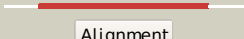

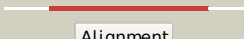

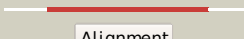




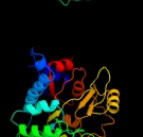




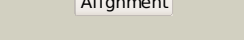

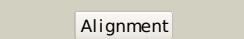







# Phyre2

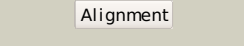
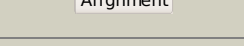
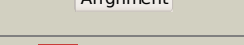
Email	I.a.kelley@imperial.ac.uk
Description	P39356
Date	Thu Jan 5 11:59:46 GMT 2012
Unique Job ID	88877637a7bae0f0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2w48D_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
2	<a href="#">c3kv1A_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor; <b>PDBTitle:</b> crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
3	<a href="#">c3nzeB_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator, sugar-binding family; <b>PDBTitle:</b> the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
4	<a href="#">d2gnpa1</a>	 Alignment		100.0	19	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
5	<a href="#">d3efba1</a>	 Alignment		100.0	22	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
6	<a href="#">d2okga1</a>	 Alignment		100.0	20	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
7	<a href="#">d2o0ma1</a>	 Alignment		100.0	23	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
8	<a href="#">c2o0mA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, sorc family; <b>PDBTitle:</b> the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
9	<a href="#">d2r5fa1</a>	 Alignment		100.0	32	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
10	<a href="#">c2bkxB_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine-6-phosphate deaminase; <b>PDBTitle:</b> structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
11	<a href="#">c2ri0B_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine-6-phosphate deaminase; <b>PDBTitle:</b> crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans

12	<a href="#">d1ne7a_</a>	Alignment		99.5	17	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> NagB-like
13	<a href="#">c3hn6D_</a>	Alignment		99.4	14	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> glucosamine-6-phosphate deaminase; <b>PDBTitle:</b> crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
14	<a href="#">d1fsfa_</a>	Alignment		99.3	19	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> NagB-like
15	<a href="#">c3e15D_</a>	Alignment		99.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> 6-phosphogluconolactonase from plasmodium vivax
16	<a href="#">c3nwpA_</a>	Alignment		99.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
17	<a href="#">c3icoA_</a>	Alignment		99.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of 6-phosphogluconolactonase from2 mycobacterium tuberculosis
18	<a href="#">c3oc6A_</a>	Alignment		99.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
19	<a href="#">c3lhiA_</a>	Alignment		99.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
20	<a href="#">d1vl1a_</a>	Alignment		99.0	12	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> NagB-like
21	<a href="#">c3lwdA_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
22	<a href="#">c2j0eA_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
23	<a href="#">c1y89B_</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> devb protein; <b>PDBTitle:</b> crystal structure of devb protein
24	<a href="#">c3cssA_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis
25	<a href="#">c1pbtA_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
26	<a href="#">c3u7jA_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
27	<a href="#">c1rp3G_</a>	Alignment	not modelled	97.5	27	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> rna polymerase sigma factor sigma-28 (flia); <b>PDBTitle:</b> cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
28	<a href="#">c3ctaA_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from

						thermoplasma2 acidophilum
29	<a href="#">d1i5za1</a>	Alignment	not modelled	97.5	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
30	<a href="#">d2bgca1</a>	Alignment	not modelled	97.5	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
31	<a href="#">d1s7oa</a>	Alignment	not modelled	97.4	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
32	<a href="#">d2oz6a1</a>	Alignment	not modelled	97.4	36	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
33	<a href="#">c3kwmC</a>	Alignment	not modelled	97.4	22	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-isomerase a
34	<a href="#">c3d0sA</a>	Alignment	not modelled	97.3	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> camp receptor protein from m.tuberculosis, camp-free form
35	<a href="#">d1xsva</a>	Alignment	not modelled	97.3	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
36	<a href="#">d2gaua1</a>	Alignment	not modelled	97.3	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
37	<a href="#">d2h6ca1</a>	Alignment	not modelled	97.2	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
38	<a href="#">c3kccA</a>	Alignment	not modelled	97.2	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> catabolite gene activator; <b>PDBTitle:</b> crystal structure of d138l mutant of catabolite gene activator protein
39	<a href="#">d1k78a1</a>	Alignment	not modelled	97.2	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
40	<a href="#">c2gauA</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp/fnr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, crp/fnr family from2 porphyromonas gingivalis (apc80792), structural genomics, mcsG
41	<a href="#">c2oz6A</a>	Alignment	not modelled	97.2	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence factor regulator; <b>PDBTitle:</b> crystal structure of virulence factor regulator from pseudomonas2 aeruginosa in complex with camp
42	<a href="#">d2coha1</a>	Alignment	not modelled	97.2	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
43	<a href="#">c1zreB</a>	Alignment	not modelled	97.1	27	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> B: <b>PDB Molecule:</b> catabolite gene activator; <b>PDBTitle:</b> 4 crystal structures of cap-dna with all base-pair2 substitutions at position 6, cap-[6g;17c]icap38 dna
44	<a href="#">d6paxa1</a>	Alignment	not modelled	97.1	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
45	<a href="#">d2d1ha1</a>	Alignment	not modelled	97.1	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
46	<a href="#">d1ft9a1</a>	Alignment	not modelled	97.1	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
47	<a href="#">c2bgcA</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> prfa; <b>PDBTitle:</b> prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
48	<a href="#">c6paxA</a>	Alignment	not modelled	97.1	22	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
49	<a href="#">c3dv8A</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp/fnr family; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator of the2 crp/fnr family (eubrec_1222) from eubacterium rectale atcc 33656 at3 2.55 a resolution
50	<a href="#">d3e5ua1</a>	Alignment	not modelled	97.1	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
51	<a href="#">c3e6dA</a>	Alignment	not modelled	97.1	26	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide-binding protein; <b>PDBTitle:</b> crystal structure of cprk c200s
52	<a href="#">c1u78A</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
53	<a href="#">c2o8xA</a>	Alignment	not modelled	97.0	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
54	<a href="#">d1pdnc</a>	Alignment	not modelled	97.0	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain

55	<a href="#">c1ft9A</a>	 Alignment	not modelled	97.0	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide oxidation system transcription <b>PDBTitle:</b> structure of the reduced (feii) co-sensing protein from r.2 rubrum
56	<a href="#">c3hheA</a>	 Alignment	not modelled	97.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
57	<a href="#">c1zybA</a>	 Alignment	not modelled	97.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator, crp family; <b>PDBTitle:</b> crystal structure of transcription regulator from bacteroides2 thetaiotaomicron vpi-5482 at 2.15 a resolution
58	<a href="#">d1ku7a</a>	 Alignment	not modelled	97.0	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
59	<a href="#">d1sfxa</a>	 Alignment	not modelled	97.0	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
60	<a href="#">d1z05a1</a>	 Alignment	not modelled	97.0	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
61	<a href="#">c3hugA</a>	 Alignment	not modelled	96.9	25	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI
62	<a href="#">c2zcwA</a>	 Alignment	not modelled	96.9	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, fnr/crp family; <b>PDBTitle:</b> crystal structure of ttha1359, a transcriptional regulator,2 crp/fnr family from thermus thermophilus hb8
63	<a href="#">c3tgnA</a>	 Alignment	not modelled	96.9	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr; <b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
64	<a href="#">c2qwwB</a>	 Alignment	not modelled	96.9	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
65	<a href="#">d1rp3a2</a>	 Alignment	not modelled	96.9	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
66	<a href="#">c3iwzB</a>	 Alignment	not modelled	96.9	29	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> catabolite activation-like protein; <b>PDBTitle:</b> the c-di-gmp responsive global regulator clp links cell-cell signaling2 to virulence gene expression in xanthomonas campestris
67	<a href="#">c1or7A</a>	 Alignment	not modelled	96.9	39	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-e factor; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
68	<a href="#">c3g3zA</a>	 Alignment	not modelled	96.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
69	<a href="#">d1ku9a</a>	 Alignment	not modelled	96.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
70	<a href="#">c1zx4B</a>	 Alignment	not modelled	96.9	33	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partition par b protein; <b>PDBTitle:</b> structure of parb bound to dna
71	<a href="#">c3fx3A</a>	 Alignment	not modelled	96.9	11	<b>PDB header:</b> camp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide-binding protein; <b>PDBTitle:</b> structure of a putative camp-binding regulatory protein from2 silicibacter pomeroyi dss-3
72	<a href="#">c3mzyA</a>	 Alignment	not modelled	96.9	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
73	<a href="#">c2it0A</a>	 Alignment	not modelled	96.8	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
74	<a href="#">c2f8mB</a>	 Alignment	not modelled	96.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> ribose 5-phosphate isomerase from plasmodium falci-parum
75	<a href="#">c2wteB</a>	 Alignment	not modelled	96.8	19	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> csa3; <b>PDBTitle:</b> the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
76	<a href="#">c3la2A</a>	 Alignment	not modelled	96.8	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> global nitrogen regulator; <b>PDBTitle:</b> crystal structure of ntca in complex with 2-oxoglutarate
77	<a href="#">d1tya</a>	 Alignment	not modelled	96.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
78	<a href="#">d2fxaa1</a>	 Alignment	not modelled	96.8	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
79	<a href="#">c2fxaB</a>	 Alignment	not modelled	96.8	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protease production regulatory protein hpr; <b>PDBTitle:</b> structure of the protease production regulatory protein hpr from2 bacillus subtilis.

80	<a href="#">c2h09A</a>	Alignment	not modelled	96.7	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> crystal structure of diphtheria toxin repressor like protein2 from e. coli
81	<a href="#">c1f5tA</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
82	<a href="#">c1m0sA</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> northeast structural genomics consortium (nesg id ir21)
83	<a href="#">d3ctaa1</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
84	<a href="#">d1or7a1</a>	Alignment	not modelled	96.7	38	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
85	<a href="#">d2etha1</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
86	<a href="#">c3e97A</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp/fnr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator of crp/fnr2 family (yp_604437.1) from deinococcus geothermalis dsm3 11300 at 1.86 a resolution
87	<a href="#">c3nrvC</a>	Alignment	not modelled	96.7	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> putative transcriptional regulator (marr/emrr family); <b>PDBTitle:</b> crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
88	<a href="#">c3bddD</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein marr; <b>PDBTitle:</b> crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
89	<a href="#">c1lkzB</a>	Alignment	not modelled	96.7	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose 5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of d-ribose-5-phosphate isomerase (rpi)2 from escherichia coli.
90	<a href="#">c1z05A</a>	Alignment	not modelled	96.6	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rok family; <b>PDBTitle:</b> crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
91	<a href="#">c1lk5C</a>	Alignment	not modelled	96.6	23	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> d-ribose-5-phosphate isomerase; <b>PDBTitle:</b> structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
92	<a href="#">d1ku3a</a>	Alignment	not modelled	96.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
93	<a href="#">c2nnnB</a>	Alignment	not modelled	96.6	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
94	<a href="#">d1z6ra1</a>	Alignment	not modelled	96.6	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
95	<a href="#">c3nqoB</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> marr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
96	<a href="#">c3deuB</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator slyA; <b>PDBTitle:</b> crystal structure of transcription regulatory protein slyA2 from salmonella typhimurium in complex with salicylate3 ligands
97	<a href="#">c3r0aB</a>	Alignment	not modelled	96.6	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
98	<a href="#">c2fa5B</a>	Alignment	not modelled	96.6	25	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator marr/emrr family; <b>PDBTitle:</b> the crystal structure of an unliganded multiple antibiotic-c-2 resistance repressor (marr) from xanthomonas campestris
99	<a href="#">d1lj9a</a>	Alignment	not modelled	96.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
100	<a href="#">d3broa1</a>	Alignment	not modelled	96.6	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
101	<a href="#">c2zdbA</a>	Alignment	not modelled	96.5	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp family; <b>PDBTitle:</b> crystal structure of tthb099, a transcriptional regulator crp family2 from thermus thermophilus hb8
102	<a href="#">c2fmyB</a>	Alignment	not modelled	96.5	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> carbon monoxide oxidation system transcription regulator <b>PDBTitle:</b> co-dependent transcription factor cooA from carboxydotherrmus2 hydrogenofomans (imidazole-bound form)
103	<a href="#">c2nyxB</a>	Alignment	not modelled	96.5	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulatory protein, rv1404; <b>PDBTitle:</b> crystal structure of rv1404 from mycobacterium tuberculosis
104	<a href="#">c2ev5B</a>	Alignment	not modelled	96.5	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator mntr;

104	<a href="#">c2ev3B</a>	Alignment	not modelled	96.3	19	<b>PDBTitle:</b> bacillus subtilis manganese transport regulator (mnt2) bound to calcium
105	<a href="#">c3bpxB</a>	Alignment	not modelled	96.5	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
106	<a href="#">c3dkwB</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> dnr protein; <b>PDBTitle:</b> crystal structure of dnr from pseudomonas aeruginosa.
107	<a href="#">c2l4aA</a>	Alignment		96.5	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
108	<a href="#">c2x4hA</a>	Alignment	not modelled	96.4	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
109	<a href="#">c1z6rC</a>	Alignment	not modelled	96.4	14	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> mlc protein; <b>PDBTitle:</b> crystal structure of mlc from escherichia coli
110	<a href="#">c2rdpA</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr; <b>PDBTitle:</b> the structure of a marr family protein from bacillus2 stearotherophilus
111	<a href="#">c3k0lA</a>	Alignment	not modelled	96.4	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein; <b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
112	<a href="#">c3l7oB</a>	Alignment	not modelled	96.4	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
113	<a href="#">c2pexA</a>	Alignment	not modelled	96.4	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator ohrr; <b>PDBTitle:</b> structure of reduced c22s ohrr from xanthomonas campestris
114	<a href="#">d1lnwa</a>	Alignment	not modelled	96.3	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
115	<a href="#">d2p7vb1</a>	Alignment	not modelled	96.3	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
116	<a href="#">d2hr3a1</a>	Alignment	not modelled	96.3	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
117	<a href="#">c2gxgA</a>	Alignment	not modelled	96.3	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
118	<a href="#">d1s3ja</a>	Alignment	not modelled	96.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
119	<a href="#">c2e7xA</a>	Alignment	not modelled	96.3	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
120	<a href="#">d2fbha1</a>	Alignment	not modelled	96.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators