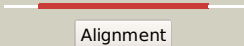

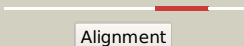

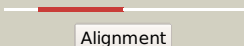





















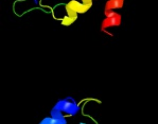






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2018 (-)_2265288_2266007
Date	Mon Aug 5 13:25:12 BST 2019
Unique Job ID	2b15cfe35f837852

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5af3A_	 Alignment		100.0	100	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
2	d2ga1a1	 Alignment		99.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like
3	c4r4eA_	 Alignment		98.9	13	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
4	c4r24B_	 Alignment		98.8	9	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
5	c2zhhA_	 Alignment		98.5	18	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
6	c2vz4A_	 Alignment		98.5	18	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	d1r8da_	 Alignment		98.5	15	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
8	c5c8eC_	 Alignment		98.5	15	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
9	c3hh0C_	 Alignment		98.5	12	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
10	c3gpvA_	 Alignment		98.5	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
11	c5i44E_	 Alignment		98.4	13	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form

12	c2jmlA_	Alignment		98.4	12	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
13	c3gp4B_	Alignment		98.4	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
14	d1r8ea1	Alignment		98.4	16	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
15	d1q06a_	Alignment		98.3	8	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
16	c5gpeB_	Alignment		98.2	11	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)
17	c3qaoA_	Alignment		98.2	13	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
18	c5xqlA_	Alignment		97.8	20	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
19	c3d6zA_	Alignment		97.8	16	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
20	c3ucsB_	Alignment		97.7	15	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
21	c5crlA_	Alignment	not modelled	97.6	19	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	97.1	27	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	97.1	26	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	96.1	15	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
25	c4j2nA_	Alignment	not modelled	95.8	15	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
26	c2ev2B_	Alignment	not modelled	95.6	13	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyl cyclase rv1264, at ph 8.5
27	c1u78A_	Alignment	not modelled	94.5	18	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
28	c4ua2B_	Alignment	not modelled	93.5	11	PDB header: dna binding protein Chain: B: PDB Molecule: regulatory protein; PDBTitle: crystal structure of dual function transcriptional regulator merr from2 bacillus megaterium mb1
						PDB header: gene regulation/dna

29	c6paxA	Alignment	not modelled	93.1	13	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
30	d2jn6a1	Alignment	not modelled	92.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
31	c2kfsA	Alignment	not modelled	90.9	16	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
32	c2rn7A	Alignment	not modelled	90.6	16	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	c1hlvA	Alignment	not modelled	89.2	19	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
34	d1pdnc	Alignment	not modelled	88.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
35	c5ydcA	Alignment	not modelled	86.8	11	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
36	c5j9iH	Alignment	not modelled	86.5	21	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
37	c6fkgC	Alignment	not modelled	86.1	22	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
38	d2coba1	Alignment	not modelled	85.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
39	c2ppxA	Alignment	not modelled	85.4	29	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
40	d2ppxa1	Alignment	not modelled	85.4	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
41	c3fmyA	Alignment	not modelled	83.1	22	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)
42	c3op9A	Alignment	not modelled	82.9	18	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
43	d1bw6a	Alignment	not modelled	82.7	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
44	c2kpiA	Alignment	not modelled	82.7	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
45	c5jaaB	Alignment	not modelled	82.6	21	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
46	d1adra	Alignment	not modelled	81.7	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
47	c2mqkA	Alignment	not modelled	81.1	9	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
48	d1b0na2	Alignment	not modelled	80.7	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
49	c3omtA	Alignment	not modelled	79.0	14	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.
50	c3ezfA	Alignment	not modelled	77.9	5	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
51	d1x57a1	Alignment	not modelled	77.6	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
52	d1lutx	Alignment	not modelled	77.3	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
53	d1k78a1	Alignment	not modelled	77.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
54	c3clcC	Alignment	not modelled	77.0	7	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

55	d1fipa_	Alignment	not modelled	76.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
56	d1hlva1	Alignment	not modelled	76.6	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
57	d1letxa	Alignment	not modelled	76.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
58	d2b5aa1	Alignment	not modelled	76.0	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
59	c3gn5B_	Alignment	not modelled	75.9	22	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)
60	c3f52A_	Alignment	not modelled	75.5	26	PDB header: transcription activator Chain: A; PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
61	c2elhA_	Alignment	not modelled	75.4	33	PDB header: dna binding protein Chain: A; PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
62	c5d4zF_	Alignment	not modelled	75.1	7	PDB header: dna binding protein Chain: F; PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
63	d1y9qa1	Alignment	not modelled	75.0	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
64	d1llib_	Alignment	not modelled	74.8	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
65	c3vk0B_	Alignment	not modelled	74.8	13	PDB header: dna binding protein Chain: B; PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 neisseria
66	c4ybaA_	Alignment	not modelled	74.6	18	PDB header: gene regulation Chain: A; PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
67	c3m1fC_	Alignment	not modelled	74.4	14	PDB header: transcription regulator Chain: C; PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
68	c5d50I_	Alignment	not modelled	74.2	13	PDB header: dna binding protein Chain: I; PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
69	d1umqa_	Alignment	not modelled	74.0	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
70	c1umqA_	Alignment	not modelled	74.0	27	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
71	c1b0nA_	Alignment	not modelled	73.6	22	PDB header: transcription regulator Chain: A; PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
72	c5woqA_	Alignment	not modelled	73.3	30	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
73	c3b7hA_	Alignment	not modelled	73.3	14	PDB header: structural protein Chain: A; PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
74	c2xcjB_	Alignment	not modelled	73.0	21	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	c2ebyA_	Alignment	not modelled	72.5	17	PDB header: transcription Chain: A; PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
76	d1r69a_	Alignment	not modelled	72.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
77	d1ntca_	Alignment	not modelled	72.4	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
78	c3dnvB_	Alignment	not modelled	72.3	14	PDB header: transcription/dna Chain: B; PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
79	d6paxa1	Alignment	not modelled	72.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
80	d2r1j1_	Alignment	not modelled	72.2	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
						PDB header: dna binding protein

81	c3trbA_	Alignment	not modelled	72.1	11	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
82	c3bs3A_	Alignment	not modelled	71.4	11	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
83	c3f6wE_	Alignment	not modelled	71.3	17	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
84	c2fjrB_	Alignment	not modelled	71.1	4	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
85	d2a6ca1	Alignment	not modelled	71.1	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
86	c3t76A_	Alignment	not modelled	71.0	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
87	c4ghjA_	Alignment	not modelled	70.6	22	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
88	c4o8bA_	Alignment	not modelled	70.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr
89	d1y7ya1	Alignment	not modelled	69.8	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
90	d1lmb3_	Alignment	not modelled	69.7	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
91	d1sq8a_	Alignment	not modelled	69.0	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
92	d1j9ia_	Alignment	not modelled	68.8	18	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
93	d1i3ja_	Alignment	not modelled	68.7	14	Fold: DNA-binding domain of intron-encoded endonucleases Superfamily: DNA-binding domain of intron-encoded endonucleases Family: DNA-binding domain of intron-encoded endonucleases
94	d2croa_	Alignment	not modelled	68.3	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
95	c3e7ID_	Alignment	not modelled	68.1	13	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
96	c2gm4B_	Alignment	not modelled	68.0	9	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimera bound to2 cleaved dna
97	c3eusB_	Alignment	not modelled	67.3	21	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
98	c2ef8A_	Alignment	not modelled	67.2	9	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
99	d1rioa_	Alignment	not modelled	66.2	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
100	d2ofya1	Alignment	not modelled	65.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
101	d2icta1	Alignment	not modelled	65.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
102	c1y9qA_	Alignment	not modelled	64.6	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
103	c5y6iB_	Alignment	not modelled	64.3	9	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of pseudomonas aeruginosa hmgr
104	c3cecA_	Alignment	not modelled	64.1	23	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
105	c2wusR_	Alignment	not modelled	64.1	26	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
106	c6f8sA_	Alignment	not modelled	63.0	23	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
107	d1uxca_	Alignment	not modelled	63.0	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LacI-like bacterial regulator

108	c2l8nA_	Alignment	not modelled	62.9	15	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
109	c2o0yB_	Alignment	not modelled	62.4	17	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
110	c2lcvA_	Alignment	not modelled	62.4	16	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	c3r4kD_	Alignment	not modelled	62.2	13	PDB header: dna binding protein Chain: D: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
112	d1lcda_	Alignment	not modelled	62.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
113	d2o38a1	Alignment	not modelled	61.9	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
114	c2o38A_	Alignment	not modelled	61.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
115	c2o8xA_	Alignment	not modelled	61.5	18	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
116	d1qpza1	Alignment	not modelled	61.3	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
117	c3kxαD_	Alignment	not modelled	61.1	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
118	c3qyxD_	Alignment	not modelled	60.7	26	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
119	d1dpua_	Alignment	not modelled	60.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of RPA32
120	c1dpuA_	Alignment	not modelled	60.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: replication protein a (rpa32) c-terminal domain; PDBTitle: solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)