

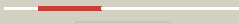





















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0744c (- )_834443_834949
Date	Fri Jul 26 01:50:32 BST 2019
Unique Job ID	9b53c7321962bbdb

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4j2nA_</a>	 Alignment		99.4	29	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
2	<a href="#">c4j2nB_</a>	 Alignment		99.4	29	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
3	<a href="#">c6amaO_</a>	 Alignment		99.0	28	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> O: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> structure of s. coelicolor/s. venezuelae bidc-smea-ssfa complex to2 3.09 angstrom
4	<a href="#">c1z4hA_</a>	 Alignment		98.9	11	<b>PDB header:</b> protein binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tor inhibition protein; <b>PDBTitle:</b> the response regulator tori belongs to a new family of2 atypical excisionase
5	<a href="#">c1y6uA_</a>	 Alignment		98.3	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excisionase from transposon tn916; <b>PDBTitle:</b> the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
6	<a href="#">c2kfsA_</a>	 Alignment		98.0	24	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical regulatory protein; <b>PDBTitle:</b> nmr structure of rv2175c
7	<a href="#">c4r24B_</a>	 Alignment		97.9	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator tnra; <b>PDBTitle:</b> complete dissection of b. subtilis nitrogen homeostatic circuitry
8	<a href="#">c5c8eC_</a>	 Alignment		97.8	17	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> light-dependent transcriptional regulator carh; <b>PDBTitle:</b> crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
9	<a href="#">c2zhhA_</a>	 Alignment		97.8	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensitive transcriptional activator soxR; <b>PDBTitle:</b> crystal structure of soxR
10	<a href="#">c5i44E_</a>	 Alignment		97.8	20	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> chromosome-anchoring protein raca; <b>PDBTitle:</b> structure of raca-dna complex; p21 form
11	<a href="#">c4r4eA_</a>	 Alignment		97.7	14	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator glnr; <b>PDBTitle:</b> structure of glnr-dna complex

12	<a href="#">d1r8da_</a>	Alignment		97.7	16	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
13	<a href="#">d1q06a_</a>	Alignment		97.7	13	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
14	<a href="#">c2vz4A_</a>	Alignment		97.5	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> the n-terminal domain of merr-like protein tipal bound to promoter dna
15	<a href="#">c3gpvA_</a>	Alignment		97.5	5	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
16	<a href="#">c3ucsB_</a>	Alignment		97.4	19	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone-modulator protein cbpm; <b>PDBTitle:</b> crystal structure of the complex between cbpa j-domain and cbpm
17	<a href="#">d1j9ia_</a>	Alignment		97.3	22	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Terminase gpNU1 subunit domain
18	<a href="#">c3hh0C_</a>	Alignment		97.3	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
19	<a href="#">d1r8ea1</a>	Alignment		97.3	14	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
20	<a href="#">c3gp4B_</a>	Alignment		97.3	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
21	<a href="#">c3qaoA_</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> merr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
22	<a href="#">c5af3A_</a>	Alignment	not modelled	97.2	25	<b>PDB header:</b> dna binding <b>Chain:</b> A: <b>PDB Molecule:</b> vapbc49; <b>PDBTitle:</b> x-ray crystal structure of rv2018 from mycobacterium tuberculosis
23	<a href="#">c5gpeB_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, merr-family; <b>PDBTitle:</b> crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
24	<a href="#">c2jmlA_</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding domain/transcriptional regulator; <b>PDBTitle:</b> solution structure of the n-terminal domain of cara repressor
25	<a href="#">c3d6zA_</a>	Alignment	not modelled	96.2	16	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug-efflux transporter 1 regulator; <b>PDBTitle:</b> crystal structure of r275e mutant of bmrr bound to dna and rhodamine
26	<a href="#">c5crlA_</a>	Alignment	not modelled	96.0	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric resistance operon regulatory protein; <b>PDBTitle:</b> crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
27	<a href="#">c5xqlA_</a>	Alignment	not modelled	95.4	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug-efflux transporter 1 regulator; <b>PDBTitle:</b> crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
28	<a href="#">c1u78A_</a>	Alignment	not modelled	94.2	15	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase;

28	<a href="#">c1076A</a>	Alignment	not modelled	94.2	13	<b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
29	<a href="#">c4lhfA</a>	Alignment	not modelled	93.8	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein cox; <b>PDBTitle:</b> crystal structure of a dna binding protein from phage p2
30	<a href="#">d1pdnc</a>	Alignment	not modelled	93.2	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
31	<a href="#">c6paxA</a>	Alignment	not modelled	93.0	25	<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
32	<a href="#">c1hlvA</a>	Alignment	not modelled	92.9	9	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
33	<a href="#">d1j5ya1</a>	Alignment	not modelled	91.9	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
34	<a href="#">d2jn6a1</a>	Alignment	not modelled	91.7	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
35	<a href="#">d1fipa</a>	Alignment	not modelled	91.6	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
36	<a href="#">d1umqa</a>	Alignment	not modelled	91.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
37	<a href="#">c1umqA</a>	Alignment	not modelled	91.6	19	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
38	<a href="#">d1biaa1</a>	Alignment	not modelled	91.5	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
39	<a href="#">c6fkgC</a>	Alignment	not modelled	91.4	19	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> rv1990c (mbca); <b>PDBTitle:</b> crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
40	<a href="#">c3eqxB</a>	Alignment	not modelled	91.3	14	<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
41	<a href="#">c1g2hA</a>	Alignment	not modelled	91.2	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein tyrr homolog; <b>PDBTitle:</b> solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
42	<a href="#">d1g2ha</a>	Alignment	not modelled	91.2	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
43	<a href="#">d1etxa</a>	Alignment	not modelled	91.1	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
44	<a href="#">d2d1ha1</a>	Alignment	not modelled	91.0	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
45	<a href="#">c3bd1B</a>	Alignment	not modelled	90.5	31	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cro protein; <b>PDBTitle:</b> structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
46	<a href="#">c2rn7A</a>	Alignment	not modelled	90.2	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfa; <b>PDBTitle:</b> nmr solution structure of tnpε protein from shigella2 flexneri. northeast structural genomics target sfr125
47	<a href="#">c2m8gX</a>	Alignment	not modelled	90.1	17	<b>PDB header:</b> transcription <b>Chain:</b> X: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> structure, function, and tethering of dna-binding domains in 542 transcriptional activators
48	<a href="#">d1pm6a</a>	Alignment	not modelled	90.0	16	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Excisionase-like
49	<a href="#">d1ntca</a>	Alignment	not modelled	89.4	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
50	<a href="#">c6j05B</a>	Alignment	not modelled	89.2	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
51	<a href="#">c3e7ID</a>	Alignment	not modelled	89.2	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
52	<a href="#">c4l5eA</a>	Alignment	not modelled	89.0	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of a. aeolicus ntrc1 dna binding domain
53	<a href="#">c2dg6A</a>	Alignment	not modelled	88.7	16	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2) <b>PDB header:</b> transcription

54	<a href="#">c2oqgA</a>	Alignment	not modelled	88.6	23	<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
55	<a href="#">d2bjca1</a>	Alignment	not modelled	87.7	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
56	<a href="#">d1rh6a_</a>	Alignment	not modelled	87.3	16	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Excisionase-like
57	<a href="#">c6j0eB_</a>	Alignment	not modelled	87.0	19	<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 for2 the mechanism of derepression
58	<a href="#">c3ezfA_</a>	Alignment	not modelled	87.0	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> para; <b>PDBTitle:</b> partition protein
59	<a href="#">c1r22B_</a>	Alignment	not modelled	86.8	24	<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
60	<a href="#">c3hefB_</a>	Alignment	not modelled	86.6	10	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gene 1 protein; <b>PDBTitle:</b> crystal structure of the bacteriophage sf6 terminase small subunit
61	<a href="#">d2ao9a1</a>	Alignment	not modelled	86.1	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
62	<a href="#">c2fjrB_</a>	Alignment	not modelled	86.1	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
63	<a href="#">c4omzG_</a>	Alignment	not modelled	85.6	11	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nlr; <b>PDBTitle:</b> crystal structure of nlr from sinorhizobium fredii
64	<a href="#">c4hamA_</a>	Alignment	not modelled	85.5	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2241 protein; <b>PDBTitle:</b> crystal structure of transcriptional antiterminator from listeria2 monocytogenes egd-e
65	<a href="#">d1r1ta_</a>	Alignment	not modelled	85.4	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
66	<a href="#">d1r1ua_</a>	Alignment	not modelled	85.2	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
67	<a href="#">c3jthA_</a>	Alignment	not modelled	84.4	17	<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
68	<a href="#">c3omtA_</a>	Alignment	not modelled	84.4	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
69	<a href="#">c2kpiA_</a>	Alignment	not modelled	84.4	26	<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
70	<a href="#">c3cuoB_</a>	Alignment	not modelled	84.1	17	<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
71	<a href="#">c3op9A_</a>	Alignment	not modelled	84.0	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> pli0006 protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator from listeria innocua
72	<a href="#">c2lkpB_</a>	Alignment	not modelled	83.7	17	<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
73	<a href="#">c5j9iH_</a>	Alignment	not modelled	83.5	14	<b>PDB header:</b> antitoxin <b>Chain:</b> H: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higa2 antitoxin c-terminal domain
74	<a href="#">c1j5yA_</a>	Alignment	not modelled	83.4	28	<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
75	<a href="#">c2zkcC_</a>	Alignment	not modelled	83.1	17	<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
76	<a href="#">d1xsva_</a>	Alignment	not modelled	83.0	38	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
77	<a href="#">c6gh5M_</a>	Alignment	not modelled	83.0	10	<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
78	<a href="#">c5fgmA_</a>	Alignment	not modelled	83.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigr; <b>PDBTitle:</b> streptomyces coelicolor sigr region 4
						<b>PDB header:</b> transcription

79	<a href="#">c5dukA</a>	Alignment	not modelled	82.9	19	<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 2 thermoplasmales archaeon scgc ab-539-n05
80	<a href="#">c5wayB</a>	Alignment	not modelled	82.7	19	<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
81	<a href="#">d1rzsA</a>	Alignment	not modelled	82.6	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
82	<a href="#">c3bs3A</a>	Alignment	not modelled	82.2	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of a putative dna-binding protein from bacteroides2 fragilis
83	<a href="#">c2ebyA</a>	Alignment	not modelled	82.2	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybaq; <b>PDBTitle:</b> crystal structure of a hypothetical protein from e. coli
84	<a href="#">d1rp3a2</a>	Alignment	not modelled	82.2	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
85	<a href="#">d1adra</a>	Alignment	not modelled	82.2	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
86	<a href="#">c2ev2B</a>	Alignment	not modelled	82.1	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> structure of rv1264n, the regulatory domain of the mycobacterial2 adenyl cyclase rv1264, at ph 8.5
87	<a href="#">c2o8xA</a>	Alignment	not modelled	82.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of 2 mycobacterium tuberculosis sigc
88	<a href="#">d1lcda</a>	Alignment	not modelled	81.9	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
89	<a href="#">c3pqkD</a>	Alignment	not modelled	81.7	9	<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
90	<a href="#">c5jaaB</a>	Alignment	not modelled	81.3	14	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higba2 toxin-antitoxin complex
91	<a href="#">d2ppxA1</a>	Alignment	not modelled	81.2	7	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
92	<a href="#">c2ppxA</a>	Alignment	not modelled	81.2	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1735; <b>PDBTitle:</b> crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
93	<a href="#">d1r69a</a>	Alignment	not modelled	81.1	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
94	<a href="#">c3gn5B</a>	Alignment	not modelled	81.1	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa (ygit/b3021); <b>PDBTitle:</b> structure of the e. coli protein mqsa (ygit/b3021)
95	<a href="#">c2jscB</a>	Alignment	not modelled	81.1	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
96	<a href="#">c5byhM</a>	Alignment	not modelled	80.8	13	<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
97	<a href="#">c4go1A</a>	Alignment	not modelled	80.7	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lsrr; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsrr from e.2 coli.
98	<a href="#">c6cmvA</a>	Alignment	not modelled	80.7	21	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrs14-like protein; <b>PDBTitle:</b> crystal structure of archaeal biofilm regulator (abfr2) from 2 sulfobolus acidocaldarius
99	<a href="#">d1luxca</a>	Alignment	not modelled	80.6	32	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
100	<a href="#">c3kxD</a>	Alignment	not modelled	80.5	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
101	<a href="#">d1s7oa</a>	Alignment	not modelled	80.4	38	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
102	<a href="#">c2xcjB</a>	Alignment	not modelled	80.4	14	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> c protein; <b>PDBTitle:</b> crystal structure of p2 c, the immunity repressor of 2 temperate e. coli phage p2
103	<a href="#">c3hugA</a>	Alignment	not modelled	80.4	21	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigI
104	<a href="#">d1x57a1</a>	Alignment	not modelled	80.3	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
						<b>Fold:</b> lambda repressor-like DNA-binding domains

105	<a href="#">d2icta1</a>	Alignment	not modelled	80.3	7	<b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
106	<a href="#">c3iwfA</a>	Alignment	not modelled	80.2	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
107	<a href="#">d1okra</a>	Alignment	not modelled	80.1	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
108	<a href="#">c1bdhA</a>	Alignment	not modelled	79.9	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
109	<a href="#">d1y7ya1</a>	Alignment	not modelled	79.9	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
110	<a href="#">d1mkma1</a>	Alignment	not modelled	79.8	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator IclR, N-terminal domain
111	<a href="#">c4r6iA</a>	Alignment	not modelled	79.7	16	<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.
112	<a href="#">c3mzyA</a>	Alignment	not modelled	79.5	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
113	<a href="#">d1y9qa1</a>	Alignment	not modelled	79.5	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Probable transcriptional regulator VC1968, N-terminal domain
114	<a href="#">c1lbgB</a>	Alignment	not modelled	79.4	27	<b>PDB header:</b> <b>PDB COMPND:</b>
115	<a href="#">c2kkoB</a>	Alignment	not modelled	79.4	12	<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.
116	<a href="#">c3vepA</a>	Alignment	not modelled	79.3	25	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-d factor; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda
117	<a href="#">c1zvva</a>	Alignment	not modelled	79.3	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpa-crh-dna complex
118	<a href="#">d3ctaa1</a>	Alignment	not modelled	79.2	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
119	<a href="#">d1b0na2</a>	Alignment	not modelled	79.2	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
120	<a href="#">c3mlfC</a>	Alignment	not modelled	79.2	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> putative transcriptional regulator from staphylococcus aureus.