



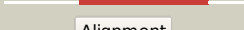

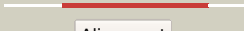









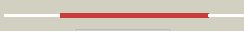







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2657c (-)_2979059_2979319
Date	Wed Aug 7 12:50:30 BST 2019
Unique Job ID	c4ccb6db4a01293a

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j2nA_	 Alignment		99.6	42	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
2	c4j2nB_	 Alignment		99.6	42	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
3	c6amaO_	 Alignment		99.1	25	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bidc-smea-ssfa complex to2 3.09 angstrom
4	c1z4hA_	 Alignment		99.1	10	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
5	c1y6uA_	 Alignment		98.8	19	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
6	c2kfsA_	 Alignment		98.2	22	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
7	c5i44E_	 Alignment		98.1	17	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
8	c4r24B_	 Alignment		98.1	18	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
9	c4r4eA_	 Alignment		98.0	17	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
10	c3gpvA_	 Alignment		98.0	17	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	c2zhhA_	 Alignment		98.0	19	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr

12	c5c8eC_	Alignment		97.9	16	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to adenosylcobalamin and a 26-bp dna segment
13	c2vz4A_	Alignment		97.8	23	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
14	d1r8ea1	Alignment		97.7	14	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
15	d1r8da_	Alignment		97.6	13	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
16	d1q06a_	Alignment		97.6	17	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
17	c3gp4B_	Alignment		97.5	20	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
18	c3qaoA_	Alignment		97.5	23	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
19	c3hh0C_	Alignment		97.5	22	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
20	c2jmlA_	Alignment		97.4	18	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
21	c3ucsB_	Alignment	not modelled	97.3	13	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
22	d1j9ia_	Alignment	not modelled	97.3	19	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
23	c5af3A_	Alignment	not modelled	97.3	20	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
24	c3d6zA_	Alignment	not modelled	96.7	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
25	c5gpeB_	Alignment	not modelled	96.5	18	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)
26	c5crlA_	Alignment	not modelled	96.0	28	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)
27	c4lhfa_	Alignment	not modelled	95.9	20	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
28	d1pm6a_	Alignment	not modelled	95.1	22	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
						PDB header: transcription

29	c5xqlA_	Alignment	not modelled	94.7	19	Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
30	d1j5ya1	Alignment	not modelled	94.6	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
31	d1biaa1	Alignment	not modelled	94.5	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
32	d2jn6a1	Alignment	not modelled	94.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
33	d1umqa_	Alignment	not modelled	94.0	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
34	c1umqA_	Alignment	not modelled	94.0	31	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
35	d1fipa_	Alignment	not modelled	93.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
36	c2rn7A_	Alignment	not modelled	93.6	27	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
37	d1g2ha_	Alignment	not modelled	93.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
38	c1g2ha_	Alignment	not modelled	93.5	12	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
39	d1etxa_	Alignment	not modelled	93.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
40	c1u78A_	Alignment	not modelled	93.0	10	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
41	c6fkgC_	Alignment	not modelled	93.0	19	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
42	c5m7nA_	Alignment	not modelled	92.5	16	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystalldirect automated mounting and cryo-cooling3 technology
43	c2m8gX_	Alignment	not modelled	92.3	28	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
44	d1rh6a_	Alignment	not modelled	92.3	22	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
45	d1ntca_	Alignment	not modelled	92.1	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
46	c3eqxB_	Alignment	not modelled	92.0	16	PDB header: dna binding protein Chain: B: PDB Molecule: fic domain containing transcriptional regulator; PDBTitle: crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
47	c3bd1B_	Alignment	not modelled	92.0	27	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
48	c4l5eA_	Alignment	not modelled	91.8	20	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
49	c1ojlD_	Alignment	not modelled	91.7	27	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
50	c3e7lD_	Alignment	not modelled	91.6	15	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
51	d1etob_	Alignment	not modelled	91.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
52	c2ev2B_	Alignment	not modelled	91.4	16	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
53	d2ao9a1	Alignment	not modelled	90.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
54	c6i05B_	Alignment	not modelled	90.0	21	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsr;

54	c0j0zB	Alignment	not modelled	90.0	41	PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
55	c40mzG	Alignment	not modelled	89.9	10	PDB header: transcription Chain: G: PDB Molecule: nolr; PDBTitle: crystal structure of nolr from sinorhizobium fredii
56	c5WayB	Alignment	not modelled	89.9	33	PDB header: transcription Chain: B: PDB Molecule: transcriptional activator; PDBTitle: mgaspn protein, mga regulator from streptococcus pneumoniae
57	c3jthA	Alignment	not modelled	89.8	15	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
58	d1pdnc	Alignment	not modelled	89.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
59	c6j0eB	Alignment	not modelled	89.5	15	PDB header: transcription Chain: B: PDB Molecule: arsenic responsive repressor arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
60	c3ezfA	Alignment	not modelled	89.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
61	c2gm4B	Alignment	not modelled	88.9	17	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
62	c2kpiA	Alignment	not modelled	88.9	19	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
63	c3omtA	Alignment	not modelled	88.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
64	c6paxA	Alignment	not modelled	88.5	21	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
65	c4i2oA	Alignment	not modelled	88.5	34	PDB header: transcription regulator/dna Chain: A: PDB Molecule: fixk2 protein; PDBTitle: the structure of fixk2 from bradyrhizobium japonicum
66	c1j5yA	Alignment	not modelled	87.7	31	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, biotin repressor family; PDBTitle: crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
67	c2oqgA	Alignment	not modelled	87.5	19	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
68	c1r22B	Alignment	not modelled	87.5	10	PDB header: transcription repressor Chain: B: PDB Molecule: transcriptional repressor smtb; PDBTitle: crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
69	c3h5tA	Alignment	not modelled	87.2	23	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
70	d1adra	Alignment	not modelled	87.1	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
71	d1r1ua	Alignment	not modelled	87.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
72	d2d1ha1	Alignment	not modelled	87.1	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
73	c2dg6A	Alignment	not modelled	86.9	17	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)
74	d2ppxa1	Alignment	not modelled	86.8	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
75	c2ppxA	Alignment	not modelled	86.8	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
76	c2fjrB	Alignment	not modelled	86.7	8	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
77	c5j9iH	Alignment	not modelled	86.7	15	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
78	d1jhfa1	Alignment	not modelled	86.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
79	d1y9qa1	Alignment	not modelled	86.6	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain

80	c2ebyA	Alignment	not modelled	86.6	32	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
81	c3t76A	Alignment	not modelled	86.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
82	c5fgmA	Alignment	not modelled	86.6	21	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
83	c2xcjB	Alignment	not modelled	86.6	11	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
84	d1r1ta	Alignment	not modelled	86.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
85	d1rzsa	Alignment	not modelled	86.4	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
86	c3bs3A	Alignment	not modelled	86.4	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
87	c4r6iA	Alignment	not modelled	86.3	41	PDB header: transcription Chain: A: PDB Molecule: anthrax toxin expression trans-acting positive regulator; PDBTitle: atxa protein, a virulence regulator from bacillus anthracis.
88	c2r0qF	Alignment	not modelled	86.1	30	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
89	c2zwcA	Alignment	not modelled	86.1	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, fnr/crp family; PDBTitle: crystal structure of ttha1359, a transcriptional regulator,2 crp/fnr family from thermus thermophilus hb8
90	d2coha1	Alignment	not modelled	85.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
91	c2lkpB	Alignment	not modelled	85.8	23	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr
92	d1x57a1	Alignment	not modelled	85.7	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
93	c2zkzC	Alignment	not modelled	85.5	17	PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
94	c5jaaB	Alignment	not modelled	85.3	14	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higba2 toxin-antitoxin complex
95	d1r69a	Alignment	not modelled	84.7	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
96	d2bjca1	Alignment	not modelled	84.6	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
97	c2o8xA	Alignment	not modelled	84.6	21	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
98	c3cuoB	Alignment	not modelled	84.5	13	PDB header: transcription regulator Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator ygav; PDBTitle: crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
99	c3vk0B	Alignment	not modelled	84.5	11	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhf from2 neisseria
100	c2kkoB	Alignment	not modelled	84.5	19	PDB header: dna binding protein Chain: B: PDB Molecule: possible transcriptional regulatory protein PDBTitle: solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
101	d1xsva	Alignment	not modelled	84.4	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
102	c3clcC	Alignment	not modelled	84.4	11	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
103	c3iwfA	Alignment	not modelled	84.3	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
104	c3op9A	Alignment	not modelled	84.3	26	PDB header: transcription regulator Chain: A: PDB Molecule: pi0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua

105	d1luxca_	Alignment	not modelled	84.3	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LacI-like bacterial regulator
106	d1utxa_	Alignment	not modelled	84.3	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
107	c3pqkD_	Alignment	not modelled	84.2	13	PDB header: transcription Chain: D: PDB Molecule: biofilm growth-associated repressor; PDBTitle: crystal structure of the transcriptional repressor bigr from xylella2 fastidiosia
108	c3mzyA_	Alignment	not modelled	84.1	18	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
109	d1y7ya1	Alignment	not modelled	83.9	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
110	d2icta1	Alignment	not modelled	83.8	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
111	d1luxda_	Alignment	not modelled	83.8	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LacI-like bacterial regulator
112	c3trbA_	Alignment	not modelled	83.8	18	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
113	c3hugA_	Alignment	not modelled	83.8	18	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigI
114	d1qpza1	Alignment	not modelled	83.7	32	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LacI-like bacterial regulator
115	d1b0na2	Alignment	not modelled	83.6	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
116	d2r1jl1	Alignment	not modelled	83.5	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
117	d1mkma1	Alignment	not modelled	83.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
118	c3fmyA_	Alignment	not modelled	83.2	15	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)
119	c4rfaA_	Alignment	not modelled	83.2	22	PDB header: transcription regulator Chain: A: PDB Molecule: lmo0740 protein; PDBTitle: crystal structure of cyclic nucleotide-binding domain containing2 protein from listeria monocytogenes egd-e
120	c2lfwA_	Alignment	not modelled	83.2	18	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1