


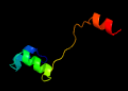
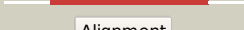

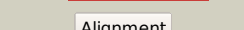

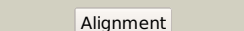





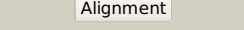

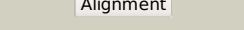

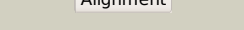

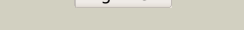








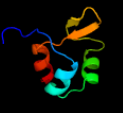











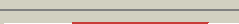
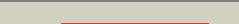







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0500A (-)_591114_591350
Date	Fri Jul 26 01:50:04 BST 2019
Unique Job ID	b3be158293eb2a84

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j2nA_	 Alignment		99.5	31	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
2	c4j2nB_	 Alignment		99.5	31	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
3	c1z4hA_	 Alignment		99.2	16	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
4	c6amaO_	 Alignment		99.1	38	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
5	c1y6uA_	 Alignment		98.9	17	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		98.3	20	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
7	c4r24B_	 Alignment		97.8	12	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
8	c2zhhA_	 Alignment		97.7	24	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxR; PDBTitle: crystal structure of soxR
9	c5i44E_	 Alignment		97.7	29	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
10	c4r4eA_	 Alignment		97.7	19	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
11	c2vz4A_	 Alignment		97.5	17	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

12	c3gpvA_	 Alignment		97.4	15	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	d1q06a_	 Alignment		97.3	7	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
14	c5af3A_	 Alignment		97.3	18	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
15	c5c8eC_	 Alignment		97.3	19	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
16	d1j9ia_	 Alignment		97.3	18	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
17	d1r8da_	 Alignment		97.2	16	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
18	d1r8ea1	 Alignment		97.2	17	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
19	c3gp4B_	 Alignment		97.2	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
20	c3hh0C_	 Alignment		97.1	11	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
21	c3qaoA_	 Alignment	not modelled	97.0	21	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
22	c3ucsB_	 Alignment	not modelled	97.0	17	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
23	c2jmlA_	 Alignment	not modelled	96.7	12	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
24	c5gpeB_	 Alignment	not modelled	96.5	16	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)
25	c5crlA_	 Alignment	not modelled	95.7	23	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)
26	c3d6zA_	 Alignment	not modelled	95.6	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
27	d1pm6a_	 Alignment	not modelled	95.6	40	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
28	c4lhfa_	 Alianment	not modelled	95.0	25	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox;

						PDBTitle: crystal structure of a dna binding protein from phage p2
29	c5xqlA_	Alignment	not modelled	94.9	15	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
30	d1j5ya1	Alignment	not modelled	94.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
31	d1rh6a_	Alignment	not modelled	93.9	38	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
32	d1biaa1	Alignment	not modelled	93.9	4	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
33	c1umqA_	Alignment	not modelled	93.5	19	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
34	d1umqa_	Alignment	not modelled	93.5	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
35	d2jn6a1	Alignment	not modelled	93.4	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cg12762-like
36	c1u78A_	Alignment	not modelled	93.3	9	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
37	c3eqxB_	Alignment	not modelled	92.8	9	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
38	d1fipa_	Alignment	not modelled	92.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
39	c2m8gX_	Alignment	not modelled	92.8	7	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
40	d1etxa_	Alignment	not modelled	92.4	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
41	d1g2ha_	Alignment	not modelled	92.4	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
42	c1g2hA_	Alignment	not modelled	92.4	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
43	c3jthA_	Alignment	not modelled	92.2	17	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
44	c6j05B_	Alignment	not modelled	92.0	21	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
45	d1pdnc_	Alignment	not modelled	91.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
46	c6paxA_	Alignment	not modelled	91.7	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
47	d1ntca_	Alignment	not modelled	91.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
48	c6fkgC_	Alignment	not modelled	91.6	30	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
49	d2d1ha1	Alignment	not modelled	91.4	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
50	c3e7ID_	Alignment	not modelled	91.3	11	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
51	c2rn7A_	Alignment	not modelled	91.2	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
52	c2oqqA_	Alignment	not modelled	91.1	21	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
53	c4omzG_	Alignment	not modelled	91.1	15	PDB header: transcription Chain: G: PDB Molecule: nolr; PDBTitle: crystal structure of nolr from sinorhizobium fredii

54	c4I5eA_	Alignment	not modelled	91.0	8	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
55	d2ao9a1	Alignment	not modelled	90.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
56	c3bd1B_	Alignment	not modelled	90.9	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
57	d1etob_	Alignment	not modelled	90.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
58	c3cuoB_	Alignment	not modelled	90.6	17	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
59	c5m7nA_	Alignment	not modelled	90.5	8	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 crystaldirect automated mounting and cryo-cooling3 technology
60	c6j0eB_	Alignment	not modelled	90.4	28	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
61	c2du9A_	Alignment	not modelled	90.3	20	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
62	c2kvvA_	Alignment	not modelled	90.3	8	PDB header: hydrolase Chain: A: PDB Molecule: putative excisionase; PDBTitle: solution nmr of putative excisionase from klebsiella pneumoniae,2 northeast structural genomics consortium target kpr49
63	c2lkpB_	Alignment	not modelled	90.2	25	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr
64	c2jscB_	Alignment	not modelled	89.6	19	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator rv1994c/mt2050; PDBTitle: nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
65	c1ojlD_	Alignment	not modelled	89.3	14	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
66	c1r22B_	Alignment	not modelled	89.2	17	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
67	d1r1ua_	Alignment	not modelled	88.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
68	c2kkoB_	Alignment	not modelled	88.5	21	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.
69	c2gm4B_	Alignment	not modelled	88.4	22	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
70	d1r1ta_	Alignment	not modelled	88.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
71	c3by6C_	Alignment	not modelled	87.8	23	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
72	c2zkzC_	Alignment	not modelled	87.6	17	PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
73	c1hlvA_	Alignment	not modelled	87.5	8	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
74	c3e6dA_	Alignment	not modelled	87.4	16	PDB header: transcription regulation Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: crystal structure of cprk c200s
75	c3f6oB_	Alignment	not modelled	87.4	23	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
76	c5kvrA_	Alignment	not modelled	87.3	20	PDB header: translation Chain: A: PDB Molecule: pyruvate dehydrogenase complex repressor; PDBTitle: x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073
77	c3f6vA_	Alignment	not modelled	87.3	19	PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: crystal structure of possible transcriptional regulator for

						arsenical2 resistance
78	c4hamA_	Alignment	not modelled	87.3	23	PDB header: transcription Chain: A: PDB Molecule: lmo2241 protein; PDBTitle: crystal structure of transcriptional antiterminator from listeria2 monocytogenes egd-e
79	c2hs5A_	Alignment	not modelled	87.1	24	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator gntr; PDBTitle: structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
80	c4r1hA_	Alignment	not modelled	86.9	25	PDB header: transcription regulator Chain: A: PDB Molecule: lmo0741 protein; PDBTitle: gntr family transcriptional regulator from listeria monocytogenes
81	c2ev2B_	Alignment	not modelled	86.8	10	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
82	c1j5yA_	Alignment	not modelled	86.6	15	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
83	c2dg6A_	Alignment	not modelled	86.5	21	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)
84	c2r0qF_	Alignment	not modelled	86.5	26	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
85	c6az6B_	Alignment	not modelled	86.4	20	PDB header: transcription Chain: B: PDB Molecule: gntr family transcriptional regulator; PDBTitle: streptococcus agalactiae gntr
86	c3bwgA_	Alignment	not modelled	86.0	23	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator yydk; PDBTitle: the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
87	c3eetA_	Alignment	not modelled	85.9	21	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntr-family transcriptional regulator; PDBTitle: crystal structure of putative gntr-family transcriptional2 regulator
88	c5wayB_	Alignment	not modelled	85.8	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional activator; PDBTitle: mgaspn protein, mga regulator from streptococcus pneumoniae
89	c2zwcA_	Alignment	not modelled	85.8	23	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	c4pqjB_	Alignment	not modelled	85.6	18	PDB header: dna binding protein Chain: B: PDB Molecule: truncated replication protein repa; PDBTitle: n-terminal domain of dna binding protein
91	c4egzA_	Alignment	not modelled	85.5	18	PDB header: transcription/dna Chain: A: PDB Molecule: arabinose metabolism transcriptional repressor; PDBTitle: crystal structure of arar(dbd) in complex with operator orr3
92	c3pqkD_	Alignment	not modelled	85.5	15	PDB header: transcription Chain: D: PDB Molecule: biofilm growth-associated repressor; PDBTitle: crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
93	c2kpiA_	Alignment	not modelled	85.3	26	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
94	d1mkma1	Alignment	not modelled	84.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lclR, N-terminal domain
95	d2coha1	Alignment	not modelled	84.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
96	c5duka_	Alignment	not modelled	84.4	22	PDB header: transcription Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
97	c3omtA_	Alignment	not modelled	84.3	21	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.
98	d1ft9a1	Alignment	not modelled	84.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
99	c2xcjB_	Alignment	not modelled	84.1	23	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
100	c3neuA_	Alignment	not modelled	84.1	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
101	c4n0ba_	Alignment	not modelled	84.1	18	PDB header: transcription activator Chain: A: PDB Molecule: hth-type transcriptional regulatory protein gabr; PDBTitle: crystal structure of bacillus subtilis gabr, an autorepressor

						and2 transcriptional activator of gabt PDB header: structural genomics, unknown function Chain: H: PDB Molecule: phage protein; PDBTitle: structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
102	c2ao9H_	Alignment	not modelled	83.8	21	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
103	c2w48D_	Alignment	not modelled	83.7	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
104	d1adra_	Alignment	not modelled	83.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
105	d1ttya_	Alignment	not modelled	83.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
106	d1xsva_	Alignment	not modelled	83.3	25	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
107	c5fgmA_	Alignment	not modelled	83.2	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
108	d1rzsA_	Alignment	not modelled	83.0	22	PDB header: dna binding protein Chain: A: PDB Molecule: chlorophenol reduction gene k; PDBTitle: crystal structure of oxidized cprk in complex with o-2 chlorophenolacetic acid
109	c2h6bA_	Alignment	not modelled	83.0	18	PDB header: transcription Chain: A: PDB Molecule: anthrax toxin expression trans-acting positive regulator; PDBTitle: atxa protein, a virulence regulator from bacillus anthracis.
110	c4r6iA_	Alignment	not modelled	82.9	19	PDB header: transcription Chain: A: PDB Molecule: gntR-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from mycobacterium smegmatis
111	c3f8mA_	Alignment	not modelled	82.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
112	d3bwga1	Alignment	not modelled	82.8	23	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
113	c3bs3A_	Alignment	not modelled	82.3	24	PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg
114	c3hosA_	Alignment	not modelled	82.2	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of a putative transcriptional regulator of the2 crp/fnr family (eubrec_1222) from eubacterium rectale atcc 33656 at3 2.55 a resolution
115	c3dv8A_	Alignment	not modelled	82.1	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, gntR family; PDBTitle: crystal structure of transcriptional regulator (gntR family member)2 from pseudomonas syringae pv. tomato str. dc3000
116	c3c7jA_	Alignment	not modelled	82.0	27	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
117	c2ebyA_	Alignment	not modelled	81.8	28	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
118	c2fjrB_	Alignment	not modelled	81.8	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
119	d1uxca_	Alignment	not modelled	81.6	27	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
120	c3t76A_	Alignment	not modelled	81.4	26	