
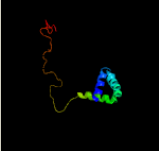
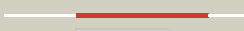


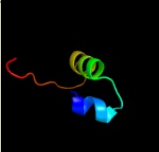











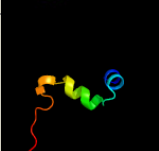




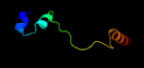





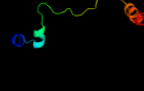




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2085 (- )_2343035_2343340
Date	Mon Aug 5 13:25:20 BST 2019
Unique Job ID	d830c5e741c6c576

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2rn7A_</a>	 Alignment		99.7	26	<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
2	<a href="#">d2jn6a1</a>	 Alignment		99.0	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
3	<a href="#">c6amaO_</a>	 Alignment		93.4	19	<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="#">c5i44E_</a>	 Alignment		92.1	38	<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
5	<a href="#">c4j2nB_</a>	 Alignment		92.0	15	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
6	<a href="#">c4j2nA_</a>	 Alignment		91.3	15	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
7	<a href="#">d1k78a1</a>	 Alignment		90.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
8	<a href="#">c5c8eC_</a>	 Alignment		90.2	14	<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 to adenosylcobalamin and a 26-bp dna segment
9	<a href="#">c1u78A_</a>	 Alignment		89.6	6	<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
10	<a href="#">d2ezla_</a>	 Alignment		89.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
11	<a href="#">c1h1vA_</a>	 Alignment		89.4	16	<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

12	<a href="#">c6paxA</a>	Alignment		89.1	14	<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
13	<a href="#">c2vz4A</a>	Alignment		88.6	14	<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
14	<a href="#">d1q06a</a>	Alignment		88.1	9	<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
15	<a href="#">d6paxa1</a>	Alignment		87.1	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
16	<a href="#">c4r4eA</a>	Alignment		86.2	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
17	<a href="#">d1j9ia</a>	Alignment		86.0	25	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Terminase gpNU1 subunit domain
18	<a href="#">d1pduc</a>	Alignment		85.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
19	<a href="#">c2jmlA</a>	Alignment		85.8	33	<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
20	<a href="#">c3gp4B</a>	Alignment		85.5	24	<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="#">d1r8da</a>	Alignment	not modelled	85.3	19	<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
22	<a href="#">c3gpvA</a>	Alignment	not modelled	84.9	10	<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
23	<a href="#">c2zhha</a>	Alignment	not modelled	84.8	13	<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
24	<a href="#">c4r24B</a>	Alignment	not modelled	83.5	15	<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
25	<a href="#">c2elhA</a>	Alignment	not modelled	83.2	24	<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
26	<a href="#">c4fcyA</a>	Alignment	not modelled	82.2	20	<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
27	<a href="#">d1hlva1</a>	Alignment	not modelled	81.9	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
28	<a href="#">d1r8ea1</a>	Alignment	not modelled	81.2	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
						<b>PDB header:</b> transcription regulator

29	<a href="#">c3qaoA</a>	Alignment	not modelled	81.1	19	<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
30	<a href="#">c3hh0C</a>	Alignment	not modelled	79.1	10	<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
31	<a href="#">c5crIA</a>	Alignment	not modelled	78.2	19	<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)
32	<a href="#">d2p7vb1</a>	Alignment	not modelled	77.3	24	<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
33	<a href="#">c1or7A</a>	Alignment	not modelled	76.2	14	<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
34	<a href="#">c3hosA</a>	Alignment	not modelled	75.4	16	<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
35	<a href="#">c5tw1F</a>	Alignment	not modelled	75.2	22	<b>PDB header:</b> transcription activator/transferase/dna <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor siga; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
36	<a href="#">c6c03A</a>	Alignment	not modelled	74.2	9	<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
37	<a href="#">c5gpeB</a>	Alignment	not modelled	73.5	14	<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)
38	<a href="#">c5af3A</a>	Alignment	not modelled	73.1	29	<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
39	<a href="#">c2cfxD</a>	Alignment	not modelled	73.0	14	<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
40	<a href="#">c2e7xA</a>	Alignment	not modelled	72.2	15	<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 lrpc/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
41	<a href="#">d1rp3a2</a>	Alignment	not modelled	71.4	18	<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
42	<a href="#">c6in7B</a>	Alignment	not modelled	70.5	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> crystal structure of algu in complex with muca(cyto)
43	<a href="#">d1or7a1</a>	Alignment	not modelled	70.5	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
44	<a href="#">c2o8xA</a>	Alignment	not modelled	70.1	18	<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
45	<a href="#">c6hn7A</a>	Alignment	not modelled	69.9	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> redirecting phage packaging protein c (rppc); <b>PDBTitle:</b> hijacking the hijackers: escherichia coli pathogenicity islands2 redirect helper phage packaging for their own benefit.
46	<a href="#">c3vdoA</a>	Alignment	not modelled	69.9	14	<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
47	<a href="#">c2kpiA</a>	Alignment	not modelled	69.8	25	<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
48	<a href="#">c3mzyA</a>	Alignment	not modelled	68.5	9	<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
49	<a href="#">c1i1gA</a>	Alignment	not modelled	67.4	19	<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
50	<a href="#">c2ia0A</a>	Alignment	not modelled	67.1	6	<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)
51	<a href="#">c2p6tH</a>	Alignment	not modelled	67.0	13	<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
52	<a href="#">c2cg4B</a>	Alignment	not modelled	66.9	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc

53	<a href="#">c2vbzA_</a>	Alignment	not modelled	66.8	10	<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
54	<a href="#">c6dvdF_</a>	Alignment	not modelled	66.6	23	<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 l) with 6 nt spacer and bromine3 labelled in position "-11
55	<a href="#">c5zx3F_</a>	Alignment	not modelled	65.5	5	<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
56	<a href="#">d1fjlb_</a>	Alignment	not modelled	65.2	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
57	<a href="#">c1l9uH_</a>	Alignment	not modelled	65.2	22	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> sigma factor siga; <b>PDBTitle:</b> thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
58	<a href="#">c2ao9H_</a>	Alignment	not modelled	64.7	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> phage protein; <b>PDBTitle:</b> structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
59	<a href="#">c6c05F_</a>	Alignment	not modelled	64.7	22	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor siga; <b>PDBTitle:</b> mycobacterium tuberculosis rnap holo/rbpa in relaxed state
60	<a href="#">d1fipa_</a>	Alignment	not modelled	64.4	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
61	<a href="#">d1etxa_</a>	Alignment	not modelled	64.4	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
62	<a href="#">d2ao9a1</a>	Alignment	not modelled	64.3	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
63	<a href="#">d2coba1</a>	Alignment	not modelled	63.6	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
64	<a href="#">c3wodF_</a>	Alignment	not modelled	63.1	24	<b>PDB header:</b> transferase/transcription <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> rna polymerase-gp39 complex
65	<a href="#">c3l1pA_</a>	Alignment	not modelled	62.8	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> pou domain, class 5, transcription factor 1; <b>PDBTitle:</b> pou protein:dna complex
66	<a href="#">c4cxfA_</a>	Alignment	not modelled	62.6	23	<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
67	<a href="#">c2fjrB_</a>	Alignment	not modelled	62.5	11	<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
68	<a href="#">d1o4xa1</a>	Alignment	not modelled	62.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
69	<a href="#">c2e1cA_</a>	Alignment	not modelled	61.2	10	<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
70	<a href="#">d1xsva_</a>	Alignment	not modelled	60.3	5	<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
71	<a href="#">d1p7jb_</a>	Alignment	not modelled	59.9	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
72	<a href="#">c2lfwA_</a>	Alignment	not modelled	59.7	5	<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
73	<a href="#">c2dmqA_</a>	Alignment	not modelled	59.7	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lim/homeobox protein lhx9; <b>PDBTitle:</b> solution structure of the homeobox domain of lim/homeobox2 protein lhx9
74	<a href="#">c3i4pA_</a>	Alignment	not modelled	59.7	11	<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
75	<a href="#">d1au7a1</a>	Alignment	not modelled	59.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
76	<a href="#">d1ttya_</a>	Alignment	not modelled	59.4	19	<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
77	<a href="#">c3d1nK_</a>	Alignment	not modelled	59.1	26	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> K: <b>PDB Molecule:</b> pou domain, class 6, transcription factor 1; <b>PDBTitle:</b> structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
78	<a href="#">c3h5tA_</a>	Alignment	not modelled	58.9	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum

79	<a href="#">c3hugA</a>	Alignment	not modelled	58.6	23	<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
80	<a href="#">c5jaaB</a>	Alignment	not modelled	58.4	29	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higa2 toxin-antitoxin complex
81	<a href="#">c3e7ID</a>	Alignment	not modelled	58.2	11	<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
82	<a href="#">c3kxD</a>	Alignment	not modelled	57.9	30	<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
83	<a href="#">c5j9iH</a>	Alignment	not modelled	57.8	29	<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
84	<a href="#">c3omtA</a>	Alignment	not modelled	57.7	16	<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.
85	<a href="#">c2da1A</a>	Alignment	not modelled	57.3	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-fetoprotein enhancer binding protein; <b>PDBTitle:</b> solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
86	<a href="#">c3bd1B</a>	Alignment	not modelled	57.3	19	<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
87	<a href="#">c2dmtA</a>	Alignment	not modelled	57.1	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein barh-like 1; <b>PDBTitle:</b> solution structure of the homeobox domain of homeobox2 protein barh-like 1
88	<a href="#">d1pufa</a>	Alignment	not modelled	57.1	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
89	<a href="#">c3vk0B</a>	Alignment	not modelled	57.0	11	<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 nhtf from2 neisseria
90	<a href="#">d1efaa1</a>	Alignment	not modelled	57.0	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
91	<a href="#">c1zgwA</a>	Alignment	not modelled	56.6	19	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ada polyprotein; <b>PDBTitle:</b> nmr structure of e. coli ada protein in complex with dna
92	<a href="#">c4pcqC</a>	Alignment	not modelled	56.5	9	<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)
93	<a href="#">d2bjca1</a>	Alignment	not modelled	56.4	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
94	<a href="#">d2hddb</a>	Alignment	not modelled	56.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
95	<a href="#">d2craa1</a>	Alignment	not modelled	56.0	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
96	<a href="#">d1ku3a</a>	Alignment	not modelled	55.7	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
97	<a href="#">c3hefB</a>	Alignment	not modelled	55.7	22	<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
98	<a href="#">c5uuxC</a>	Alignment	not modelled	54.7	14	<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
99	<a href="#">d2cuea1</a>	Alignment	not modelled	54.6	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
100	<a href="#">c5fgmA</a>	Alignment	not modelled	54.5	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigr; <b>PDBTitle:</b> streptomycetes coelicolor sigr region 4
101	<a href="#">d1ntca</a>	Alignment	not modelled	54.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
102	<a href="#">d2hsga1</a>	Alignment	not modelled	54.3	19	<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
103	<a href="#">d1du0a</a>	Alignment	not modelled	54.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
104	<a href="#">c1hf0A</a>	Alignment	not modelled	54.1	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> octamer-binding transcription factor 1; <b>PDBTitle:</b> crystal structure of the dna-binding domain of oct-1 bound to dna as a2 dimer <b>Fold:</b> DNA/RNA-binding 3-helical bundle

105	<a href="#">d1ku7a_</a>	Alignment	not modelled	54.1	24	<b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
106	<a href="#">c5wurB_</a>	Alignment	not modelled	54.0	18	<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
107	<a href="#">c4o8bA_</a>	Alignment	not modelled	53.7	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator bswr
108	<a href="#">c1rp3G_</a>	Alignment	not modelled	53.6	18	<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
109	<a href="#">d1lcda_</a>	Alignment	not modelled	53.4	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GaIR/LacI-like bacterial regulator
110	<a href="#">c3vepA_</a>	Alignment	not modelled	53.3	18	<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
111	<a href="#">d2cg4a1</a>	Alignment	not modelled	53.3	13	<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
112	<a href="#">c2gm4B_</a>	Alignment	not modelled	52.7	14	<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
113	<a href="#">c3ucsB_</a>	Alignment	not modelled	52.6	25	<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
114	<a href="#">c2jvIA_</a>	Alignment	not modelled	52.5	31	<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
115	<a href="#">d1bw6a_</a>	Alignment	not modelled	52.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
116	<a href="#">c2ebyA_</a>	Alignment	not modelled	52.3	6	<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
117	<a href="#">c5yszA_</a>	Alignment	not modelled	52.1	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> transcriptional regulator celr-cellobiose complex
118	<a href="#">c2dmsA_</a>	Alignment	not modelled	51.9	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein otx2; <b>PDBTitle:</b> solution structure of the homeobox domain of homeobox2 protein otx2
119	<a href="#">c6fkgC_</a>	Alignment	not modelled	51.3	18	<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.
120	<a href="#">d1bw5a_</a>	Alignment	not modelled	51.2	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain