Phyre^2

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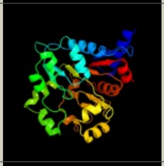
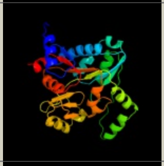
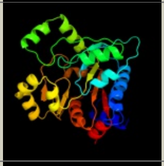
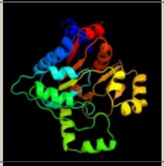
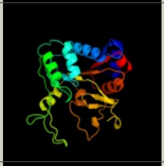
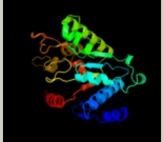
Detailed template information

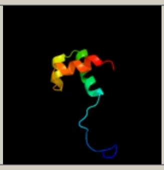
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w48D_	Alignment		100.0	26	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
2	c3kv1A_	Alignment		100.0	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
3	c3nzeB_	Alignment		100.0	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator, sugar-binding family; **PDBTitle:** the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
4	d2gnpa1	Alignment		100.0	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
5	d3efba1	Alignment		100.0	26	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
6	d2okga1	Alignment		100.0	25	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
7	c2o0mA_	Alignment		100.0	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, sorc family; **PDBTitle:** the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
8	d2o0ma1	Alignment		100.0	26	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
9	d2r5fa1	Alignment		100.0	33	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
10	c2bkxB_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
11	c2ri0B_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans

12	d1ne7a_	Alignment		99.5	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
13	c3hn6D_	Alignment		99.4	13	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
14	d1fsfa_	Alignment		99.4	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
15	c3e15D_	Alignment		99.3	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** 6-phosphogluconolactonase from plasmodium vivax
16	c2j0eA_	Alignment		99.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
17	c3nwpA_	Alignment		99.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
18	c3lwdA_	Alignment		99.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
19	c3icoA_	Alignment		99.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from2 mycobacterium tuberculosis
20	c3cssA_	Alignment		99.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis
21	c3oc6A_	Alignment	not modelled	99.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
22	c1pbtA_	Alignment	not modelled	99.0	12	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
23	d1vl1a_	Alignment	not modelled	99.0	12	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
24	c1y89B_	Alignment	not modelled	99.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**devb protein; **PDBTitle:** crystal structure of devb protein
25	c3lhiA_	Alignment	not modelled	99.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
26	c1rp3G_	Alignment	not modelled	97.7	19	**PDB header:**transcription **Chain:** G: **PDB Molecule:**rna polymerase sigma factor sigma-28 (flia); **PDBTitle:** cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
27	d1i5za1	Alignment	not modelled	97.6	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
28	d2bgca1	Alignment	not modelled	97.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like

29	c3u7jA_	Alignment	not modelled	97.6	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
30	d1s7oa_	Alignment	not modelled	97.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
31	d2oz6a1	Alignment	not modelled	97.5	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
32	d1xsva_	Alignment	not modelled	97.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
33	d2gaua1	Alignment	not modelled	97.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
34	c3d0sA_	Alignment	not modelled	97.4	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** camp receptor protein from m.tuberculosis, camp-free form
35	d2d1ha1	Alignment	not modelled	97.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
36	d2h6ca1	Alignment	not modelled	97.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
37	c3kccA_	Alignment	not modelled	97.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**catabolite gene activator; **PDBTitle:** crystal structure of d138l mutant of catabolite gene activator protein
38	c2gauA_	Alignment	not modelled	97.4	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, crp/fnr family; **PDBTitle:** crystal structure of transcriptional regulator, crp/fnr family from2 porphyromonas gingivalis (apc80792), structural genomics, mcsg
39	d2coha1	Alignment	not modelled	97.3	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
40	c2bgcA_	Alignment	not modelled	97.3	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prfa; **PDBTitle:** prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
41	c2oz6A_	Alignment	not modelled	97.3	30	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**virulence factor regulator; **PDBTitle:** crystal structure of virulence factor regulator from pseudomonas2 aeruginosa in complex with camp
42	c2o8xA_	Alignment	not modelled	97.3	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
43	c1zreB_	Alignment	not modelled	97.3	27	**PDB header:**gene regulation/dna **Chain:** B: **PDB Molecule:**catabolite gene activator; **PDBTitle:** 4 crystal structures of cap-dna with all base-pair2 substitutions at position 6, cap-[6g;17c]icap38 dna
44	d3e5ua1	Alignment	not modelled	97.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
45	d1k78a1	Alignment	not modelled	97.2	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
46	d1ft9a1	Alignment	not modelled	97.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
47	d1ku7a_	Alignment	not modelled	97.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
48	c3dv8A_	Alignment	not modelled	97.2	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, crp/fnr family; **PDBTitle:** crystal structure of a putative transcriptional regulator of the2 crp/fnr family (eubrec_1222) from eubacterium rectale atcc 33656 at3 2.55 a resolution
49	c3hugA_	Alignment	not modelled	97.2	19	**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
50	c3e6dA_	Alignment	not modelled	97.2	27	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cyclic nucleotide-binding protein; **PDBTitle:** crystal structure of cprk c200s
51	d1rp3a2	Alignment	not modelled	97.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
52	c1zybA_	Alignment	not modelled	97.2	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator, crp family; **PDBTitle:** crystal structure of transcription regulator from bacteroides2 thetaiotaomicron vpi-5482 at 2.15 a resolution
53	c1or7A_	Alignment	not modelled	97.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
						PDB header:transcription **Chain:** A: **PDB Molecule:**carbon monoxide oxidation system

54	c1ft9A_	Alignment	not modelled	97.1	28	transcription **PDBTitle:** structure of the reduced (feii) co-sensing protein from r.2 rubrum
55	c2zcwA_	Alignment	not modelled	97.1	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, fnr/crp family; **PDBTitle:** crystal structure of ttha1359, a transcriptional regulator,2 crp/fnr family from thermus thermophilus hb8
56	d1sfxa_	Alignment	not modelled	97.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
57	c6paxA_	Alignment	not modelled	97.1	22	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
58	d6paxa1	Alignment	not modelled	97.1	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
59	c3mzyA_	Alignment	not modelled	97.1	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor; **PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
60	c3tgnA_	Alignment	not modelled	97.1	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**adc operon repressor adcr; **PDBTitle:** crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
61	c3iwzB_	Alignment	not modelled	97.1	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**catabolite activation-like protein; **PDBTitle:** the c-di-gmp responsive global regulator clp links cell-cell signaling2 to virulence gene expression in xanthomonas campestris
62	c3ctaA_	Alignment	not modelled	97.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase; **PDBTitle:** crystal structure of riboflavin kinase from thermoplasma2 acidophilum
63	c3g3zA_	Alignment	not modelled	97.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
64	c2qwwB_	Alignment	not modelled	97.0	18	**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
65	d1z05a1	Alignment	not modelled	97.0	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
66	c1zx4B_	Alignment	not modelled	97.0	30	**PDB header:**translation **Chain:** B: **PDB Molecule:**plasmid partition par b protein; **PDBTitle:** structure of parb bound to dna
67	d1ttya_	Alignment	not modelled	97.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
68	c3fx3A_	Alignment	not modelled	97.0	22	**PDB header:**camp-binding protein **Chain:** A: **PDB Molecule:**cyclic nucleotide-binding protein; **PDBTitle:** structure of a putative camp-binding regulatory protein from2 silicibacter pomeroyi dss-3
69	c1u78A_	Alignment	not modelled	97.0	15	**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
70	d1pdnc_	Alignment	not modelled	97.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
71	d1or7a1	Alignment	not modelled	97.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
72	d1ku9a_	Alignment	not modelled	97.0	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
73	c2fxaB_	Alignment	not modelled	96.9	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.
74	c3nrvC_	Alignment	not modelled	96.9	29	**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
75	c3la2A_	Alignment	not modelled	96.9	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**global nitrogen regulator; **PDBTitle:** crystal structure of ntca in complex with 2-oxoglutarate
76	d1ku3a_	Alignment	not modelled	96.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
77	c3bddD_	Alignment	not modelled	96.9	28	**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
78	d2fxaa1	Alignment	not modelled	96.9	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
						Fold:DNA/RNA-binding 3-helical bundle

79	d3ctaa1	Alignment	not modelled	96.9	24	**Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
80	c3r0aB_	Alignment	not modelled	96.9	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
81	d1lnwa_	Alignment	not modelled	96.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
82	c3e97A_	Alignment	not modelled	96.9	30	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, crp/fnr family; **PDBTitle:** crystal structure of transcriptional regulator of crp/fnr2 family (yp_604437.1) from deinococcus geothermalis dsm3 11300 at 1.86 a resolution
83	d2etha1	Alignment	not modelled	96.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
84	c3nqoB_	Alignment	not modelled	96.8	17	**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
85	d2fbha1	Alignment	not modelled	96.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
86	c2nnnB_	Alignment	not modelled	96.8	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
87	c2it0A_	Alignment	not modelled	96.8	20	**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
88	c2wteB_	Alignment	not modelled	96.8	15	**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.
89	c2h09A_	Alignment	not modelled	96.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
90	c3deuB_	Alignment	not modelled	96.8	15	**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
91	c1i1gA_	Alignment	not modelled	96.8	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
92	d3broa1	Alignment	not modelled	96.8	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
93	c2fa5B_	Alignment	not modelled	96.8	29	**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
94	c3hruA_	Alignment	not modelled	96.8	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
95	d1lj9a_	Alignment	not modelled	96.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
96	c1z05A_	Alignment	not modelled	96.7	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, rok family; **PDBTitle:** crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
97	c1f5tA_	Alignment	not modelled	96.7	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
98	c2nyxB_	Alignment	not modelled	96.7	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
99	c3bpxB_	Alignment	not modelled	96.7	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of marr
100	c2zdbA_	Alignment	not modelled	96.7	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, crp family; **PDBTitle:** crystal structure of tthb099, a transcriptional regulator crp family2 from thermus thermophilus hb8
101	c2e7xA_	Alignment	not modelled	96.7	18	**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
102	c2fmyB_	Alignment	not modelled	96.7	44	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**carbon monoxide oxidation system transcription regulator **PDBTitle:** co-dependent transcription factor cooa from carboxydothermus2 hydrogenoformans (imidazole-bound form)
103	c1z6rC_	Alignment	not modelled	96.7	6	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
						PDB header:transcription regulator

104	c3dkwB_	Alignment	not modelled	96.7	19	**Chain:** B: **PDB Molecule:**dnr protein; **PDBTitle:** crystal structure of dnr from pseudomonas aeruginosa.
105	c2ev5B_	Alignment	not modelled	96.6	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
106	d1z6ra1	Alignment	not modelled	96.6	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
107	d2p7vb1	Alignment	not modelled	96.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
108	c2elhA_	Alignment		96.6	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
109	c3k0lA_	Alignment	not modelled	96.6	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
110	c2x4hA_	Alignment	not modelled	96.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
111	c2pexA_	Alignment	not modelled	96.6	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator ohrr; **PDBTitle:** structure of reduced c22s ohrr from xanthamonas campestris
112	d1s3ja_	Alignment	not modelled	96.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
113	c2gxgA_	Alignment	not modelled	96.5	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**146aa long hypothetical transcriptional regulator; **PDBTitle:** crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
114	c3f3xA_	Alignment	not modelled	96.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
115	c2rdpA_	Alignment	not modelled	96.5	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
116	d2hr3a1	Alignment	not modelled	96.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
117	c3bj6B_	Alignment	not modelled	96.5	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
118	c1r71B_	Alignment	not modelled	96.4	12	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna
119	d2cg4a1	Alignment	not modelled	96.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
120	d1mkma1	Alignment	not modelled	96.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain