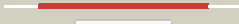


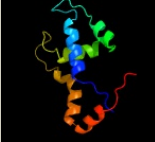
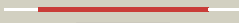


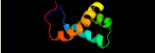



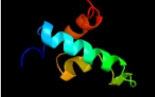
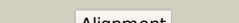















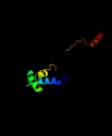

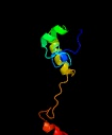


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3381c (- )_3796215_3796541
Date	Fri Aug 9 18:20:04 BST 2019
Unique Job ID	85a11447dd2bc172

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2rn7A_</a>	 Alignment		99.9	43	<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
2	<a href="#">d2jn6a1</a>	 Alignment		99.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
3	<a href="#">c1hlvA_</a>	 Alignment		97.8	19	<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
4	<a href="#">c2elhA_</a>	 Alignment		97.5	18	<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
5	<a href="#">d1hlva1</a>	 Alignment		97.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
6	<a href="#">d1bw6a_</a>	 Alignment		97.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
7	<a href="#">c1u78A_</a>	 Alignment		97.0	10	<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="#">c6paxA_</a>	 Alignment		97.0	19	<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
9	<a href="#">d6paxa1</a>	 Alignment		96.9	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
10	<a href="#">d1pdnc_</a>	 Alignment		96.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
11	<a href="#">d1k78a1</a>	 Alignment		96.7	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain

12	<a href="#">c2gloA</a>	Alignment		96.3	14	<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
13	<a href="#">d2coba1</a>	Alignment		95.7	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
14	<a href="#">c2w48D</a>	Alignment		94.7	14	<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
15	<a href="#">c3hefB</a>	Alignment		94.5	18	<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="#">c2pbxB</a>	Alignment		94.2	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin/protease regulatory protein; <b>PDBTitle:</b> vibrio cholerae hapr
17	<a href="#">c1iufA</a>	Alignment		93.5	6	<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
18	<a href="#">c2k27A</a>	Alignment		93.1	19	<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
19	<a href="#">c2mqkA</a>	Alignment		92.8	13	<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
20	<a href="#">c4go1A</a>	Alignment		92.6	15	<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.
21	<a href="#">c2m8eA</a>	Alignment	not modelled	91.6	13	<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
22	<a href="#">c4lfuA</a>	Alignment	not modelled	90.3	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> crystal structure of escherichia coli sdia in the space group c2
23	<a href="#">c3sztB</a>	Alignment	not modelled	90.2	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
24	<a href="#">d1or7a1</a>	Alignment	not modelled	89.9	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
25	<a href="#">c2lvsA</a>	Alignment	not modelled	89.4	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of a crispr repeat binding protein
26	<a href="#">c3e7qB</a>	Alignment	not modelled	89.4	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
27	<a href="#">c1zljE</a>	Alignment	not modelled	88.6	12	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
28	<a href="#">d1a04a1</a>	Alignment	not modelled	88.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)

29	<a href="#">d2ezla_</a>	Alignment	not modelled	88.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
30	<a href="#">c2q0aA_</a>	Alignment	not modelled	88.3	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional activator protein trar; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
31	<a href="#">c6jqsA_</a>	Alignment	not modelled	88.2	5	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> structure of transcription factor, gere
32	<a href="#">c4cxfA_</a>	Alignment	not modelled	87.9	21	<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
33	<a href="#">c3mzyA_</a>	Alignment	not modelled	87.9	12	<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
34	<a href="#">d1rp3a2</a>	Alignment	not modelled	87.5	17	<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
35	<a href="#">c1h0mD_</a>	Alignment	not modelled	87.3	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional activator protein trar; <b>PDBTitle:</b> three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
36	<a href="#">c2krfB_</a>	Alignment	not modelled	87.0	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma; <b>PDBTitle:</b> nmr solution structure of the dna binding domain of competence protein2 a
37	<a href="#">c4j2nB_</a>	Alignment	not modelled	86.9	20	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
38	<a href="#">d1ijwc_</a>	Alignment	not modelled	86.8	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
39	<a href="#">c1dipA_</a>	Alignment	not modelled	86.5	32	<b>PDB header:</b> acetylation <b>Chain:</b> A: <b>PDB Molecule:</b> delta-sleep-inducing peptide immunoreactive <b>PDBTitle:</b> the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
40	<a href="#">c2jpcA_</a>	Alignment	not modelled	86.3	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
41	<a href="#">c3vdoA_</a>	Alignment	not modelled	85.9	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
42	<a href="#">c3qp5C_</a>	Alignment	not modelled	85.8	10	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> cvir transcriptional regulator; <b>PDBTitle:</b> crystal structure of cvir bound to antagonist chlorolactone (cl)
43	<a href="#">c3frwF_</a>	Alignment	not modelled	85.7	10	<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
44	<a href="#">c1or7A_</a>	Alignment	not modelled	85.6	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
45	<a href="#">d1l3la1</a>	Alignment	not modelled	85.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
46	<a href="#">c3hugA_</a>	Alignment	not modelled	85.5	7	<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
47	<a href="#">d1hcra_</a>	Alignment	not modelled	85.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
48	<a href="#">c3vepA_</a>	Alignment	not modelled	85.1	21	<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
49	<a href="#">c3t0yA_</a>	Alignment	not modelled	85.0	21	<b>PDB header:</b> transcription regulator/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
50	<a href="#">c4j2nA_</a>	Alignment	not modelled	85.0	20	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
51	<a href="#">d1p4wa_</a>	Alignment	not modelled	84.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
52	<a href="#">c2o8xA_</a>	Alignment	not modelled	84.8	10	<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
53	<a href="#">c5uxxC_</a>	Alignment	not modelled	84.8	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
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

54	<a href="#">d1fsea_</a>	Alignment	not modelled	84.3	10	<b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
55	<a href="#">d2fq4a1</a>	Alignment	not modelled	84.2	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
56	<a href="#">c2r0qF_</a>	Alignment	not modelled	84.0	29	<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
57	<a href="#">c6amaO_</a>	Alignment	not modelled	83.9	20	<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
58	<a href="#">d1yioa1</a>	Alignment	not modelled	83.9	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
59	<a href="#">c1x3uA_</a>	Alignment	not modelled	83.9	7	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein fixj; <b>PDBTitle:</b> solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
60	<a href="#">c3korD_</a>	Alignment	not modelled	83.8	13	<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
61	<a href="#">c5fgmA_</a>	Alignment	not modelled	83.8	24	<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
62	<a href="#">c5c8eC_</a>	Alignment	not modelled	83.6	18	<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
63	<a href="#">c2rnjA_</a>	Alignment	not modelled	83.4	7	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> nmr structure of the s. aureus vvar dna binding domain
64	<a href="#">d1fup_</a>	Alignment	not modelled	83.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
65	<a href="#">c5scr1A_</a>	Alignment	not modelled	82.8	24	<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)
66	<a href="#">d1trra_</a>	Alignment	not modelled	82.2	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
67	<a href="#">d2ao9a1</a>	Alignment	not modelled	82.1	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
68	<a href="#">c5zx3F_</a>	Alignment	not modelled	82.0	17	<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
69	<a href="#">c6j05B_</a>	Alignment	not modelled	81.6	14	<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
70	<a href="#">c3c3wB_</a>	Alignment	not modelled	81.3	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulatory protein devr; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
71	<a href="#">d1jhga_</a>	Alignment	not modelled	81.3	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
72	<a href="#">c2dg7A_</a>	Alignment	not modelled	80.8	20	<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 sco03372 from streptomyces coelicolor a3(2)
73	<a href="#">c6in7B_</a>	Alignment	not modelled	80.6	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)
74	<a href="#">c6dvdF_</a>	Alignment	not modelled	80.6	14	<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
75	<a href="#">c3gpvA_</a>	Alignment	not modelled	80.4	7	<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
76	<a href="#">c5dukA_</a>	Alignment	not modelled	80.4	14	<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
77	<a href="#">d2oi8a1</a>	Alignment	not modelled	80.3	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
78	<a href="#">c5wurB_</a>	Alignment	not modelled	80.1	17	<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
						<b>PDB header:</b> dna binding protein

79	<a href="#">c2l4aA</a>	Alignment	not modelled	79.9	12	<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
80	<a href="#">c2kpiA</a>	Alignment	not modelled	79.0	18	<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
81	<a href="#">c6c03A</a>	Alignment	not modelled	78.5	17	<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
82	<a href="#">c2lfwA</a>	Alignment	not modelled	78.3	17	<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
83	<a href="#">c2f07A</a>	Alignment	not modelled	78.3	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yvdt; <b>PDBTitle:</b> crystal structure of yvdt from bacillus subtilis
84	<a href="#">c2ao9H</a>	Alignment	not modelled	78.2	17	<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
85	<a href="#">c4r4eA</a>	Alignment	not modelled	77.9	10	<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
86	<a href="#">d1xsva</a>	Alignment	not modelled	77.4	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> YlxM/p13-like
87	<a href="#">c3ivpD</a>	Alignment	not modelled	77.3	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative transposon-related dna-binding protein; <b>PDBTitle:</b> the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
88	<a href="#">c2gd7B</a>	Alignment	not modelled	77.1	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hexim1 protein; <b>PDBTitle:</b> the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
89	<a href="#">c2gm4B</a>	Alignment	not modelled	76.8	9	<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
90	<a href="#">c2l0kA</a>	Alignment	not modelled	76.6	15	<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
91	<a href="#">c5m9eA</a>	Alignment	not modelled	76.4	17	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> microtubule integrity protein mal3; <b>PDBTitle:</b> interactions between the mal3 eb1-like domain and dis1
92	<a href="#">c5i44E</a>	Alignment	not modelled	76.4	16	<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
93	<a href="#">d1ntca</a>	Alignment	not modelled	76.0	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
94	<a href="#">c5jvmA</a>	Alignment	not modelled	75.9	16	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of kinesin-like protein kif3c and <b>PDBTitle:</b> the neck-linker and alpha 7 helix of mus musculus kif3c
95	<a href="#">d1t33a1</a>	Alignment	not modelled	75.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
96	<a href="#">c2d6yA</a>	Alignment	not modelled	75.4	20	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr family regulatory protein; <b>PDBTitle:</b> crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)
97	<a href="#">c3gziA</a>	Alignment	not modelled	75.1	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
98	<a href="#">d1rioA</a>	Alignment	not modelled	75.1	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
99	<a href="#">c2guhA</a>	Alignment	not modelled	74.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
100	<a href="#">d2g7sa1</a>	Alignment	not modelled	74.6	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
101	<a href="#">c3gp4B</a>	Alignment	not modelled	74.3	16	<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
102	<a href="#">d1lui5a1</a>	Alignment	not modelled	74.2	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
103	<a href="#">d1pb6a1</a>	Alignment	not modelled	74.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain



104	<a href="#">c4fcyA_</a>	Alignment	not modelled	73.1	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
105	<a href="#">d1jt6a1</a>	Alignment	not modelled	73.1	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
106	<a href="#">d1r1ua_</a>	Alignment	not modelled	72.6	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
107	<a href="#">d1llib_</a>	Alignment	not modelled	72.5	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
108	<a href="#">d2cg4a1</a>	Alignment	not modelled	72.4	16	<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="#">c4r24B_</a>	Alignment	not modelled	72.3	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
110	<a href="#">c2k9qB_</a>	Alignment	not modelled	71.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
111	<a href="#">d2vkv1</a>	Alignment	not modelled	71.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
112	<a href="#">c4dzmA_</a>	Alignment	not modelled	71.5	36	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil peptide cc-di; <b>PDBTitle:</b> a de novo designed coiled coil cc-di
113	<a href="#">c4dzmB_</a>	Alignment	not modelled	71.5	36	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coiled-coil peptide cc-di; <b>PDBTitle:</b> a de novo designed coiled coil cc-di
114	<a href="#">c2m8gX_</a>	Alignment	not modelled	71.4	18	<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
115	<a href="#">c1rp3G_</a>	Alignment	not modelled	71.4	13	<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
116	<a href="#">c1ui6B_</a>	Alignment	not modelled	71.1	17	<b>PDB header:</b> antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> a-factor receptor homolog; <b>PDBTitle:</b> crystal structure of gamma-butyrolactone receptor (arpa-like protein)
117	<a href="#">c1umqA_</a>	Alignment	not modelled	71.1	21	<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
118	<a href="#">d1umqa_</a>	Alignment	not modelled	71.1	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
119	<a href="#">c2ia0A_</a>	Alignment	not modelled	70.8	15	<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)
120	<a href="#">d1v7ba1</a>	Alignment	not modelled	70.5	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain