Phyre^2

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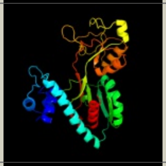
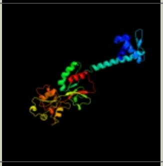
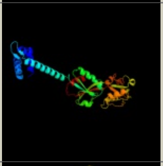
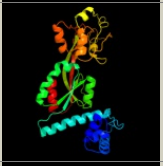
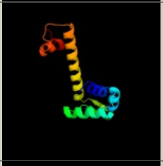
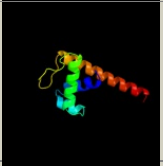
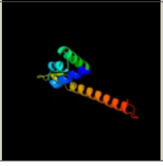
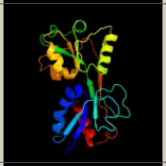
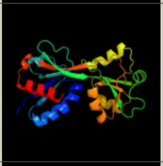
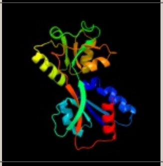
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2esnC_	Alignment		100.0	21	**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
2	c3t1bB_	Alignment		100.0	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** crystal structure of the full-length aphb n100e variant
3	c3hhgF_	Alignment		100.0	12	**PDB header:**transcription regulator **Chain:** F: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
4	c3fzjC_	Alignment		100.0	15	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** tsar low resolution crystal structure, tetragonal form
5	c1iz1B_	Alignment		100.0	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**lysr-type regulatory protein; **PDBTitle:** crystal structure of cbnr, a lysr family transcriptional2 regulator
6	c3ispA_	Alignment		100.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator **PDBTitle:** crystal structure of argp from mycobacterium tuberculosis
7	c3fzvC_	Alignment		100.0	15	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
8	c1b9nA_	Alignment		99.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein (mode); **PDBTitle:** regulator from escherichia coli
9	d2esna1	Alignment		99.9	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LysR-like transcriptional regulators
10	c3m1eA_	Alignment		99.9	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of benm_dbd
11	d1b9ma1	Alignment		99.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of molybdate-dependent transcriptional regulator ModE

12	d1ixca1	Alignment		99.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LysR-like transcriptional regulators
13	d1utha_	Alignment		99.8	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
14	c2ijlB_	Alignment		99.7	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**molybdenum-binding transcriptional repressor; **PDBTitle:** the structure of a putative mode from agrobacterium tumefaciens.
15	c3oxnD_	Alignment		99.7	18	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
16	c2uyeA_	Alignment		99.7	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein; **PDBTitle:** double mutant y110s,f111v dntr from burkholderia sp. strain2 dnt in complex with thiocyanate
17	c2hxrA_	Alignment		99.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator cynr; **PDBTitle:** structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
18	d2esna2	Alignment		99.7	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
19	d2fyia1	Alignment		99.6	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
20	c3jv9B_	Alignment		99.6	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** the structure of a reduced form of oxyr from n. meningitidis
21	c3hhfB_	Alignment	not modelled	99.6	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** structure of crga regulatory domain, a lysr-type transcriptional2 regulator from neisseria meningitidis.
22	c3kosA_	Alignment	not modelled	99.6	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator ampr; **PDBTitle:** structure of the ampr effector binding domain from citrobacter2 freundii
23	c3ho7A_	Alignment	not modelled	99.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**oxyr; **PDBTitle:** crystal structure of oxyr from porphyromonas gingivalis
24	c2ql3G_	Alignment	not modelled	99.6	15	**PDB header:**transcription **Chain:** G: **PDB Molecule:**probable transcriptional regulator, lysr family protein; **PDBTitle:** crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
25	c3fd3A_	Alignment	not modelled	99.6	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**chromosome replication initiation inhibitor protein; **PDBTitle:** structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
26	c1al3A_	Alignment	not modelled	99.6	15	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cys regulon transcriptional activator cysb; **PDBTitle:** cofactor binding fragment of cysb from klebsiella aerogenes
27	d1al3a_	Alignment	not modelled	99.6	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
						Fold: Periplasmic binding protein-like II

28	d1i6aa_	Alignment	not modelled	99.6	17	**Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
29	d1ixca2	Alignment	not modelled	99.5	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
30	c2h9qC_	Alignment	not modelled	99.5	16	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** crystal structure of the effector binding domain of a catm2 variant (r156h)
31	c3mz1D_	Alignment	not modelled	99.5	12	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a possible transcription regulator protein2 from sinorhizobium meliloti 1021
32	c3n6uA_	Alignment	not modelled	99.5	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
33	c2f7cA_	Alignment	not modelled	99.5	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** catm effector binding domain with its effector cis,cis-muconate
34	c2h9bB_	Alignment	not modelled	99.4	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
35	c2f78A_	Alignment	not modelled	99.3	12	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** benm effector binding domain with its effector benzoate
36	c2qsxB_	Alignment	not modelled	99.2	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** crystal structure of putative transcriptional regulator lysr from2 vibrio parahaemolyticus
37	c3onmB_	Alignment	not modelled	99.2	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator lrha; **PDBTitle:** effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis
38	c2x4hA_	Alignment	not modelled	98.2	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
39	c3boqB_	Alignment	not modelled	98.1	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
40	c3ctaA_	Alignment	not modelled	98.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase; **PDBTitle:** crystal structure of riboflavin kinase from thermoplasma2 acidophilum
41	c3nrvC_	Alignment	not modelled	97.9	16	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**putative transcriptional regulator (marr/emrr family); **PDBTitle:** crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
42	d2fbha1	Alignment	not modelled	97.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
43	c3bpxB_	Alignment	not modelled	97.8	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of marr
44	c2gxgA_	Alignment	not modelled	97.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**146aa long hypothetical transcriptional regulator; **PDBTitle:** crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
45	c3g3zA_	Alignment	not modelled	97.8	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
46	c2nyxB_	Alignment	not modelled	97.8	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
47	c2nnnB_	Alignment	not modelled	97.8	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
48	d1lj9a_	Alignment	not modelled	97.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
49	c2h09A_	Alignment	not modelled	97.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
50	c3fm5D_	Alignment	not modelled	97.7	14	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator; **PDBTitle:** x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1
51	d1lnwa_	Alignment	not modelled	97.7	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
52	d1jgsa_	Alignment	not modelled	97.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
53	c3e6mD_	Alignment	not modelled	97.7	14	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**marr family transcriptional regulator; **PDBTitle:** the crystal structure of a marr family transcriptional2

						regulator from silicibacter pomeroyi dss.
54	d2bv6a1	Alignment	not modelled	97.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
55	d2fxaa1	Alignment	not modelled	97.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
56	c2fa5B_	Alignment	not modelled	97.7	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator marr/emrr family; **PDBTitle:** the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
57	c3hruA_	Alignment	not modelled	97.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
58	c3ecoB_	Alignment	not modelled	97.7	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mepr; **PDBTitle:** crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
59	c1fx7C_	Alignment	not modelled	97.7	13	**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
60	c3cdhB_	Alignment	not modelled	97.7	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3
61	c3f3xA_	Alignment	not modelled	97.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
62	c1f5tA_	Alignment	not modelled	97.6	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
63	c3cjnA_	Alignment	not modelled	97.6	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
64	c2rdpA_	Alignment	not modelled	97.6	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
65	d2etha1	Alignment	not modelled	97.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
66	d1s3ja_	Alignment	not modelled	97.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
67	c3nqoB_	Alignment	not modelled	97.5	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**marr-family transcriptional regulator; **PDBTitle:** crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
68	d1p4xa1	Alignment	not modelled	97.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
69	d3broa1	Alignment	not modelled	97.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
70	c2it0A_	Alignment	not modelled	97.5	15	**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
71	c2pexA_	Alignment	not modelled	97.5	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator ohrr; **PDBTitle:** structure of reduced c22s ohrr from xanthamonas campestris
72	c2fxaB_	Alignment	not modelled	97.5	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protease production regulatory protein hpr; **PDBTitle:** structure of the protease production regulatory protein hpr from2 bacillus subtilis.
73	c3hrmA_	Alignment	not modelled	97.5	7	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator sarz; **PDBTitle:** crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
74	d1ub9a_	Alignment	not modelled	97.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
75	c3bjaA_	Alignment	not modelled	97.5	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
76	c3k0lA_	Alignment	not modelled	97.5	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
77	d2fbia1	Alignment	not modelled	97.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
78	d2fbka1	Alignment	not modelled	97.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family: MarR-like transcriptional regulators
79	d2hr3a1	Alignment	not modelled	97.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
80	c3s2wB_	Alignment	not modelled	97.4	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1
81	c1g3wA_	Alignment	not modelled	97.4	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
82	d2a61a1	Alignment	not modelled	97.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
83	d2frha1	Alignment	not modelled	97.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
84	d1p4xa2	Alignment	not modelled	97.2	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
85	c3oopA_	Alignment	not modelled	97.2	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2960 protein; **PDBTitle:** the structure of a protein with unknown function from listeria innocua2 clip11262
86	d3ctaa1	Alignment	not modelled	97.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
87	c2qwwB_	Alignment	not modelled	97.2	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
88	c3jw4C_	Alignment	not modelled	97.2	12	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, marr/emrr family; **PDBTitle:** the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
89	c3bj6B_	Alignment	not modelled	97.2	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
90	d3deua1	Alignment	not modelled	97.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
91	c3kp3B_	Alignment	not modelled	97.1	8	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
92	d1z91a1	Alignment	not modelled	97.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
93	c1p4xA_	Alignment	not modelled	97.0	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**staphylococcal accessory regulator a homologue; **PDBTitle:** crystal structure of sars protein from staphylococcus aureus
94	c2ev5B_	Alignment	not modelled	97.0	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
95	c3deuB_	Alignment	not modelled	97.0	10	**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
96	c2oqgA_	Alignment	not modelled	97.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
97	d1hsja1	Alignment	not modelled	96.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
98	d2f2ea1	Alignment	not modelled	96.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**HxlR-like
99	c1r22B_	Alignment	not modelled	96.6	17	**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
100	d1r7ja_	Alignment	not modelled	96.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Archaeal DNA-binding protein
101	c3r0aB_	Alignment	not modelled	96.6	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
102	d1r1ua_	Alignment	not modelled	96.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
103	c2kkoB_	Alignment	not modelled	96.5	11	**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.
104	c3onqB_	Alignment	not modelled	96.5	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**regulator of polyketide synthase expression; **PDBTitle:** crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
105	c2zkzC_	Alignment	not modelled	96.5	19	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional repressor pagr; **PDBTitle:** crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
106	c2wteB_	Alignment	not modelled	96.4	18	**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.
107	c3f6vA_	Alignment	not modelled	96.3	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
108	c3f6oB_	Alignment	not modelled	96.2	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
109	c3cuoB_	Alignment	not modelled	96.2	15	**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
110	c2ia0A_	Alignment	not modelled	96.2	24	**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)
111	c2dbbA_	Alignment	not modelled	96.0	27	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
112	d1r1ta_	Alignment	not modelled	96.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
113	c3bddD_	Alignment	not modelled	95.9	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein marr; **PDBTitle:** crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
114	c3jthA_	Alignment	not modelled	95.6	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
115	d1u2wa1	Alignment	not modelled	95.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
116	c3df8A_	Alignment	not modelled	95.6	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible hxlr family transcriptional factor; **PDBTitle:** the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1
117	c2ewnA_	Alignment	not modelled	95.6	20	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
118	c2l4aA_	Alignment	not modelled	95.6	20	**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
119	d1stza1	Alignment	not modelled	95.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
120	d1a04a1	Alignment	not modelled	95.5	10	**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)