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
112	d1e3oc2	Alignment	not modelled	96.1	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
113	c1ic8B	Alignment	not modelled	96.0	7	PDB header: transcription/dna Chain: B: PDB Molecule: hepatocyte nuclear factor 1-alpha; PDBTitle: hepatocyte nuclear factor 1a bound to dna : mody3 gene product
114	c3l1pA	Alignment	not modelled	96.0	21	PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex
115	c1au7B	Alignment	not modelled	96.0	20	PDB header: transcription/dna Chain: B: PDB Molecule: protein pit-1; PDBTitle: pit-1 mutant/dna complex
116	d1r71a	Alignment	not modelled	95.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
117	c3d1nK	Alignment	not modelled	95.4	19	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
118	c3k2zA	Alignment	not modelled	95.3	13	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
119	c3vwba	Alignment	not modelled	95.1	17	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 ic5b promoter
120	d2auwa1	Alignment	not modelled	95.1	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like