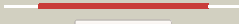



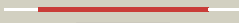






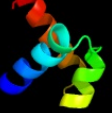














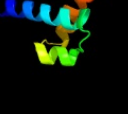



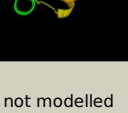


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD075A (-) _850345_850530
Date	Fri Jul 26 01:50:33 BST 2019
Unique Job ID	7c3853dd1e1dbb2c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2jn6a1</a>	 Alignment		98.9	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
2	<a href="#">c2rn7A_</a>	 Alignment		98.6	33	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfa; <b>PDBTitle:</b> nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
3	<a href="#">c6paxA_</a>	 Alignment		98.6	23	<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
4	<a href="#">d1pdnc_</a>	 Alignment		98.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
5	<a href="#">d1k78a1</a>	 Alignment		98.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
6	<a href="#">d6paxa1</a>	 Alignment		98.2	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
7	<a href="#">c1u78A_</a>	 Alignment		98.1	19	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
8	<a href="#">c2elhA_</a>	 Alignment		97.9	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
9	<a href="#">c4fcyA_</a>	 Alignment		97.8	24	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposase; <b>PDBTitle:</b> crystal structure of the bacteriophage mu transpososome
10	<a href="#">c1hlvA_</a>	 Alignment		97.7	17	<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
11	<a href="#">c3hosA_</a>	 Alignment		97.5	13	<b>PDB header:</b> transferase, dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element mariner, complete cds; <b>PDBTitle:</b> crystal structure of the mariner mos1 paired end complex with mg

12	<a href="#">d1hlva1</a>	Alignment		97.5	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
13	<a href="#">d1bw6a_</a>	Alignment		97.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
14	<a href="#">c2k27A_</a>	Alignment		97.1	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
15	<a href="#">c3hefB_</a>	Alignment		97.0	24	<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
16	<a href="#">c3frwF_</a>	Alignment		96.9	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trpr protein from ruminococcus obeum
17	<a href="#">c3korD_</a>	Alignment		96.8	23	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
18	<a href="#">c4go1A_</a>	Alignment		96.7	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator Isrr; <b>PDBTitle:</b> crystal structure of full length transcription repressor Isrr from e.2 coli.
19	<a href="#">d1ntca_</a>	Alignment		96.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
20	<a href="#">d2oa4a1</a>	Alignment		96.6	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> SPO1678-like
21	<a href="#">c2w48D_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
22	<a href="#">c2r0qF_</a>	Alignment	not modelled	96.4	24	<b>PDB header:</b> recombination/dna <b>Chain:</b> F: <b>PDB Molecule:</b> putative transposon tn552 dna-invertase bin3; <b>PDBTitle:</b> crystal structure of a serine recombinase- dna regulatory2 complex
23	<a href="#">d2coba1</a>	Alignment	not modelled	96.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
24	<a href="#">c2jrtA_</a>	Alignment	not modelled	96.2	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
25	<a href="#">d1umqa_</a>	Alignment	not modelled	96.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
26	<a href="#">c1umqA_</a>	Alignment	not modelled	96.2	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
27	<a href="#">d1fipa_</a>	Alignment	not modelled	96.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

28	<a href="#">d1jhga_</a>	Alignment	not modelled	96.2	13	<b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
29	<a href="#">d1trra_</a>	Alignment	not modelled	96.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
30	<a href="#">d1etxa_</a>	Alignment	not modelled	96.0	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
31	<a href="#">c3e7ID_</a>	Alignment	not modelled	96.0	14	<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
32	<a href="#">c2gm4B_</a>	Alignment	not modelled	95.6	24	<b>PDB header:</b> recombination, dna <b>Chain:</b> B: <b>PDB Molecule:</b> transposon gamma-delta resolvase; <b>PDBTitle:</b> an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
33	<a href="#">c4l5eA_</a>	Alignment	not modelled	95.5	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
34	<a href="#">c2cg4B_</a>	Alignment	not modelled	95.4	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
35	<a href="#">c2m8eA_</a>	Alignment	not modelled	95.4	19	<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 pai subdomain of sleeping beauty transposase
36	<a href="#">d1xsva_</a>	Alignment	not modelled	95.3	27	<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
37	<a href="#">d1j5ya1</a>	Alignment	not modelled	95.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
38	<a href="#">c2oqgA_</a>	Alignment	not modelled	95.3	29	<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
39	<a href="#">c2l0kA_</a>	Alignment	not modelled	95.3	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein d; <b>PDBTitle:</b> nmr solution structure of a transcription factor spoiiiid in complex2 with dna
40	<a href="#">c1or7A_</a>	Alignment	not modelled	95.2	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-e factor; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
41	<a href="#">c4j2nA_</a>	Alignment	not modelled	95.1	39	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
42	<a href="#">c4p96B_</a>	Alignment	not modelled	95.0	28	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from vibrio cholerae
43	<a href="#">c2gloA_</a>	Alignment	not modelled	95.0	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> brinker cg9653-pa; <b>PDBTitle:</b> solution structure of the brinker dna binding domain in2 complex with the omb enhancer
44	<a href="#">c4j2nB_</a>	Alignment	not modelled	95.0	41	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
45	<a href="#">d2ezla_</a>	Alignment	not modelled	95.0	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
46	<a href="#">c2ia0A_</a>	Alignment	not modelled	95.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
47	<a href="#">c5m7nA_</a>	Alignment	not modelled	95.0	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
48	<a href="#">d1rp3a2</a>	Alignment	not modelled	94.9	14	<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
49	<a href="#">d1ulya_</a>	Alignment	not modelled	94.9	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
50	<a href="#">c1j5yA_</a>	Alignment	not modelled	94.9	22	<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
51	<a href="#">c2cfxD_</a>	Alignment	not modelled	94.9	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
52	<a href="#">c1r22B_</a>	Alignment	not modelled	94.8	21	<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
53	<a href="#">d1r1ua_</a>	Alignment	not modelled	94.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators

54	<a href="#">c5dukA</a>	Alignment	not modelled	94.8	26	<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 from2 thermoplasmatales archaeon scgc ab-539-n05
55	<a href="#">d1biaa1</a>	Alignment	not modelled	94.7	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
56	<a href="#">c2m8gX</a>	Alignment	not modelled	94.6	16	<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
57	<a href="#">c6ep3B</a>	Alignment	not modelled	94.6	30	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> lmo0651 protein; <b>PDBTitle:</b> lar controls the expression of the listeria monocytogenes agr system2 and mediates virulence.
58	<a href="#">c3i4pA</a>	Alignment	not modelled	94.6	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
59	<a href="#">c5uxxC</a>	Alignment	not modelled	94.6	24	<b>PDB header:</b> dna binding protein/unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> co-crystal structure of the sigma factor rpoE in complex with the2 anti-sigma factor nepr from bartonella quintana
60	<a href="#">c2e7xA</a>	Alignment	not modelled	94.6	16	<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
61	<a href="#">c2w7nA</a>	Alignment	not modelled	94.5	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
62	<a href="#">c2lkpB</a>	Alignment	not modelled	94.5	19	<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
63	<a href="#">d1r1ta</a>	Alignment	not modelled	94.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
64	<a href="#">c4omzG</a>	Alignment	not modelled	94.5	24	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
65	<a href="#">c3hugA</a>	Alignment	not modelled	94.5	16	<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
66	<a href="#">c2o8xA</a>	Alignment	not modelled	94.5	23	<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 of2 mycobacterium tuberculosis sigc
67	<a href="#">c3f6oB</a>	Alignment	not modelled	94.5	12	<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
68	<a href="#">c2vbzA</a>	Alignment	not modelled	94.4	17	<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
69	<a href="#">d1etob</a>	Alignment	not modelled	94.3	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
70	<a href="#">c2p6tH</a>	Alignment	not modelled	94.3	19	<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
71	<a href="#">c3mzyA</a>	Alignment	not modelled	94.3	13	<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
72	<a href="#">c6c03A</a>	Alignment	not modelled	94.2	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative rna polymerase ecf-subfamily sigma factor; <b>PDBTitle:</b> the crystal structure streptomyces venezuelae rsbn-bldn complex
73	<a href="#">d2ao9a1</a>	Alignment	not modelled	94.2	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
74	<a href="#">c2mqkA</a>	Alignment	not modelled	94.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent target dna activator b; <b>PDBTitle:</b> solution structure of n terminal domain of the mub aaa+ atpase
75	<a href="#">c5zx3F</a>	Alignment	not modelled	94.1	23	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigh; <b>PDBTitle:</b> mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
76	<a href="#">c2dbbA</a>	Alignment	not modelled	94.1	15	<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
77	<a href="#">c2di3A</a>	Alignment	not modelled	94.0	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory proteins, gntr family; <b>PDBTitle:</b> crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
78	<a href="#">d2isya1</a>	Alignment	not modelled	94.0	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
						<b>PDB header:</b> dna binding protein

79	<a href="#">c5z4yB_</a>	Alignment	not modelled	93.8	20	<b>Chain:</b> B: <b>PDB Molecule:</b> cys regulon transcriptional activator; <b>PDBTitle:</b> crystal structure of pacysb ntd domain with space group p4
80	<a href="#">c3vdoA_</a>	Alignment	not modelled	93.8	12	<b>PDB header:</b> dna binding protein/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor sigk; <b>PDBTitle:</b> structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
81	<a href="#">c5j9iH_</a>	Alignment	not modelled	93.8	22	<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
82	<a href="#">c1i1gA_</a>	Alignment	not modelled	93.8	18	<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
83	<a href="#">c6az6B_</a>	Alignment	not modelled	93.8	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> gntR family transcriptional regulator; <b>PDBTitle:</b> streptococcus agalactiae gntR
84	<a href="#">c2e1cA_</a>	Alignment	not modelled	93.7	11	<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
85	<a href="#">c3vepA_</a>	Alignment	not modelled	93.7	29	<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 sig4 in complex with its negative regulator rsda
86	<a href="#">c1e2xA_</a>	Alignment	not modelled	93.7	24	<b>PDB header:</b> transcriptional regulation <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from e.2 coli
87	<a href="#">d1or7a1</a>	Alignment	not modelled	93.6	23	<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
88	<a href="#">c6j05B_</a>	Alignment	not modelled	93.6	22	<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
89	<a href="#">c2jscB_</a>	Alignment	not modelled	93.6	22	<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
90	<a href="#">c6dvdF_</a>	Alignment	not modelled	93.6	18	<b>PDB header:</b> transferase/dna <b>Chain:</b> F: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigl; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
91	<a href="#">d1g3wa1</a>	Alignment	not modelled	93.5	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
92	<a href="#">c4cxA_</a>	Alignment	not modelled	93.5	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor cnrh; <b>PDBTitle:</b> structure of cnrh in complex with the cytosolic domain of cnry
93	<a href="#">d1s7oa_</a>	Alignment	not modelled	93.5	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> YlxM/p13-like
94	<a href="#">c3jthA_</a>	Alignment	not modelled	93.4	27	<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
95	<a href="#">c3f6vA_</a>	Alignment	not modelled	93.4	22	<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
96	<a href="#">c3fmsA_</a>	Alignment	not modelled	93.4	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntR family; <b>PDBTitle:</b> crystal structure of tm0439, a gntR transcriptional regulator
97	<a href="#">c5fgmA_</a>	Alignment	not modelled	93.4	20	<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
98	<a href="#">c2kpiA_</a>	Alignment	not modelled	93.3	23	<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
99	<a href="#">c3b7hA_</a>	Alignment	not modelled	93.3	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
100	<a href="#">d1vz0a1</a>	Alignment	not modelled	93.2	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
101	<a href="#">d1stza1</a>	Alignment	not modelled	93.2	24	<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
102	<a href="#">d2cyya1</a>	Alignment	not modelled	93.1	11	<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
103	<a href="#">c2lfwA_</a>	Alignment	not modelled	93.1	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> phyr sigma-like domain; <b>PDBTitle:</b> nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1

104	<a href="#">d1g2ha_</a>	Alignment	not modelled	93.1	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
105	<a href="#">c1g2hA_</a>	Alignment	not modelled	93.1	21	<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
106	<a href="#">d1jhfa1</a>	Alignment	not modelled	93.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
107	<a href="#">c2gqgB_</a>	Alignment	not modelled	93.0	17	<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 (lrp)
108	<a href="#">d2cg4a1</a>	Alignment	not modelled	93.0	17	<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
109	<a href="#">c6j0eB_</a>	Alignment	not modelled	93.0	17	<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
110	<a href="#">c4pcqC_</a>	Alignment	not modelled	92.9	22	<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)
111	<a href="#">c2hs5A_</a>	Alignment	not modelled	92.8	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator gntr; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
112	<a href="#">c4egzA_</a>	Alignment	not modelled	92.7	26	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> arabinose metabolism transcriptional repressor; <b>PDBTitle:</b> crystal structure of arar(dbd) in complex with operator orr3
113	<a href="#">c1iufA_</a>	Alignment	not modelled	92.7	7	<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
114	<a href="#">c2l4aA_</a>	Alignment	not modelled	92.6	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
115	<a href="#">c2kkoB_</a>	Alignment	not modelled	92.5	19	<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="#">d1ilga1</a>	Alignment	not modelled	92.5	15	<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
117	<a href="#">c5wurB_</a>	Alignment	not modelled	92.4	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigw; <b>PDBTitle:</b> crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
118	<a href="#">c1rp3G_</a>	Alignment	not modelled	92.4	15	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> rna polymerase sigma factor sigma-28 (flia); <b>PDBTitle:</b> cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm
119	<a href="#">c6amaO_</a>	Alignment	not modelled	92.4	26	<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 bldc-smea-ssfa complex to2 3.09 angstrom
120	<a href="#">c2jvIA_</a>	Alignment	not modelled	92.4	6	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> trmbf1; <b>PDBTitle:</b> nmr structure of the c-terminal domain of mbf1 of trichoderma reesei