Phyre2

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Description	P54901
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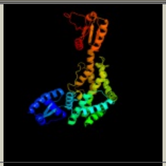
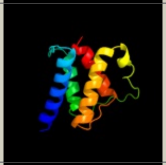
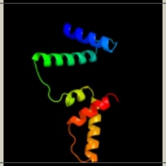
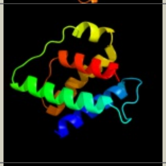
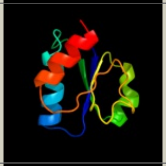
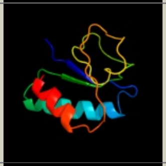
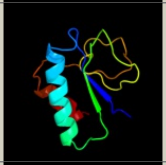
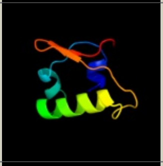
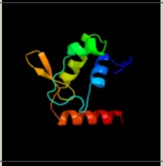
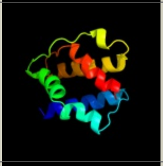
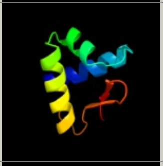
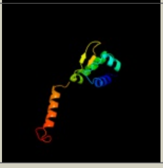
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sqnB_	Alignment		100.0	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**conserved domain protein; **PDBTitle:** putative mga family transcriptional regulator from enterococcus2 faecalis
2	c1h99A_	Alignment		100.0	14	**PDB header:**transcriptional antiterminator **Chain:** A: **PDB Molecule:**transcription antiterminator lict; **PDBTitle:** prd of lict antiterminator from bacillus subtilis
3	d1h99a2	Alignment		99.7	14	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
4	c3gwhB_	Alignment		99.6	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional antiterminator (bglg family); **PDBTitle:** crystallographic ab initio protein solution far below atomic2 resolution
5	d1h99a1	Alignment		99.6	20	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
6	c1tvmA_	Alignment		99.2	14	**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
7	c3czcA_	Alignment		98.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
8	d1vkra_	Alignment		98.9	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
9	c1vkrA_	Alignment		98.9	14	**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
10	d1j5ya1	Alignment		98.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
11	c1j5yA_	Alignment		98.5	18	**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

12	d1biaa1	Alignment		98.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
13	d1o57a1	Alignment		97.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of Bacillus PurR
14	c2ewnA_	Alignment		97.0	19	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
15	c3neuA_	Alignment		96.9	9	**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
16	c3nufB_	Alignment		96.7	23	**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
17	c3by6C_	Alignment		96.5	5	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
18	c1f5tA_	Alignment		96.4	16	**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
19	d1stza1	Alignment		96.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
20	c1o57A_	Alignment		96.2	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
21	c2h09A_	Alignment	not modelled	96.1	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
22	d2d1ha1	Alignment	not modelled	96.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
23	c2l4aA_	Alignment		96.0	17	**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
24	d3bwga1	Alignment	not modelled	95.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
25	c2du9A_	Alignment	not modelled	95.6	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
26	c3hruA_	Alignment	not modelled	95.5	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
27	c2hs5A_	Alignment	not modelled	95.4	15	**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
						PDB header:transcription

28	c2y75F_	Alignment	not modelled	95.3	13	**Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
29	c2it0A_	Alignment	not modelled	95.2	19	**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
30	d1mkma1	Alignment	not modelled	95.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
31	c3bwgA_	Alignment	not modelled	95.1	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yydk; **PDBTitle:** the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
32	c3nbmA_	Alignment	not modelled	95.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
33	c1g3wA_	Alignment	not modelled	95.0	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
34	d1r1ua_	Alignment	not modelled	95.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
35	d1ku7a_	Alignment	not modelled	95.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
36	d2isya1	Alignment	not modelled	94.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
37	c2kkoB_	Alignment	not modelled	94.8	17	**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.
38	c3ihuA_	Alignment	not modelled	94.8	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution
39	d1ku9a_	Alignment	not modelled	94.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
40	c1r22B_	Alignment	not modelled	94.7	14	**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
41	d1ku3a_	Alignment	not modelled	94.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
42	c1e2xA_	Alignment	not modelled	94.7	23	**PDB header:**transcriptional regulation **Chain:** A: **PDB Molecule:**fatty acid metabolism regulator protein; **PDBTitle:** fadr, fatty acid responsive transcription factor from e.2 coli
43	d1g3wa1	Alignment	not modelled	94.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
44	c3fmsA_	Alignment	not modelled	94.6	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of tm0439, a gntr transcriptional2 regulator
45	d1iiba_	Alignment	not modelled	94.6	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
46	c3edpB_	Alignment	not modelled	94.6	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lin2111 protein; **PDBTitle:** the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
47	d1ttya_	Alignment	not modelled	94.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
48	c3f8mA_	Alignment	not modelled	94.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**gntr-family protein transcriptional regulator; **PDBTitle:** crystal structure of phnf from mycobacterium smegmatis
49	d1i1ga1	Alignment	not modelled	94.5	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
50	d1hw1a1	Alignment	not modelled	94.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
51	d2hs5a1	Alignment	not modelled	94.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
52	c1fx7C_	Alignment	not modelled	94.4	15	**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

53	d2cg4a1	Alignment	not modelled	94.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
54	c3cuoB_	Alignment	not modelled	94.1	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
55	c1kgsA_	Alignment	not modelled	94.1	13	**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
56	c3lwfD_	Alignment	not modelled	94.0	8	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
57	c2vbzA_	Alignment	not modelled	94.0	11	**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
58	c2x4hA_	Alignment	not modelled	94.0	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
59	c2q0oA_	Alignment	not modelled	93.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
60	d2cyya1	Alignment	not modelled	93.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
61	c2jscB_	Alignment	not modelled	93.8	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
62	d2p7vb1	Alignment	not modelled	93.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
63	c2hwvA_	Alignment	not modelled	93.7	14	**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.
64	c2l0kA_	Alignment	not modelled	93.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage iii sporulation protein d; **PDBTitle:** nmr solution structure of a transcription factor spoiiid in complex2 with dna
65	c2di3A_	Alignment	not modelled	93.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bacterial regulatory proteins, gntr family; **PDBTitle:** crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
66	c3i4pA_	Alignment	not modelled	93.5	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
67	d2cfxa1	Alignment	not modelled	93.4	2	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
68	c2cfxD_	Alignment	not modelled	93.3	3	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
69	c3k69A_	Alignment	not modelled	93.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
70	c2ia0A_	Alignment	not modelled	93.1	15	**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)
71	c3r0aB_	Alignment	not modelled	93.1	5	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
72	c2cg4B_	Alignment	not modelled	93.1	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
73	d2p5ka1	Alignment	not modelled	93.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
74	c2dbbA_	Alignment	not modelled	92.9	8	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
75	c3pqkD_	Alignment	not modelled	92.8	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
76	c2p6tH_	Alignment	not modelled	92.8	14	**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
77	c1iz1B_	Alignment	not modelled	92.7	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**lysr-type regulatory protein; **PDBTitle:** crystal structure of cbnr, a lysr family transcriptional2

						regulator
78	c2oqrA_	Alignment	not modelled	92.6	14	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
79	d1jhfa1	Alignment	not modelled	92.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
80	c3jthA_	Alignment	not modelled	92.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
81	d1ulya_	Alignment	not modelled	92.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein PH1932
82	c2e7xA_	Alignment	not modelled	92.4	11	**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
83	d1u2wa1	Alignment	not modelled	92.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
84	c2e1cA_	Alignment	not modelled	92.4	14	**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
85	d1p2fa1	Alignment	not modelled	92.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
86	c1i1gA_	Alignment	not modelled	92.3	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
87	d1xsva_	Alignment	not modelled	92.3	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
88	d1i5za1	Alignment	not modelled	92.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
89	c3t1bB_	Alignment	not modelled	92.1	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** crystal structure of the full-length aphb n100e variant
90	d1b4aa1	Alignment	not modelled	92.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
91	c1zljE_	Alignment	not modelled	92.0	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
92	d1or7a1	Alignment	not modelled	92.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
93	d2fxaa1	Alignment	not modelled	91.9	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
94	d1v4ra1	Alignment	not modelled	91.9	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
95	c1h0mD_	Alignment	not modelled	91.8	14	**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
96	c2zkzC_	Alignment	not modelled	91.7	7	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional repressor pagr; **PDBTitle:** crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
97	c1mkmA_	Alignment	not modelled	91.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
98	d2ev0a1	Alignment	not modelled	91.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
99	c2esnC_	Alignment	not modelled	91.4	10	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
100	d1rp3a2	Alignment	not modelled	91.3	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
101	d1r1ta_	Alignment	not modelled	91.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
102	c3f6vA_	Alignment	not modelled	91.3	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
103	c1b4aA_	Alignment	not modelled	91.2	18	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor;

103	c1b4aA_	Alignment	not modelled	91.2	18	**PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus
104	d2hr3a1	Alignment	not modelled	91.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
105	d2p4wa1	Alignment	not modelled	91.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF1790-like
106	c3deuB_	Alignment	not modelled	90.9	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator slya; **PDBTitle:** crystal structure of transcription regulatory protein slya2 from salmonella typhimurium in complex with salicylate3 ligands
107	d2oz6a1	Alignment	not modelled	90.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
108	c2v79B_	Alignment	not modelled	90.9	8	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
109	d2esna1	Alignment	not modelled	90.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LysR-like transcriptional regulators
110	c2wteB_	Alignment	not modelled	90.7	12	**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.
111	c2pmuD_	Alignment	not modelled	90.7	13	**PDB header:**transcription regulation **Chain:** D: **PDB Molecule:**response regulator phop; **PDBTitle:** crystal structure of the dna-binding domain of phop
112	c3ereD_	Alignment	not modelled	90.6	14	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
113	d2h6ca1	Alignment	not modelled	90.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
114	d1ub9a_	Alignment	not modelled	90.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
115	c3g3zA_	Alignment	not modelled	90.4	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
116	c3fzjC_	Alignment	not modelled	90.4	10	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** tsar low resolution crystal structure, tetragonal form
117	c2oqgA_	Alignment	not modelled	90.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
118	c1u78A_	Alignment	not modelled	90.0	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
119	c3hr4C_	Alignment	not modelled	89.9	17	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
120	c3hugA_	Alignment	not modelled	89.8	15	**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