
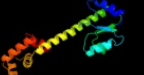


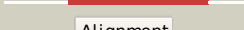

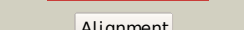



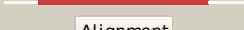







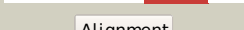












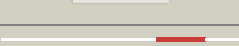



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zn2A_</a>	 Alignment		99.8	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator styr
2	<a href="#">c1h0mD_</a>	 Alignment		99.7	10	<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 protein2 trar bound to its autoinducer and to its target dna
3	<a href="#">c3c3wB_</a>	 Alignment		99.7	11	<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
4	<a href="#">c2q0oA_</a>	 Alignment		99.7	10	<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
5	<a href="#">c3sztB_</a>	 Alignment		99.7	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
6	<a href="#">c3qp5C_</a>	 Alignment		99.7	16	<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)
7	<a href="#">c1rnlA_</a>	 Alignment		99.7	13	<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
8	<a href="#">c3klnC_</a>	 Alignment		99.6	17	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
9	<a href="#">d1p4wa_</a>	 Alignment		99.6	16	<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)
10	<a href="#">c1zljE_</a>	 Alignment		99.5	19	<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
11	<a href="#">d1fsea_</a>	 Alignment		99.5	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)

12	<a href="#">c2krfB_</a>	Alignment		99.4	19	<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
13	<a href="#">c3cloC_</a>	Alignment		99.4	17	<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
14	<a href="#">d1a04a1</a>	Alignment		99.4	23	<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)
15	<a href="#">d1l3la1</a>	Alignment		99.4	16	<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)
16	<a href="#">d1yioa1</a>	Alignment		99.4	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)
17	<a href="#">c2rniA_</a>	Alignment		99.4	20	<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
18	<a href="#">c1x3uA_</a>	Alignment		99.4	21	<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
19	<a href="#">c2jpcA_</a>	Alignment		99.3	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
20	<a href="#">c1kgsA_</a>	Alignment		99.1	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding response regulator d; <b>PDBTitle:</b> crystal structure at 1.50 a of an ompR/phob homolog from thermotoga2 maritima
21	<a href="#">c3q9sA_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> crystal structure of rra(1-215) from deinococcus radiodurans
22	<a href="#">c2oqrA_</a>	Alignment	not modelled	98.8	11	<b>PDB header:</b> transcription,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory transduction protein regx3; <b>PDBTitle:</b> the structure of the response regulator regx3 from mycobacterium2 tuberculosis
23	<a href="#">c1ys7B_</a>	Alignment	not modelled	98.7	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein prra; <b>PDBTitle:</b> crystal structure of the response regulator protein prra complexed with2 mg2+
24	<a href="#">c2gwrA_</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator mtra; <b>PDBTitle:</b> crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
25	<a href="#">c1p2fA_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompR/phob homolog
26	<a href="#">c3r0jA_</a>	Alignment	not modelled	98.3	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> possible two component system response transcriptional <b>PDBTitle:</b> structure of phop from mycobacterium tuberculosis
27	<a href="#">d1ttya_</a>	Alignment	not modelled	98.3	9	<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
28	<a href="#">d1rp3a2</a>	Alignment	not modelled	98.1	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> Sigma4 domain

29	<a href="#">dlxsva_</a>	Alignment	not modelled	98.1	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> YlxM/p13-like
30	<a href="#">d2p7vb1</a>	Alignment	not modelled	98.1	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> Sigma4 domain
31	<a href="#">c2o8xA_</a>	Alignment	not modelled	98.1	15	<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
32	<a href="#">d1smvf2</a>	Alignment	not modelled	98.1	7	<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="#">d1or7a1</a>	Alignment	not modelled	98.1	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
34	<a href="#">c3hugA_</a>	Alignment	not modelled	98.1	14	<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 sigl
35	<a href="#">d1ku3a_</a>	Alignment	not modelled	98.0	6	<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
36	<a href="#">d1ku7a_</a>	Alignment	not modelled	98.0	7	<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="#">c3mzyA_</a>	Alignment	not modelled	98.0	30	<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
38	<a href="#">d1s7oa_</a>	Alignment	not modelled	97.9	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> YlxM/p13-like
39	<a href="#">c1rp3G_</a>	Alignment	not modelled	97.8	14	<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-sigma2 complex, sigma-28/flgm
40	<a href="#">c1or7A_</a>	Alignment	not modelled	97.8	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
41	<a href="#">c2hqrA_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
42	<a href="#">c2q1zA_</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rpoe, ecf sigc; <b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides sigc in complex with the2 anti-sigma chr
43	<a href="#">d1s8na_</a>	Alignment	not modelled	97.3	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
44	<a href="#">c3t72o_</a>	Alignment	not modelled	97.2	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> O: <b>PDB Molecule:</b> pho box dna (strand 1); <b>PDBTitle:</b> phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
45	<a href="#">c1l9uH_</a>	Alignment	not modelled	97.1	7	<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
46	<a href="#">c2a6eF_</a>	Alignment	not modelled	96.9	7	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> crystal structure of the t. thermophilus rna polymerase2 holoenzyme
47	<a href="#">d2cg4a1</a>	Alignment	not modelled	96.9	7	<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
48	<a href="#">d1jhfa1</a>	Alignment	not modelled	96.8	14	<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
49	<a href="#">c3cwoX_</a>	Alignment	not modelled	96.6	8	<b>PDB header:</b> de novo protein <b>Chain:</b> X: <b>PDB Molecule:</b> beta/alpha-barrel protein based on 1thf and 1trny; <b>PDBTitle:</b> a beta/alpha-barrel built by the combination of fragments2 from different folds
50	<a href="#">c2wteB_</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> csa3; <b>PDBTitle:</b> the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
51	<a href="#">c1u78A_</a>	Alignment	not modelled	96.3	14	<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
52	<a href="#">d1biaa1</a>	Alignment	not modelled	96.3	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
53	<a href="#">d1stza1</a>	Alignment	not modelled	96.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain

54	<a href="#">c2vbzA</a>	Alignment	not modelled	96.2	14	<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
55	<a href="#">d2cyya1</a>	Alignment	not modelled	96.2	12	<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
56	<a href="#">d2cfxa1</a>	Alignment	not modelled	96.2	12	<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
57	<a href="#">c2cg4B</a>	Alignment	not modelled	96.1	7	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
58	<a href="#">c2p6H</a>	Alignment	not modelled	96.1	14	<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
59	<a href="#">d2d1ha1</a>	Alignment	not modelled	96.1	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
60	<a href="#">dlilga1</a>	Alignment	not modelled	96.0	12	<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
61	<a href="#">c3iwfA</a>	Alignment	not modelled	96.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
62	<a href="#">c2e1cA</a>	Alignment	not modelled	95.9	12	<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
63	<a href="#">c2l4aA</a>	Alignment	not modelled	95.9	13	<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
64	<a href="#">dlj5ya1</a>	Alignment	not modelled	95.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
65	<a href="#">c2e7xA</a>	Alignment	not modelled	95.9	14	<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
66	<a href="#">c3iydF</a>	Alignment	not modelled	95.8	11	<b>PDB header:</b> transcription/dna <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
67	<a href="#">c3cz5B</a>	Alignment	not modelled	95.8	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> two-component response regulator, luxr family; <b>PDBTitle:</b> crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
68	<a href="#">c2dbbA</a>	Alignment	not modelled	95.7	12	<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
69	<a href="#">c3r0aB</a>	Alignment	not modelled	95.6	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
70	<a href="#">cli1ga</a>	Alignment	not modelled	95.6	12	<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
71	<a href="#">c3k2zA</a>	Alignment	not modelled	95.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> crystal structure of a lexa protein from thermotoga maritima
72	<a href="#">c2x4hA</a>	Alignment	not modelled	95.6	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
73	<a href="#">c1b9nA</a>	Alignment	not modelled	95.4	6	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein (mode); <b>PDBTitle:</b> regulator from escherichia coli
74	<a href="#">c2fa5B</a>	Alignment	not modelled	95.2	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator marr/emrr family; <b>PDBTitle:</b> the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
75	<a href="#">c2ia0A</a>	Alignment	not modelled	95.2	12	<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)
76	<a href="#">c3deuB</a>	Alignment	not modelled	95.2	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator slyA; <b>PDBTitle:</b> crystal structure of transcription regulatory protein slyA2 from salmonella typhimurium in complex with salicylate3 ligands
77	<a href="#">d3broa1</a>	Alignment	not modelled	95.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
78	<a href="#">d1ys7a2</a>	Alignment	not modelled	95.2	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related

79	<a href="#">c3cuoB</a>		Alignment	not modelled	95.1	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
80	<a href="#">d3deua1</a>		Alignment	not modelled	95.1	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
81	<a href="#">c2nnnB</a>		Alignment	not modelled	95.0	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
82	<a href="#">c2cfxD</a>		Alignment	not modelled	95.0	12	<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
83	<a href="#">d1rlua</a>		Alignment	not modelled	94.9	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
84	<a href="#">d2fbha1</a>		Alignment	not modelled	94.8	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
85	<a href="#">c3fm5D</a>		Alignment	not modelled	94.8	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1
86	<a href="#">d2p4wa1</a>		Alignment	not modelled	94.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
87	<a href="#">c3tgnA</a>		Alignment	not modelled	94.8	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr; <b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
88	<a href="#">d1okra</a>		Alignment	not modelled	94.8	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
89	<a href="#">c3eulB</a>		Alignment	not modelled	94.7	7	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> possible nitrate/nitrite response transcriptional <b>PDBTitle:</b> structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
90	<a href="#">c6paxA</a>		Alignment	not modelled	94.7	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
91	<a href="#">c3cjnA</a>		Alignment	not modelled	94.7	4	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
92	<a href="#">d1ku9a</a>		Alignment	not modelled	94.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
93	<a href="#">d1pdnc</a>		Alignment	not modelled	94.6	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
94	<a href="#">c3frwF</a>		Alignment	not modelled	94.6	13	<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 trp protein from ruminococcus obeum
95	<a href="#">d1p6ra</a>		Alignment	not modelled	94.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
96	<a href="#">d1ixca1</a>		Alignment	not modelled	94.5	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
97	<a href="#">c3bj6B</a>		Alignment	not modelled	94.5	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcription regulator sp03579
98	<a href="#">c2rdpA</a>		Alignment	not modelled	94.4	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr; <b>PDBTitle:</b> the structure of a marr family protein from bacillus2 stearothermophilus
99	<a href="#">c3i4pA</a>		Alignment	not modelled	94.4	10	<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
100	<a href="#">d1rlta</a>		Alignment	not modelled	94.4	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
101	<a href="#">c2r0qF</a>		Alignment	not modelled	94.4	15	<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
102	<a href="#">c2zxiB</a>		Alignment	not modelled	94.3	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein walr; <b>PDBTitle:</b> crystal structure of yycf dna-binding domain from staphylococcus2 aureus
103	<a href="#">c2hwvA</a>		Alignment	not modelled	94.3	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator vicr; <b>PDBTitle:</b> crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
104	<a href="#">c3k0A</a>		Alignment	not modelled	94.3	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein;



104	<a href="#">c3kviA_</a>	Alignment	not modelled	94.3	11	<b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
105	<a href="#">d2esna1</a>	Alignment	not modelled	94.2	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
106	<a href="#">c1r22B_</a>	Alignment	not modelled	94.2	5	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
107	<a href="#">c2vn2B_</a>	Alignment	not modelled	94.2	19	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome replication initiation protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
108	<a href="#">d2a61a1</a>	Alignment	not modelled	94.2	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
109	<a href="#">d1sfxa_</a>	Alignment	not modelled	94.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
110	<a href="#">c3bpxB_</a>	Alignment	not modelled	94.2	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
111	<a href="#">d1gxqa_</a>	Alignment	not modelled	94.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
112	<a href="#">c3eq2A_</a>	Alignment	not modelled	94.1	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator; <b>PDBTitle:</b> structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
113	<a href="#">c3m1eA_</a>	Alignment	not modelled	94.0	13	<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
114	<a href="#">c3b2nA_</a>	Alignment	not modelled	94.0	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein q99uf4; <b>PDBTitle:</b> crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
115	<a href="#">c2ijlB_</a>	Alignment	not modelled	94.0	9	<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.
116	<a href="#">c3ispA_</a>	Alignment	not modelled	93.9	15	<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
117	<a href="#">d2hr3a1</a>	Alignment	not modelled	93.9	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
118	<a href="#">c2gxgA_</a>	Alignment	not modelled	93.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfobus tokodaii strain7
119	<a href="#">d1lnwa_</a>	Alignment	not modelled	93.9	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
120	<a href="#">d1k78a1</a>	Alignment	not modelled	93.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain