


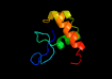


















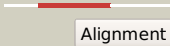

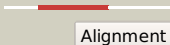

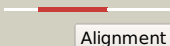







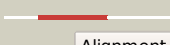







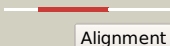
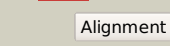
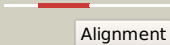
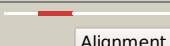

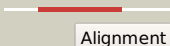


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2308 (-) _2580429_2581145
Date	Mon Aug 5 13:25:45 BST 2019
Unique Job ID	b20c98d4c5398055

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5af3A_	 Alignment		100.0	23	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
2	d2ga1a1	 Alignment		99.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like
3	c4r24B_	 Alignment		98.6	16	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
4	c4r4eA_	 Alignment		98.6	14	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
5	c5c8eC_	 Alignment		98.2	21	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
6	c2vz4A_	 Alignment		98.1	16	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
7	c2zhhA_	 Alignment		98.1	15	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
8	d1r8ea1	 Alignment		98.1	14	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
9	c3gp4B_	 Alignment		98.0	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
10	c2jmlA_	 Alignment		98.0	14	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
11	d1r8da_	 Alignment		98.0	12	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators

12	c3gpvA	 Alignment		98.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
13	c3hh0C	 Alignment		98.0	10	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
14	c5gpeB	 Alignment		98.0	12	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, merr-family; PDBTitle: crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
15	c5i44E	 Alignment		97.9	14	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
16	d1q06a	 Alignment		97.8	15	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
17	c5xqlA	 Alignment		97.7	10	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
18	c3d6zA	 Alignment		97.7	14	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrr bound to dna and rhodamine
19	c3qaoA	 Alignment		97.7	12	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
20	c3ucsB	 Alignment		97.5	11	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
21	c5scrA	 Alignment	not modelled	97.3	12	PDB header: metal binding protein Chain: A: PDB Molecule: mercuric resistance operon regulatory protein; PDBTitle: crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
22	c6amaO	 Alignment	not modelled	96.7	19	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
23	c2dg6A	 Alignment	not modelled	96.1	23	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
24	c4j2nB	 Alignment	not modelled	95.0	8	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
25	c2kfsA	 Alignment	not modelled	94.7	19	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
26	c4j2nA	 Alignment	not modelled	94.3	13	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
27	d2jn6a1	 Alignment	not modelled	92.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
28	c1hlvA	 Alignment	not modelled	90.4	9	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna

29	c2ev2B	Alignment	not modelled	89.2	8	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cylcase rv1264, at ph 8.5
30	c1u78A	Alignment	not modelled	89.2	8	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
31	c4ua2B	Alignment	not modelled	88.4	7	PDB header: dna binding protein Chain: B: PDB Molecule: regulatory protein; PDBTitle: crystal structure of dual function transcriptional regulator merr from2 bacillus megaterium mb1
32	c2rn7A	Alignment	not modelled	86.7	18	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
33	c5ydcA	Alignment	not modelled	84.4	9	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator rv1828; PDBTitle: crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis
34	c6fkqC	Alignment	not modelled	83.6	26	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
35	c5j9iH	Alignment	not modelled	83.5	15	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
36	c2ppxA	Alignment	not modelled	82.5	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
37	d2ppxA1	Alignment	not modelled	82.5	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
38	d2coba1	Alignment	not modelled	81.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
39	c3op9A	Alignment	not modelled	80.3	12	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
40	c2kpiA	Alignment	not modelled	80.1	30	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
41	d1bw6a	Alignment	not modelled	79.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
42	d1adra	Alignment	not modelled	79.7	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
43	c2mqkA	Alignment	not modelled	79.6	26	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
44	c3fmyA	Alignment	not modelled	79.0	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)
45	c3omtA	Alignment	not modelled	76.0	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.
46	c5jaaB	Alignment	not modelled	76.0	15	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
47	d1b0na2	Alignment	not modelled	74.4	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
48	c5d50l	Alignment	not modelled	74.1	13	PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
49	d2a6ca1	Alignment	not modelled	73.5	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
50	c1b0nA	Alignment	not modelled	73.3	11	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
51	d1utxa	Alignment	not modelled	73.3	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
52	d1hlva1	Alignment	not modelled	73.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
53	d1y9qa1	Alignment	not modelled	73.1	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
54	c3b7hA	Alignment	not modelled	72.6	22	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11

55	d2b5aa1	Alignment	not modelled	72.3	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
56	c4o8bA	Alignment	not modelled	72.3	24	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr
57	c3clcC	Alignment	not modelled	71.9	4	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
58	c5d4zF	Alignment	not modelled	71.8	15	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
59	d1lib	Alignment	not modelled	71.3	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
60	c3vk0B	Alignment	not modelled	71.2	12	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 heisseria
61	c2ebyA	Alignment	not modelled	71.1	17	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
62	c3f52A	Alignment	not modelled	71.0	13	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
63	c3bd1B	Alignment	not modelled	70.9	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
64	c3gn5B	Alignment	not modelled	70.5	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)
65	c4ybaA	Alignment	not modelled	69.8	15	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
66	d1etxa	Alignment	not modelled	69.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
67	d1x57a1	Alignment	not modelled	69.7	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
68	c5woqA	Alignment	not modelled	69.7	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
69	d1fipa	Alignment	not modelled	69.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
70	d1umqa	Alignment	not modelled	69.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
71	c1umqA	Alignment	not modelled	69.5	14	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
72	d1r69a	Alignment	not modelled	69.5	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
73	c3t76A	Alignment	not modelled	69.3	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
74	c2xcjB	Alignment	not modelled	69.3	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
75	c3trbA	Alignment	not modelled	69.2	10	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
76	c2fjrB	Alignment	not modelled	69.1	0	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
77	d1lmb3	Alignment	not modelled	69.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
78	c6paxA	Alignment	not modelled	68.8	17	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
79	d2r1jl1	Alignment	not modelled	68.8	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
80	c3bs3A	Alignment	not modelled	68.8	15	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

81	c3f6wE	Alignment	not modelled	68.0	19	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
82	c3ezfA	Alignment	not modelled	67.6	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
83	c3m1fC	Alignment	not modelled	67.2	12	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
84	c3dnnB	Alignment	not modelled	66.9	23	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
85	d1y7ya1	Alignment	not modelled	66.7	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
86	d1i3ja	Alignment	not modelled	66.6	10	Fold: DNA-binding domain of intron-encoded endonucleases Superfamily: DNA-binding domain of intron-encoded endonucleases Family: DNA-binding domain of intron-encoded endonucleases
87	d2croa	Alignment	not modelled	65.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
88	c4ghjA	Alignment	not modelled	64.5	22	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
89	c3eusB	Alignment	not modelled	64.5	12	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
90	c2l8nA	Alignment	not modelled	64.1	12	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
91	c2lcvA	Alignment	not modelled	63.4	12	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
92	d1ntca	Alignment	not modelled	62.3	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
93	c4l5eA	Alignment	not modelled	62.2	16	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
94	d2icta1	Alignment	not modelled	62.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
95	d1sq8a	Alignment	not modelled	61.7	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
96	c3cecA	Alignment	not modelled	61.7	18	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
97	c4fcyA	Alignment	not modelled	61.4	16	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
98	d1pdnc	Alignment	not modelled	61.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
99	c2o38A	Alignment	not modelled	61.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
100	d2o38a1	Alignment	not modelled	61.1	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
101	c2ef8A	Alignment	not modelled	61.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
102	d1rioa	Alignment	not modelled	60.6	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
103	c3e7lD	Alignment	not modelled	60.6	21	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
104	d2ofya1	Alignment	not modelled	60.0	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
105	d1lcda	Alignment	not modelled	59.5	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Gair/Laci-like bacterial regulator
106	c6f8sA	Alignment	not modelled	59.2	14	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
107	c1v0aA	Alignment	not modelled	58.9	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth 3 family;

107	c1y2qA_	Alignment	not modelled	58.9	19	PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
108	d2hsqa1	Alignment	not modelled	57.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
109	c2wusR_	Alignment	not modelled	57.1	13	PDB header: structural protein Chain: R; PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
110	c3zhiA_	Alignment	not modelled	56.7	16	PDB header: transcription Chain: A; PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage tp901-1
111	d1luxca_	Alignment	not modelled	56.5	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
112	d1qpza1	Alignment	not modelled	56.4	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
113	d2bjca1	Alignment	not modelled	53.3	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
114	c2jvIA_	Alignment	not modelled	52.8	35	PDB header: transcription Chain: A; PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
115	c3kxaD_	Alignment	not modelled	52.8	26	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
116	c3qyxD_	Alignment	not modelled	52.6	21	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
117	c5chhA_	Alignment	not modelled	51.7	16	PDB header: transcription Chain: A; PDB Molecule: arac family transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
118	c2m8gX_	Alignment	not modelled	51.6	26	PDB header: transcription Chain: X; PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
119	c1z4hA_	Alignment	not modelled	51.1	9	PDB header: protein binding, dna binding protein Chain: A; PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
120	c1g2hA_	Alignment	not modelled	50.4	6	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae