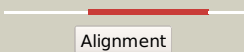

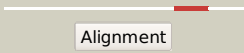

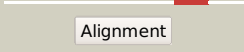





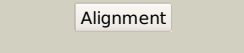

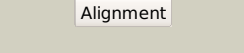



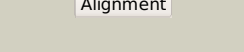

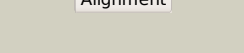
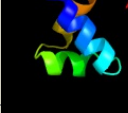
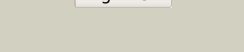



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2242_(-)_2515312_2516556
Date	Mon Aug 5 13:25:37 BST 2019
Unique Job ID	ac64516ecc20b77c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3onqB_</a>	 Alignment		100.0	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of polyketide synthase expression; <b>PDBTitle:</b> crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
2	<a href="#">d1ntca_</a>	 Alignment		96.8	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
3	<a href="#">d1fipa_</a>	 Alignment		96.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
4	<a href="#">c3m1eA_</a>	 Alignment		96.6	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of benm_dbd
5	<a href="#">c1umqA_</a>	 Alignment		96.5	26	<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
6	<a href="#">d1umqa_</a>	 Alignment		96.5	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
7	<a href="#">c5z4yB_</a>	 Alignment		96.5	11	<b>PDB header:</b> dna binding protein <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
8	<a href="#">c5fo5A_</a>	 Alignment		96.5	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator metr; <b>PDBTitle:</b> structure of the dna-binding domain of escherichia coli methionine2 biosynthesis regulator metr
9	<a href="#">c2esnC_</a>	 Alignment		96.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
10	<a href="#">d2esna1</a>	 Alignment		96.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
11	<a href="#">c3ispA_</a>	 Alignment		96.2	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator <b>PDBTitle:</b> crystal structure of argp from mycobacterium tuberculosis

12	<a href="#">c1iz1B_</a>	Alignment		96.2	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysr-type regulatory protein; <b>PDBTitle:</b> crystal structure of cbnr, a lysr family transcriptional2 regulator
13	<a href="#">d1etxa_</a>	Alignment		96.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
14	<a href="#">c5y9sD_</a>	Alignment		96.2	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> vv2_1132; <b>PDBTitle:</b> crystal structure of vv2_1132, a lysr family transcriptional regulator
15	<a href="#">c2m8gX_</a>	Alignment		96.2	23	<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
16	<a href="#">d1etob_</a>	Alignment		96.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
17	<a href="#">c3t1bB_</a>	Alignment		96.2	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> crystal structure of the full-length aphb n100e variant
18	<a href="#">d1b9ma1</a>	Alignment		96.1	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> N-terminal domain of molybdate-dependent transcriptional regulator ModE
19	<a href="#">c3fzjC_</a>	Alignment		95.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> lysr type regulator of tsambcd; <b>PDBTitle:</b> tsar low resolution crystal structure, tetragonal form
20	<a href="#">d1ixca1</a>	Alignment		95.8	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
21	<a href="#">c1zljE_</a>	Alignment	not modelled	95.7	21	<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
22	<a href="#">c3k1nB_</a>	Alignment	not modelled	95.7	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of full-length benm
23	<a href="#">c1b9nA_</a>	Alignment	not modelled	95.6	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein (mode); <b>PDBTitle:</b> regulator from escherichia coli
24	<a href="#">c5y2vA_</a>	Alignment	not modelled	95.6	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco operon transcriptional regulator; <b>PDBTitle:</b> strcutrue of the full-length ccmr complexed with 2-og from2 synechocystis pcc6803
25	<a href="#">c4pzjA_</a>	Alignment	not modelled	95.5	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> 1.60 angstrom resolution crystal structure of a transcriptional2 regulator of the lysr family from eggerthella lenta dsm 2243
26	<a href="#">c1g2hA_</a>	Alignment	not modelled	95.5	19	<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
27	<a href="#">d1g2ha_</a>	Alignment	not modelled	95.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
28	<a href="#">c3hugA_</a>	Alignment	not modelled	95.5	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
29	<a href="#">c3fzvC_</a>	Alignment	not modelled	95.4	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
30	<a href="#">c5ydwB_</a>	Alignment	not modelled	95.4	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell density-dependent motility repressor; <b>PDBTitle:</b> full-length structure of hypt from salmonella typhimuriuma2 (hypochlorite-specific lysr-type transcriptional regulator)
31	<a href="#">c4I5eA_</a>	Alignment	not modelled	95.3	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
32	<a href="#">c5m7nA_</a>	Alignment	not modelled	95.3	19	<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 crystal direct automated mounting and cryo-cooling3 technology
33	<a href="#">c3hhgF_</a>	Alignment	not modelled	95.2	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> structure of crga, a lysr-type transcriptional regulator from 2 neisseria meningitidis.
34	<a href="#">c6g4rE_</a>	Alignment	not modelled	95.1	14	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> hydrogen peroxide-inducible genes activator; <b>PDBTitle:</b> corynebacterium glutamicum oxyr c206s mutant, h2o2-bound
35	<a href="#">c3e7ID_</a>	Alignment	not modelled	95.0	6	<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
36	<a href="#">d1or7a1</a>	Alignment	not modelled	95.0	21	<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
37	<a href="#">c4lfuA_</a>	Alignment	not modelled	94.9	18	<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
38	<a href="#">d1rp3a2</a>	Alignment	not modelled	94.3	8	<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
39	<a href="#">c6c03A_</a>	Alignment	not modelled	94.2	11	<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
40	<a href="#">c2ijjB_</a>	Alignment	not modelled	94.2	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> molybdenum-binding transcriptional repressor; <b>PDBTitle:</b> the structure of a putative mode from agrobacterium tumefaciens.
41	<a href="#">c3qp5C_</a>	Alignment	not modelled	94.2	11	<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)
42	<a href="#">d1a04a1</a>	Alignment	not modelled	94.1	18	<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)
43	<a href="#">c3sztB_</a>	Alignment	not modelled	94.0	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
44	<a href="#">c2rnjA_</a>	Alignment	not modelled	94.0	13	<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
45	<a href="#">d1l3la1</a>	Alignment	not modelled	94.0	21	<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="#">c1ojlD_</a>	Alignment	not modelled	93.9	30	<b>PDB header:</b> response regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulatory protein zrar; <b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
47	<a href="#">d1fsea_</a>	Alignment	not modelled	93.8	21	<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)
48	<a href="#">c6jqsa_</a>	Alignment	not modelled	93.7	15	<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
49	<a href="#">d1p4wa_</a>	Alignment	not modelled	93.7	20	<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)
50	<a href="#">c2krfB_</a>	Alignment	not modelled	93.4	15	<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
51	<a href="#">d1yioa1</a>	Alignment	not modelled	93.2	15	<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	93.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc

53	<a href="#">c2q0aA</a>	Alignment	not modelled	93.0	13	<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
54	<a href="#">c3vepA</a>	Alignment	not modelled	92.9	19	<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
55	<a href="#">c5fgmA</a>	Alignment	not modelled	92.8	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
56	<a href="#">c1h0mD</a>	Alignment	not modelled	92.7	21	<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
57	<a href="#">c6ideA</a>	Alignment	not modelled	92.4	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator luxr family; <b>PDBTitle:</b> crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
58	<a href="#">c5o8yG</a>	Alignment	not modelled	92.3	16	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> transcriptional regulatory protein rcsb; <b>PDBTitle:</b> conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
59	<a href="#">c1x3uA</a>	Alignment	not modelled	92.0	15	<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="#">c6dvdF</a>	Alignment	not modelled	91.9	16	<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
61	<a href="#">d2cg4a1</a>	Alignment	not modelled	91.2	21	<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
62	<a href="#">c3cloC</a>	Alignment	not modelled	90.9	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
63	<a href="#">c2jpcA</a>	Alignment	not modelled	90.6	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
64	<a href="#">c6in7B</a>	Alignment	not modelled	90.5	20	<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)
65	<a href="#">c4if4A</a>	Alignment	not modelled	90.3	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the magnesium and berylliofluoride-activated vvar2 from staphylococcus aureus
66	<a href="#">c5zx3F</a>	Alignment	not modelled	90.1	16	<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
67	<a href="#">c2cfxD</a>	Alignment	not modelled	89.7	21	<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
68	<a href="#">c2e1cA</a>	Alignment	not modelled	89.7	16	<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
69	<a href="#">c4x6gG</a>	Alignment	not modelled	89.5	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> oxyr; <b>PDBTitle:</b> full-length oxyr c199d from pseudomonas aeruginosa
70	<a href="#">d2cfxa1</a>	Alignment	not modelled	89.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
71	<a href="#">c1or7A</a>	Alignment	not modelled	89.2	21	<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
72	<a href="#">c2vbzA</a>	Alignment	not modelled	89.1	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
73	<a href="#">c2cg4B</a>	Alignment	not modelled	88.8	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
74	<a href="#">c4czdA</a>	Alignment	not modelled	88.6	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
75	<a href="#">c2lfwA</a>	Alignment	not modelled	88.4	20	<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
76	<a href="#">c5hevC</a>	Alignment	not modelled	88.4	16	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the berylliofluoride-activated liar from2 enterococcus faecium
77	<a href="#">c2l4aA</a>	Alignment	not modelled	88.2	14	<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

78	<a href="#">d1i1ga1</a>	Alignment	not modelled	88.1	28	<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
79	<a href="#">c2e7xA</a>	Alignment	not modelled	87.8	21	<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
80	<a href="#">d1xsva</a>	Alignment	not modelled	87.7	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
81	<a href="#">c2p6tH</a>	Alignment	not modelled	87.6	21	<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
82	<a href="#">d2cyya1</a>	Alignment	not modelled	87.5	10	<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
83	<a href="#">d2coba1</a>	Alignment	not modelled	87.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
84	<a href="#">c3i4pA</a>	Alignment	not modelled	87.1	15	<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
85	<a href="#">c3klnC</a>	Alignment	not modelled	87.0	28	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
86	<a href="#">c2dbbA</a>	Alignment	not modelled	86.5	10	<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
87	<a href="#">c1i1gA</a>	Alignment	not modelled	86.2	24	<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
88	<a href="#">c2q1zA</a>	Alignment	not modelled	86.1	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rpoe, ecf sigE; <b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides sigE in complex with the2 anti-sigma chrr
89	<a href="#">c4cxfA</a>	Alignment	not modelled	86.0	17	<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
90	<a href="#">c5f64C</a>	Alignment	not modelled	86.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> positive transcription regulator evga; <b>PDBTitle:</b> putative positive transcription regulator (sensor evgs) from shigella2 flexneri
91	<a href="#">c5chhA</a>	Alignment	not modelled	85.8	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arac family transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
92	<a href="#">d2jn6a1</a>	Alignment	not modelled	85.8	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
93	<a href="#">c3mzyA</a>	Alignment	not modelled	85.0	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
94	<a href="#">c4pccC</a>	Alignment	not modelled	84.8	28	<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)
95	<a href="#">d1s7oa</a>	Alignment	not modelled	84.7	13	<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
96	<a href="#">c3vdoA</a>	Alignment	not modelled	84.4	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
97	<a href="#">c1zn2A</a>	Alignment	not modelled	83.1	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator styr
98	<a href="#">c2gqqB</a>	Alignment	not modelled	82.4	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
99	<a href="#">c1u78A</a>	Alignment	not modelled	82.4	21	<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
100	<a href="#">c3t0yA</a>	Alignment	not modelled	82.3	11	<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
101	<a href="#">c2ia0A</a>	Alignment	not modelled	81.8	21	<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)
102	<a href="#">c5uxxC</a>	Alignment	not modelled	81.2	17	<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>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, asnc



103	<a href="#">c4czdD_</a>	Alignment	not modelled	81.0	12	family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
104	<a href="#">c4yn8A_</a>	Alignment	not modelled	80.7	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator chra; <b>PDBTitle:</b> crystal structure of response regulator chra in heme-sensing two2 component system
105	<a href="#">d1jhfa1</a>	Alignment	not modelled	80.3	17	<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
106	<a href="#">c3hyiA_</a>	Alignment	not modelled	80.3	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> protein duf199/whia; <b>PDBTitle:</b> crystal structure of full-length duf199/whia from therratoga maritima
107	<a href="#">d1ttya_</a>	Alignment	not modelled	79.7	16	<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
108	<a href="#">d1smyf2</a>	Alignment	not modelled	79.3	11	<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
109	<a href="#">c5ae5A_</a>	Alignment	not modelled	78.4	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lysr-type regulatory protein; <b>PDBTitle:</b> structures of inactive and activated dntr provide conclusive evidence2 for the mechanism of action of lysr transcription factors
110	<a href="#">c1rn1A_</a>	Alignment	not modelled	77.8	18	<b>PDB header:</b> signal transduction protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite response regulator protein narl; <b>PDBTitle:</b> the nitrate/nitrite response regulator protein narl from narl
111	<a href="#">c4g6qA_</a>	Alignment	not modelled	77.1	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein kfla 6221 from2 krillibella flavida dsm 17836
112	<a href="#">c4ch7A_</a>	Alignment	not modelled	77.0	5	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nird-like protein; <b>PDBTitle:</b> crystal structure of the siroheme decarboxylase nirdl
113	<a href="#">d1ulya_</a>	Alignment	not modelled	76.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
114	<a href="#">c4uiqA_</a>	Alignment	not modelled	76.6	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> globin-coupled sensor with diguanylate cyclase activity; <b>PDBTitle:</b> isolated globin domain of the bordetella pertussis globin-2 coupled sensor with a heme at the dimer interface
115	<a href="#">c5xe7A_</a>	Alignment	not modelled	76.5	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigj; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
116	<a href="#">c6amaQ_</a>	Alignment	not modelled	76.3	28	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> O: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> structure of s. coelicolor/s. venezuelae bidc-smea-ssfa complex to2 3.09 angstrom
117	<a href="#">c2rn7A_</a>	Alignment	not modelled	75.8	19	<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
118	<a href="#">c5wurB_</a>	Alignment	not modelled	75.7	9	<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
119	<a href="#">c4zvbD_</a>	Alignment	not modelled	75.2	7	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> diguanylate cyclase dosc; <b>PDBTitle:</b> crystal structure of globin domain of the e. coli dosc - form ii2 (ferrous)
120	<a href="#">c5z7iC_</a>	Alignment	not modelled	73.7	23	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle regulatory protein gcra; <b>PDBTitle:</b> caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna