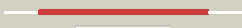























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1657_(argR)_1870849_1871361
Date	Fri Aug 2 13:30:25 BST 2019
Unique Job ID	1e842601cc74ac90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ereD_</a>	 Alignment		100.0	100	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
2	<a href="#">c1b4aA_</a>	 Alignment		100.0	33	<b>PDB header:</b> repressor <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> structure of the arginine repressor from bacillus stearothermophilus
3	<a href="#">c3v4gA_</a>	 Alignment		100.0	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
4	<a href="#">c5jvoA_</a>	 Alignment		99.9	54	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor from the pathogenic2 bacterium corynebacterium pseudotuberculosis
5	<a href="#">c3cagF_</a>	 Alignment		99.9	100	<b>PDB header:</b> dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
6	<a href="#">d1f9na1</a>	 Alignment		99.9	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
7	<a href="#">d1b4aa1</a>	 Alignment		99.9	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
8	<a href="#">d2p5ka1</a>	 Alignment		99.9	37	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
9	<a href="#">d1b4ba_</a>	 Alignment		99.9	36	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
10	<a href="#">d2p5ma1</a>	 Alignment		99.9	32	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
11	<a href="#">d1aoya_</a>	 Alignment		99.8	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain

12	<a href="#">dlxxaa_</a>	Alignment		99.8	33	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
13	<a href="#">dlbiaa1</a>	Alignment		96.6	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
14	<a href="#">c5unkA_</a>	Alignment		96.4	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sleeping beauty transposase; <b>PDBTitle:</b> nmr structure of the red subdomain of the sleeping beauty transposase
15	<a href="#">dlj5ya1</a>	Alignment		96.3	34	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
16	<a href="#">d2d1ha1</a>	Alignment		96.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
17	<a href="#">dlmzba_</a>	Alignment		95.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FUR-like
18	<a href="#">c2xigA_</a>	Alignment		95.2	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
19	<a href="#">c5fd6A_</a>	Alignment		95.2	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> zinc-bound manganese uptake regulator
20	<a href="#">c4razB_</a>	Alignment		95.0	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding transcriptional dual regulator of siderophore <b>PDBTitle:</b> crystal structure of magnetospirillum gryphiswaldense msr-1 holo-fur
21	<a href="#">c3mwmA_</a>	Alignment	not modelled	95.0	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal uptake regulation protein; <b>PDBTitle:</b> graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
22	<a href="#">c4a0zA_</a>	Alignment	not modelled	94.8	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor fapr; <b>PDBTitle:</b> structure of the global transcription regulator fapr from2 staphylococcus aureus in complex with malonyl-coa
23	<a href="#">c2oqgA_</a>	Alignment	not modelled	94.7	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1
24	<a href="#">c4mtdA_</a>	Alignment	not modelled	94.7	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> zinc uptake regulation protein; <b>PDBTitle:</b> zinc uptake regulator complexed with zinc and dna
25	<a href="#">c2o03A_</a>	Alignment	not modelled	94.6	21	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable zinc uptake regulation protein furb; <b>PDBTitle:</b> crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
26	<a href="#">c4i7hA_</a>	Alignment	not modelled	94.6	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> peroxide stress sensing regulator; <b>PDBTitle:</b> structural basis for peroxide sensing and gene regulation by perr from2 streptococcus pyogenes
27	<a href="#">c6dk4A_</a>	Alignment	not modelled	94.3	19	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of campylobacter jejuni peroxide stress regulator
28	<a href="#">c2fe3B_</a>	Alignment	not modelled	94.3	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxide operon regulator; <b>PDBTitle:</b> the crystal structure of bacillus subtilis perr-zn reveals a

						novel2 zn(cys)4 structural redox switch
29	<a href="#">d1stza1</a>	Alignment	not modelled	94.3	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
30	<a href="#">c1r22B</a>	Alignment	not modelled	94.2	25	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
31	<a href="#">d1r1ua</a>	Alignment	not modelled	94.1	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
32	<a href="#">c6j05B</a>	Alignment	not modelled	93.9	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
33	<a href="#">c3pgkD</a>	Alignment	not modelled	93.8	28	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> biofilm growth-associated repressor; <b>PDBTitle:</b> crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
34	<a href="#">c2w57A</a>	Alignment	not modelled	93.5	24	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
35	<a href="#">c3eyyA</a>	Alignment	not modelled	93.4	16	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative iron uptake regulatory protein; <b>PDBTitle:</b> structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
36	<a href="#">c1j5yA</a>	Alignment	not modelled	93.3	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, biotin repressor family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
37	<a href="#">c5n19B</a>	Alignment	not modelled	93.3	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator (fur family); <b>PDBTitle:</b> crystal structure of a peroxide stress regulator from leptospira2 interrogans
38	<a href="#">c2lkpB</a>	Alignment	not modelled	93.2	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, arsr family; <b>PDBTitle:</b> solution structure of apo-nmtr
39	<a href="#">c3cuoB</a>	Alignment	not modelled	93.2	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
40	<a href="#">c2zkzC</a>	Alignment	not modelled	93.1	18	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional repressor pagr; <b>PDBTitle:</b> crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
41	<a href="#">c3f6vA</a>	Alignment	not modelled	93.1	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for arsenical2 resistance
42	<a href="#">c4omzG</a>	Alignment	not modelled	93.0	26	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
43	<a href="#">c2kkoB</a>	Alignment	not modelled	92.6	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulatory protein <b>PDBTitle:</b> 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.
44	<a href="#">c2jscB</a>	Alignment	not modelled	92.5	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator rv1994c/mt2050; <b>PDBTitle:</b> nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
45	<a href="#">d1r1ta</a>	Alignment	not modelled	91.9	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
46	<a href="#">c4pcqC</a>	Alignment	not modelled	91.8	25	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> possible transcriptional regulatory protein (probably <b>PDBTitle:</b> crystal structure of mtbaldr (rv2779c)
47	<a href="#">c2e1cA</a>	Alignment	not modelled	91.7	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
48	<a href="#">c5nbcD</a>	Alignment	not modelled	91.5	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> structure of prokaryotic transcription factors
49	<a href="#">c5zhcA</a>	Alignment	not modelled	91.5	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of the padr-family transcriptional regulator rv34882 of mycobacterium tuberculosis h37rv
50	<a href="#">c3jthA</a>	Alignment	not modelled	91.3	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription activator hlyu; <b>PDBTitle:</b> crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
51	<a href="#">c4etsB</a>	Alignment	not modelled	91.1	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of campylobacter jejuni ferric uptake regulator
52	<a href="#">c6j0eB</a>	Alignment	not modelled	90.9	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> arsenic responsive repressor arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors:

						implications for the mechanism of derepression
53	<a href="#">c5wayB_</a>	Alignment	not modelled	90.6	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional activator; <b>PDBTitle:</b> mgaspn protein, mga regulator from streptococcus pneumoniae
54	<a href="#">c5dukA_</a>	Alignment	not modelled	90.3	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna binding protein; <b>PDBTitle:</b> n-terminal structure of putative dna binding transcription factor from thermoplasmatales archaeon scgc ab-539-n05
55	<a href="#">d2foka3</a>	Alignment	not modelled	90.1	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Restriction endonuclease FokI, N-terminal (recognition) domain
56	<a href="#">d1u2wa1</a>	Alignment	not modelled	90.1	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
57	<a href="#">c2fu4B_</a>	Alignment	not modelled	90.1	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
58	<a href="#">c2o8kA_</a>	Alignment	not modelled	89.6	30	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
59	<a href="#">d1ub9a_</a>	Alignment	not modelled	89.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
60	<a href="#">c3f6oB_</a>	Alignment	not modelled	89.3	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of arsr family transcriptional regulator, 2 rha00566
61	<a href="#">c5jlsA_</a>	Alignment	not modelled	89.1	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adhesin competence repressor; <b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from streptococcus pyogenes (c-terminally his tagged)
62	<a href="#">c2dbbA_</a>	Alignment	not modelled	88.9	24	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061
63	<a href="#">d1sfxa_</a>	Alignment	not modelled	88.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
64	<a href="#">d1z05a1</a>	Alignment	not modelled	88.4	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
65	<a href="#">d1foka3</a>	Alignment	not modelled	88.0	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Restriction endonuclease FokI, N-terminal (recognition) domain
66	<a href="#">c2ahqA_</a>	Alignment	not modelled	87.7	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
67	<a href="#">c2x4hA_</a>	Alignment	not modelled	87.6	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from sulfobolus solfataricus
68	<a href="#">c6gh5M_</a>	Alignment	not modelled	87.1	23	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor,rna polymerase sigma-54 <b>PDBTitle:</b> cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
69	<a href="#">c3ctaA_</a>	Alignment	not modelled	87.1	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma acidophilum
70	<a href="#">d2p4wa1</a>	Alignment	not modelled	87.0	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
71	<a href="#">c5nwtM_</a>	Alignment	not modelled	86.5	23	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor,rna polymerase sigma-54 <b>PDBTitle:</b> crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
72	<a href="#">c5i0pA_</a>	Alignment	not modelled	86.2	22	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor etv6, transcription factor etv6, <b>PDBTitle:</b> symmetry-based assembly of a two-dimensional protein lattice
73	<a href="#">c1i1gA_</a>	Alignment	not modelled	86.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
74	<a href="#">c3sqnA_</a>	Alignment	not modelled	85.9	28	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> putative mga family transcriptional regulator from enterococcus2 faecalis
75	<a href="#">c4r6iA_</a>	Alignment	not modelled	85.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> anthrax toxin expression trans-acting positive regulator; <b>PDBTitle:</b> atxa protein, a virulence regulator from bacillus anthracis.
76	<a href="#">c2p6tH_</a>	Alignment	not modelled	85.9	18	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> transcriptional regulator, lrp/asnc family; <b>PDBTitle:</b> crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
77	<a href="#">c2vbzA_</a>	Alignment	not modelled	85.2	19	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2

						tuberculosis complexed with l-tryptophan <b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
78	<a href="#">c6paxA_</a>	Alignment	not modelled	84.9	20	
79	<a href="#">c2wteB_</a>	Alignment	not modelled	84.4	23	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> csa3; <b>PDBTitle:</b> the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
80	<a href="#">c5d4zF_</a>	Alignment	not modelled	84.2	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> repressor; <b>PDBTitle:</b> crystal structure of repressor from salmonella-temperate phage
81	<a href="#">c3k2zA_</a>	Alignment	not modelled	83.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> crystal structure of a lexa protein from thermotoga maritima
82	<a href="#">c2gqqB_</a>	Alignment	not modelled	83.8	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (Irp)
83	<a href="#">c5d50I_</a>	Alignment	not modelled	83.4	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> repressor; <b>PDBTitle:</b> crystal structure of rep-ant complex from salmonella-temperate phage
84	<a href="#">c1iufA_</a>	Alignment	not modelled	83.1	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> centromere abp1 protein; <b>PDBTitle:</b> low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
85	<a href="#">d2etha1</a>	Alignment	not modelled	83.1	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
86	<a href="#">c4esfA_</a>	Alignment	not modelled	82.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> padr-like transcriptional regulator; <b>PDBTitle:</b> crystal structure of padr-like transcriptional regulator (bce3449)2 from bacillus cereus strain atcc 10987
87	<a href="#">c2mt3A_</a>	Alignment	not modelled	82.7	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-54 factor; <b>PDBTitle:</b> structure of -24 dna binding domain of sigma 54 from e.coli
88	<a href="#">c3r0aB_</a>	Alignment	not modelled	82.6	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
89	<a href="#">c5zqhA_</a>	Alignment	not modelled	82.5	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> padr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of streptococcus transcriptional regulator
90	<a href="#">c5byhM_</a>	Alignment	not modelled	82.0	25	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor; <b>PDBTitle:</b> crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
91	<a href="#">c5xpgB_</a>	Alignment	not modelled	81.9	33	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv0081; <b>PDBTitle:</b> crystal structure of m.tuberculosis rv0081
92	<a href="#">c2fjrB_</a>	Alignment	not modelled	81.9	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of bacteriophage 186
93	<a href="#">c4o6jA_</a>	Alignment	not modelled	81.8	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent transcription repressor related protein; <b>PDBTitle:</b> crystal structure of t. acidophilum ider
94	<a href="#">d2cg4a1</a>	Alignment	not modelled	81.6	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
95	<a href="#">c1z6rC_</a>	Alignment	not modelled	81.5	17	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> mlc protein; <b>PDBTitle:</b> crystal structure of mlc from escherichia coli
96	<a href="#">c4ijaA_</a>	Alignment	not modelled	81.4	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> xylr protein; <b>PDBTitle:</b> structure of s. aureus methicillin resistance factor mecR2
97	<a href="#">c2hoeA_</a>	Alignment	not modelled	81.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine kinase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
98	<a href="#">c2it0A_</a>	Alignment	not modelled	80.8	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
99	<a href="#">c4nb5D_</a>	Alignment	not modelled	80.7	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
100	<a href="#">c2kpiA_</a>	Alignment	not modelled	80.5	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
101	<a href="#">c1z05A_</a>	Alignment	not modelled	79.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rok family; <b>PDBTitle:</b> crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
102	<a href="#">d1pdnc_</a>	Alignment	not modelled	78.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
103	<a href="#">c5ui5I_</a>	Alignment	not modelled	78.8	28	<b>PDB header:</b> transcription/dna <b>Chain:</b> I: <b>PDB Molecule:</b> rna polymerase sigma factor rpon;

103	<a href="#">c3urjI_</a>	Alignment	not modelled	78.8	48	<b>PDBTitle:</b> crystal structure of aquifex aeolicus sigman bound to promoter dna <b>PDB header:</b> transcription regulator
104	<a href="#">c3cjnA_</a>	Alignment	not modelled	78.5	34	<b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
105	<a href="#">c3elkA_</a>	Alignment	not modelled	78.5	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator ta0346; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum
106	<a href="#">c2gxgA_</a>	Alignment	not modelled	78.4	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
107	<a href="#">c3vk0B_</a>	Alignment	not modelled	78.2	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of hypothetical transcription factor nhft from2 neisseria
108	<a href="#">c4czdD_</a>	Alignment	not modelled	78.0	19	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
109	<a href="#">c5h20A_</a>	Alignment	not modelled	78.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative padr-family transcriptional regulatory protein; <b>PDBTitle:</b> x-ray structure of padr-like transcription factor from bacteroid2 fragilis
110	<a href="#">d1g3wa1</a>	Alignment	not modelled	77.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
111	<a href="#">c4esbA_</a>	Alignment	not modelled	77.6	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, padr family; <b>PDBTitle:</b> crystal structure of padr-like transcriptional regulator (bc4206) from2 bacillus cereus strain atcc 14579
112	<a href="#">c3qyxD_</a>	Alignment	not modelled	77.4	31	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> esx-1 secretion-associated regulator espr; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
113	<a href="#">d1lnwa_</a>	Alignment	not modelled	77.0	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
114	<a href="#">c5zc2B_</a>	Alignment	not modelled	76.8	18	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
115	<a href="#">d1i1ga1</a>	Alignment	not modelled	76.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
116	<a href="#">c2e7xA_</a>	Alignment	not modelled	76.5	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
117	<a href="#">c5yhxH_</a>	Alignment	not modelled	76.3	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> zinc transport transcriptional regulator; <b>PDBTitle:</b> structure of lactococcus lactis zitri, wild type
118	<a href="#">c3eqxB_</a>	Alignment	not modelled	76.2	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> fic domain containing transcriptional regulator; <b>PDBTitle:</b> crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
119	<a href="#">c2qwwB_</a>	Alignment	not modelled	75.8	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
120	<a href="#">c6c28C_</a>	Alignment	not modelled	75.8	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> transcriptional repressor, cour, bound to p-coumaroyl-coa