




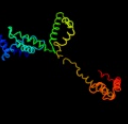















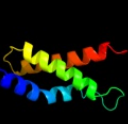


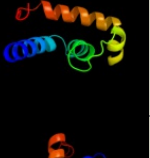

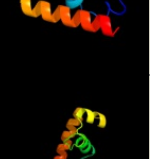
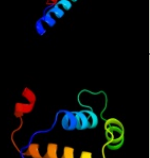
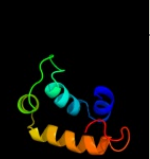

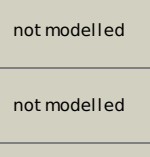


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2a6eF_</a>	 Alignment		100.0	46	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> crystal structure of the t. thermophilus rna polymerase2 holoenzyme
2	<a href="#">c3iydF_</a>	 Alignment		100.0	40	<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
3	<a href="#">c1l9uH_</a>	 Alignment		100.0	47	<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
4	<a href="#">c1ku2A_</a>	 Alignment		100.0	57	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> sigma factor siga; <b>PDBTitle:</b> crystal structure of thermus aquaticus rna polymerase sigma2 subunit fragment containing regions 1.2 to 3.1
5	<a href="#">d1ku2a2</a>	 Alignment		100.0	66	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
6	<a href="#">d1smyf3</a>	 Alignment		100.0	66	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
7	<a href="#">c1rp3G_</a>	 Alignment		100.0	24	<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
8	<a href="#">d1siga_</a>	 Alignment		100.0	50	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
9	<a href="#">c1or7A_</a>	 Alignment		99.9	18	<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
10	<a href="#">c2q1zA_</a>	 Alignment		99.9	18	<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
11	<a href="#">d1rp3a3</a>	 Alignment		99.8	27	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors

12	<a href="#">c3mzyA_</a>	Alignment		99.8	23	<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 from <i>Mycobacterium tuberculosis</i> H37Rv to 2.5 Å
13	<a href="#">d1smyf2</a>	Alignment		99.7	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
14	<a href="#">c3t72o_</a>	Alignment		99.6	34	<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
15	<a href="#">d1ku7a_</a>	Alignment		99.6	35	<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
16	<a href="#">d1ku3a_</a>	Alignment		99.5	41	<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
17	<a href="#">c3hugA_</a>	Alignment		99.4	23	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI
18	<a href="#">d2p7vb1</a>	Alignment		99.4	40	<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
19	<a href="#">d1ttya_</a>	Alignment		99.4	42	<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
20	<a href="#">d1rp3a2</a>	Alignment		99.3	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
21	<a href="#">d1or7a2</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
22	<a href="#">d1or7b2</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
23	<a href="#">d1or7a1</a>	Alignment	not modelled	99.1	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
24	<a href="#">c2o7gA_</a>	Alignment	not modelled	99.1	20	<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 pribnow box recognition region of sigC from <i>Mycobacterium tuberculosis</i> H37Rv
25	<a href="#">d1ku2a1</a>	Alignment	not modelled	99.0	40	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma3 domain
26	<a href="#">d1xsva_</a>	Alignment	not modelled	99.0	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
27	<a href="#">d1s7oa_</a>	Alignment	not modelled	98.9	15	<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
28	<a href="#">c2o8xA_</a>	Alignment	not modelled	98.9	16	<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 of <i>Mycobacterium tuberculosis</i> sigC <b>PDB header:</b> protein binding

29	<a href="#">c1l0oC_</a>	Alignment	not modelled	98.8	22	<b>Chain:</b> C: <b>PDB Molecule:</b> sigma factor; <b>PDBTitle:</b> crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
30	<a href="#">d1l0oc_</a>	Alignment	not modelled	98.8	22	<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="#">d1h3la_</a>	Alignment	not modelled	98.5	14	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
32	<a href="#">d1rp3a1</a>	Alignment	not modelled	98.4	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> Sigma3 domain
33	<a href="#">d1yioa1</a>	Alignment	not modelled	98.2	13	<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)
34	<a href="#">c3qp5C_</a>	Alignment	not modelled	98.0	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)
35	<a href="#">c3n0rA_</a>	Alignment	not modelled	98.0	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr stress response regulator at 1.25 angstrom2 resolution
36	<a href="#">c2q0oA_</a>	Alignment	not modelled	97.9	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
37	<a href="#">c1x3uA_</a>	Alignment	not modelled	97.9	13	<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
38	<a href="#">c3sztB_</a>	Alignment	not modelled	97.9	23	<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
39	<a href="#">c1h0mD_</a>	Alignment	not modelled	97.8	23	<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
40	<a href="#">c1zljE_</a>	Alignment	not modelled	97.8	26	<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 hypoxi2 response regulator dosr c-terminal domain
41	<a href="#">d1a04a1</a>	Alignment	not modelled	97.8	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)
42	<a href="#">c2krfB_</a>	Alignment	not modelled	97.6	11	<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
43	<a href="#">c2rnjA_</a>	Alignment	not modelled	97.6	15	<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
44	<a href="#">d1fsea_</a>	Alignment	not modelled	97.6	26	<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)
45	<a href="#">d1l3la1</a>	Alignment	not modelled	97.5	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)
46	<a href="#">d1p4wa_</a>	Alignment	not modelled	97.5	19	<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)
47	<a href="#">c3cloC_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> transcription <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
48	<a href="#">c3c3wB_</a>	Alignment	not modelled	97.4	24	<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
49	<a href="#">c3klinC_</a>	Alignment	not modelled	97.2	11	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
50	<a href="#">c1zn2A_</a>	Alignment	not modelled	97.0	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 styrr
51	<a href="#">c2w48D_</a>	Alignment	not modelled	97.0	17	<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
52	<a href="#">c2jpcA_</a>	Alignment	not modelled	96.9	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
53	<a href="#">c1rn1A_</a>	Alignment	not modelled	96.7	16	<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
						<b>PDB header:</b> dna binding protein/dna

54	<a href="#">c1u78A_</a>	Alignment	not modelled	96.1	21	<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
55	<a href="#">d2d1ha1</a>	Alignment	not modelled	95.5	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
56	<a href="#">d1jhfa1</a>	Alignment	not modelled	95.2	19	<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
57	<a href="#">c2bnoA_</a>	Alignment	not modelled	94.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
58	<a href="#">c2w7nA_</a>	Alignment	not modelled	94.7	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation
59	<a href="#">c2o38A_</a>	Alignment	not modelled	94.1	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative xre family transcriptional regulator
60	<a href="#">d2o38a1</a>	Alignment	not modelled	94.1	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
61	<a href="#">d2cfxa1</a>	Alignment	not modelled	94.0	14	<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="#">d1pdnc_</a>	Alignment	not modelled	93.9	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
63	<a href="#">c6paxA_</a>	Alignment	not modelled	93.8	18	<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
64	<a href="#">c2x4ha_</a>	Alignment	not modelled	93.8	11	<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
65	<a href="#">d1stza1</a>	Alignment	not modelled	93.7	23	<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
66	<a href="#">d1trra_</a>	Alignment	not modelled	93.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
67	<a href="#">d2ofya1</a>	Alignment	not modelled	93.6	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
68	<a href="#">d2cg4a1</a>	Alignment	not modelled	93.5	14	<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
69	<a href="#">c3r0aB_</a>	Alignment	not modelled	93.3	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="#">c3fymA_</a>	Alignment	not modelled	93.2	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the 1a structure of ymfM, a putative dna-binding membrane2 protein from staphylococcus aureus
71	<a href="#">c2elha_</a>	Alignment	not modelled	93.1	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cgl1849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cgl1849-pa
72	<a href="#">c3k2za_</a>	Alignment	not modelled	93.0	15	<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
73	<a href="#">c3op9A_</a>	Alignment	not modelled	92.8	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> pli0006 protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator from listeria innocua
74	<a href="#">c2kpiA_</a>	Alignment	not modelled	92.8	9	<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
75	<a href="#">c2l4aA_</a>	Alignment	not modelled	92.7	12	<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
76	<a href="#">c2p6th_</a>	Alignment	not modelled	92.6	11	<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
77	<a href="#">d1k78a1</a>	Alignment	not modelled	92.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
78	<a href="#">c2vbza_</a>	Alignment	not modelled	92.6	21	<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
79	<a href="#">c2cg4B_</a>	Alignment	not modelled	92.5	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc

80	<a href="#">d1jhga_</a>	Alignment	not modelled	92.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
81	<a href="#">d2b5aa1</a>	Alignment	not modelled	92.4	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
82	<a href="#">c2fjrB_</a>	Alignment	not modelled	92.4	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of bacteriophage 186
83	<a href="#">d2a6ca1</a>	Alignment	not modelled	92.3	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
84	<a href="#">d1biaa1</a>	Alignment	not modelled	92.3	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
85	<a href="#">c2cfxD_</a>	Alignment	not modelled	92.3	16	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator Irpc; <b>PDBTitle:</b> structure of b.subtilis Irpc
86	<a href="#">d2cyya1</a>	Alignment	not modelled	92.3	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
87	<a href="#">d2b0la1</a>	Alignment	not modelled	92.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Cody HTH domain
88	<a href="#">d1vz0a1</a>	Alignment	not modelled	92.3	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
89	<a href="#">c3f6wE_</a>	Alignment	not modelled	92.3	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> xre-family like protein; <b>PDBTitle:</b> xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
90	<a href="#">c2wteB_</a>	Alignment	not modelled	92.3	6	<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 sulfolobus solfataricus at 1.8 angstrom resolution.
91	<a href="#">d1nr3a_</a>	Alignment	not modelled	92.2	19	<b>Fold:</b> DNA-binding protein Tfx <b>Superfamily:</b> DNA-binding protein Tfx <b>Family:</b> DNA-binding protein Tfx
92	<a href="#">c2r0qF_</a>	Alignment	not modelled	92.2	22	<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
93	<a href="#">d2croa_</a>	Alignment	not modelled	92.1	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
94	<a href="#">c2dbbA_</a>	Alignment	not modelled	92.0	13	<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
95	<a href="#">d1i1ga1</a>	Alignment	not modelled	92.0	9	<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
96	<a href="#">c3hyiA_</a>	Alignment	not modelled	91.9	21	<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 thermatoga maritima
97	<a href="#">c1b0nA_</a>	Alignment	not modelled	91.8	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> protein (sinr protein); <b>PDBTitle:</b> sinr protein/sini protein complex
98	<a href="#">d1adra_</a>	Alignment	not modelled	91.8	19	<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="#">c2e7xA_</a>	Alignment	not modelled	91.8	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 Irp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
100	<a href="#">d1y7ya1</a>	Alignment	not modelled	91.8	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
101	<a href="#">c2it0A_</a>	Alignment	not modelled	91.7	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
102	<a href="#">c1y9qA_</a>	Alignment	not modelled	91.5	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
103	<a href="#">c3frwF_</a>	Alignment	not modelled	91.4	12	<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
104	<a href="#">c2ia0A_</a>	Alignment	not modelled	91.3	11	<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)
105	<a href="#">c3kxD_</a>	Alignment	not modelled	91.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of ngo0477 from neisseria gonorrhoeae
						<b>PDB header:</b> transcription



106	<a href="#">c3nqoB_</a>	Alignment	not modelled	91.1	15	<b>Chain:</b> B: <b>PDB Molecule:</b> marr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
107	<a href="#">c3clcC_</a>	Alignment	not modelled	91.1	22	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.esp13961 tetramer in complex with its natural 35 base-pair operator
108	<a href="#">d1ft9a1</a>	Alignment	not modelled	91.0	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
109	<a href="#">dli5za1</a>	Alignment	not modelled	91.0	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
110	<a href="#">c2e1cA_</a>	Alignment	not modelled	90.9	14	<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
111	<a href="#">c2wusR_</a>	Alignment	not modelled	90.9	13	<b>PDB header:</b> structural protein <b>Chain:</b> R: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> bacterial actin mreB assembles in complex with cell shape2 protein rodz
112	<a href="#">c3f52A_</a>	Alignment	not modelled	90.8	11	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> clp gene regulator (clgr); <b>PDBTitle:</b> crystal structure of the clp gene regulator clgr from c. glutamicum
113	<a href="#">d2oz6a1</a>	Alignment	not modelled	90.7	37	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
114	<a href="#">cli1gA_</a>	Alignment	not modelled	90.7	11	<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
115	<a href="#">d2ao9a1</a>	Alignment	not modelled	90.7	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
116	<a href="#">c3mlfC_</a>	Alignment	not modelled	90.7	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> putative transcriptional regulator from staphylococcus aureus.
117	<a href="#">c3korD_</a>	Alignment	not modelled	90.7	10	<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
118	<a href="#">c3fmyA_</a>	Alignment	not modelled	90.7	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
119	<a href="#">c1r22B_</a>	Alignment	not modelled	90.7	17	<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
120	<a href="#">d6paxa1</a>	Alignment	not modelled	90.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain