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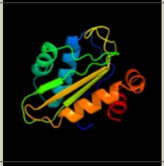
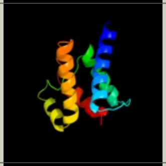
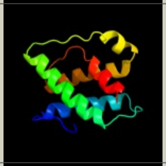
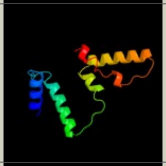
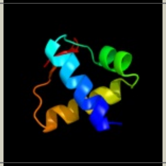
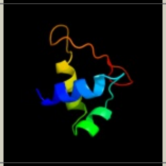
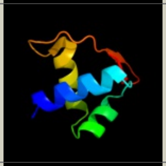
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sqnB_	Alignment		100.0	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**conserved domain protein; **PDBTitle:** putative mga family transcriptional regulator from enterococcus2 faecalis
2	c3bjvA_	Alignment		99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpa; **PDBTitle:** the crystal structure of a putative pts iia(ptxa) from streptococcus2 mutans
3	c2oq3A_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific cryptic phosphotransferase **PDBTitle:** solution structure of the mannitol- specific cryptic2 phosphotransferase enzyme iia cmtb from escherichia coli
4	c2oqtD_	Alignment		99.9	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein spy0176; **PDBTitle:** structural genomics, the crystal structure of a putative2 pts iia domain from streptococcus pyogenes m1 gas
5	c3oxpB_	Alignment		99.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
6	c3oxpA_	Alignment		99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
7	c2a0jA_	Alignment		99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, nitrogen regulatory iia protein; **PDBTitle:** crystal structure of nitrogen regulatory protein iia-ntr from2 neisseria meningitidis
8	c3urrB_	Alignment		99.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts iia-like nitrogen-regulatory protein ptsn; **PDBTitle:** structure of pts iia-like nitrogen-regulatory protein ptsn (bth_i0484)2 (ptsn)
9	d1a3aa_	Alignment		99.9	18	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
10	d1a6ja_	Alignment		99.9	20	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
11	c1h99A_	Alignment		99.9	8	**PDB header:**transcriptional antiterminator **Chain:** A: **PDB Molecule:**transcription antiterminator lict; **PDBTitle:** prd of lict antiterminator from bacillus subtilis

12	d1xiza_	Alignment		99.8	15	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
13	d1h99a2	Alignment		99.6	7	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
14	d1h99a1	Alignment		99.5	8	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
15	c3gwhB_	Alignment		99.5	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional antiterminator (bglg family); **PDBTitle:** crystallographic ab initio protein solution far below atomic2 resolution
16	d1j5ya1	Alignment		98.9	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
17	d1biaa1	Alignment		98.8	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
18	c1j5yA_	Alignment		98.7	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, biotin repressor family; **PDBTitle:** crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
19	c1tvmA_	Alignment		98.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
20	d1vkra_	Alignment		98.2	12	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
21	c1vkrA_	Alignment	not modelled	98.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
22	c3czcA_	Alignment	not modelled	98.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
23	c2ewnA_	Alignment	not modelled	97.6	27	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
24	d1stza1	Alignment	not modelled	97.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
25	d2cg4a1	Alignment	not modelled	97.3	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
26	c1u78A_	Alignment	not modelled	97.3	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
27	c2q0oA_	Alignment	not modelled	97.2	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
28	c1h0mD_	Alignment	not modelled	97.2	13	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing

							protein2 trar bound to its autoinducer and to its target dna
29	c3sztB_		Alignment	not modelled	97.2	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
30	c3qp5C_		Alignment	not modelled	97.1	23	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
31	c1ys7B_		Alignment	not modelled	97.1	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
32	d1l3la1		Alignment	not modelled	97.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
33	d1a04a1		Alignment	not modelled	96.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
34	d1p4wa_		Alignment	not modelled	96.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
35	c2cg4B_		Alignment	not modelled	96.8	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
36	c2rnjA_		Alignment	not modelled	96.8	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
37	c1zljE_		Alignment	not modelled	96.8	17	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
38	d1fsea_		Alignment	not modelled	96.8	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
39	c3cloC_		Alignment	not modelled	96.8	21	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 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
40	c2oqrA_		Alignment	not modelled	96.7	19	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
41	d1yioa1		Alignment	not modelled	96.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
42	c2krfB_		Alignment	not modelled	96.6	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
43	c3c3wB_		Alignment	not modelled	96.6	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
44	c1kgsA_		Alignment	not modelled	96.5	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna binding response regulator d; **PDBTitle:** crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
45	c2hqrA_		Alignment	not modelled	96.5	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
46	c3hruA_		Alignment	not modelled	96.5	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
47	c1stzB_		Alignment	not modelled	96.5	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
48	c2hwvA_		Alignment	not modelled	96.5	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding response regulator vicr; **PDBTitle:** crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
49	d1i1ga1		Alignment	not modelled	96.5	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
50	c2it0A_		Alignment	not modelled	96.4	16	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
51	c2l4aA_		Alignment	not modelled	96.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
52	c1x3uA_		Alignment	not modelled	96.4	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj; **PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
53	d2cfxa1		Alignment	not modelled	96.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
54	d1ys7a1	Alignment	not modelled	96.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
55	d2cyya1	Alignment	not modelled	96.3	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
56	c3nufB_	Alignment	not modelled	96.3	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**prd-containing transcription regulator; **PDBTitle:** crystal structure of a prd-containing transcription regulator2 (lsei_2718) from lactobacillus casei atcc 334 at 1.38 a resolution
57	c2zxjB_	Alignment	not modelled	96.2	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein walr; **PDBTitle:** crystal structure of yycf dna-binding domain from staphylococcus2 aureus
58	c1rnlA_	Alignment	not modelled	96.2	17	**PDB header:**signal transduction protein **Chain:** A: **PDB Molecule:**nitrate/nitrite response regulator protein narl; **PDBTitle:** the nitrate/nitrite response regulator protein narl from narl
59	c2gwrA_	Alignment	not modelled	96.1	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dna-binding response regulator mtra; **PDBTitle:** crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
60	c2vbzA_	Alignment	not modelled	96.0	24	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
61	d1gxqa_	Alignment	not modelled	96.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
62	c2pmuD_	Alignment	not modelled	96.0	10	**PDB header:**transcription regulation **Chain:** D: **PDB Molecule:**response regulator phop; **PDBTitle:** crystal structure of the dna-binding domain of phop
63	c2dbbA_	Alignment	not modelled	96.0	26	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
64	c2jpcA_	Alignment	not modelled	95.9	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
65	c1p4xA_	Alignment	not modelled	95.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**staphylococcal accessory regulator a homologue; **PDBTitle:** crystal structure of sars protein from staphylococcus aureus
66	d1o57a1	Alignment	not modelled	95.9	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of Bacillus PurR
67	c2ia0A_	Alignment	not modelled	95.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator pf0864; **PDBTitle:** transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
68	c3lmmA_	Alignment	not modelled	95.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the dip2311 protein from2 corynebacterium diphtheriae, northeast structural genomics3 consortium target cdr35
69	c1f5tA_	Alignment	not modelled	95.9	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
70	c2p6tH_	Alignment	not modelled	95.8	26	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
71	c2x4hA_	Alignment	not modelled	95.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
72	c2e1cA_	Alignment	not modelled	95.7	29	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
73	c3hosA_	Alignment	not modelled	95.7	20	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
74	c1i1gA_	Alignment	not modelled	95.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
75	d1t6sa1	Alignment	not modelled	95.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ScpB/YpuH-like
76	c2jzyA_	Alignment	not modelled	95.7	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein pcor; **PDBTitle:** solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
77	c2qufB	Alignment	not modelled	95.7	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor pf0095;

77	[illegible]	Alignment	not modelled	95.7	17	**PDBTitle:** crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus
78	c2e7xA_	Alignment	not modelled	95.6	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
79	d1xsva_	Alignment	not modelled	95.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
80	c1r22B_	Alignment	not modelled	95.6	18	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**transcriptional repressor smtb; **PDBTitle:** crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
81	c3neuA_	Alignment	not modelled	95.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1836 protein; **PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
82	c3r0jA_	Alignment	not modelled	95.5	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
83	c3q9vB_	Alignment	not modelled	95.5	25	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
84	c2cfxD_	Alignment	not modelled	95.5	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
85	c2h09A_	Alignment	not modelled	95.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
86	d1r1ta_	Alignment	not modelled	95.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
87	c3by6C_	Alignment	not modelled	95.4	20	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
88	c2oqgA_	Alignment	not modelled	95.4	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
89	c2hqnA_	Alignment	not modelled	95.3	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
90	d1opca_	Alignment	not modelled	95.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
91	d1r1ua_	Alignment	not modelled	95.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
92	c2gqqB_	Alignment	not modelled	95.2	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**leucine-responsive regulatory protein; **PDBTitle:** crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
93	d1jhfa1	Alignment	not modelled	95.2	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
94	d2d1ha1	Alignment	not modelled	95.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
95	d1rp3a2	Alignment	not modelled	95.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
96	c3i4pA_	Alignment	not modelled	95.0	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
97	c3f6vA_	Alignment	not modelled	94.9	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
98	d1s7oa_	Alignment	not modelled	94.9	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
99	c2k4jA_	Alignment	not modelled	94.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** arsr dna binding domain
100	c1fx7C_	Alignment	not modelled	94.8	16	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
101	d1p2fa1	Alignment	not modelled	94.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
102	c2zhhA_	Alignment	not modelled	94.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr;

						PDBTitle: crystal structure of soxr
103	c3jthA_	Alignment	not modelled	94.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
104	c2wteB_	Alignment	not modelled	94.7	21	**PDB header:**antiviral protein **Chain:** B: **PDB Molecule:**csa3; **PDBTitle:** the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
105	c2kkoB_	Alignment	not modelled	94.7	25	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**possible transcriptional regulatory protein **PDBTitle:** solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
106	c3hh0C_	Alignment	not modelled	94.6	13	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
107	d1kgsa1	Alignment	not modelled	94.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
108	d1or7a1	Alignment	not modelled	94.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
109	c2jscB_	Alignment	not modelled	94.5	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
110	c1p2fA_	Alignment	not modelled	94.5	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
111	c3hugA_	Alignment	not modelled	94.5	13	**PDB header:**transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
112	c3f6oB_	Alignment	not modelled	94.4	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
113	c1g3wA_	Alignment	not modelled	94.2	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
114	d2p4wa1	Alignment	not modelled	94.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF1790-like
115	c3eqxB_	Alignment	not modelled	94.1	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**fic domain containing transcriptional regulator; **PDBTitle:** crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
116	c2du9A_	Alignment	not modelled	94.1	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
117	d1r8ea1	Alignment	not modelled	94.1	12	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
118	d3bwga1	Alignment	not modelled	94.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
119	c2hs5A_	Alignment	not modelled	93.8	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator gntr; **PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
120	c2z99A_	Alignment	not modelled	93.8	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of scpb from mycobacterium tuberculosis