


















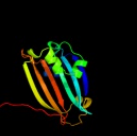





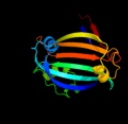







# Phyre2

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Description	P13669
Date	Thu Jan 5 11:33:42 GMT 2012
Unique Job ID	2f27cf03cc5bdac6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3bwgA_</a>	 Alignment		100.0	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yydk; <b>PDBTitle:</b> the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
2	<a href="#">c3f8mA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gntr-family protein transcriptional regulator; <b>PDBTitle:</b> crystal structure of phnf from mycobacterium smegmatis
3	<a href="#">c3edpB_</a>	 Alignment		100.0	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lin2111 protein; <b>PDBTitle:</b> the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
4	<a href="#">c3eetA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative gntr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative gntr-family transcriptional2 regulator
5	<a href="#">c2wv0H_</a>	 Alignment		100.0	29	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> hth-type transcriptional repressor yvoa; <b>PDBTitle:</b> crystal structure of the gntr-hutc family member yvoa from2 bacillus subtilis
6	<a href="#">c3f8lC_</a>	 Alignment		99.9	18	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional repressor phnf; <b>PDBTitle:</b> crystal structure of the effector domain of phnf from mycobacterium2 smegmatis
7	<a href="#">d2fa1a1</a>	 Alignment		99.9	20	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
8	<a href="#">d2p19a1</a>	 Alignment		99.9	21	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
9	<a href="#">d2ooia1</a>	 Alignment		99.9	18	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
10	<a href="#">d2oggal</a>	 Alignment		99.9	25	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
11	<a href="#">d3cnva1</a>	 Alignment		99.9	19	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain

12	<a href="#">c3neuA</a>	Alignment		99.9	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin1836 protein; <b>PDBTitle:</b> the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
13	<a href="#">c3by6C</a>	Alignment		99.9	28	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> predicted transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator from oenococcus oeni
14	<a href="#">d2ra5a1</a>	Alignment		99.9	18	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
15	<a href="#">c2ra5A</a>	Alignment		99.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator2 from streptomyces coelicolor
16	<a href="#">c2du9A</a>	Alignment		99.9	34	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> predicted transcriptional regulators; <b>PDBTitle:</b> crystal structure of the transcriptional factor from c.glutamicum
17	<a href="#">d3bwga2</a>	Alignment		99.9	23	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
18	<a href="#">d2ikka1</a>	Alignment		99.8	23	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
19	<a href="#">c3hfiA</a>	Alignment		99.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative regulator; <b>PDBTitle:</b> the crystal structure of the putative regulator from escherichia coli2 cft073
20	<a href="#">d1v4ra1</a>	Alignment		99.8	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
21	<a href="#">c2di3A</a>	Alignment	not modelled	99.8	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory proteins, gntR family; <b>PDBTitle:</b> crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
22	<a href="#">c1e2xA</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> transcriptional regulation <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from e.2 coli
23	<a href="#">d2pkha1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
24	<a href="#">c3fmsA</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntR family; <b>PDBTitle:</b> crystal structure of tm0439, a gntR transcriptional2 regulator
25	<a href="#">d3bwga1</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
26	<a href="#">d1hw1a1</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
27	<a href="#">c3tqnC</a>	Alignment	not modelled	99.8	32	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, gntR family; <b>PDBTitle:</b> structure of the transcriptional regulator of the gntR family, from2 coxiella burnetii.
28	<a href="#">c3lheA</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> gntR family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of a gntR2 family transcriptional regulator from bacillus anthracis3 str. Sterne
						<b>PDB header:</b> transcription regulator

29	<a href="#">c3c7jA_</a>	Alignment	not modelled	99.8	38	<b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000
30	<a href="#">c3ihuA_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntr family; <b>PDBTitle:</b> crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution
31	<a href="#">c3ic7A_</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron
32	<a href="#">c2hs5A_</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator gntr; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
33	<a href="#">d2hs5a1</a>	Alignment	not modelled	99.7	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GnTR-like transcriptional regulators
34	<a href="#">d3ddva1</a>	Alignment	not modelled	99.7	26	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
35	<a href="#">d1biaa1</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
36	<a href="#">c2h09A_</a>	Alignment	not modelled	98.1	24	<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
37	<a href="#">d1stza1</a>	Alignment	not modelled	97.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
38	<a href="#">c1f5tA_</a>	Alignment	not modelled	97.7	12	<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
39	<a href="#">d1jhfa1</a>	Alignment	not modelled	97.7	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
40	<a href="#">c2it0A_</a>	Alignment	not modelled	97.6	15	<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
41	<a href="#">d1g3wa1</a>	Alignment	not modelled	97.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
42	<a href="#">d1j5ya1</a>	Alignment	not modelled	97.3	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
43	<a href="#">d2isya1</a>	Alignment	not modelled	97.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
44	<a href="#">c1j5yA_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, biotin repressor family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
45	<a href="#">c3hruA_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metalloregulator scar; <b>PDBTitle:</b> crystal structure of scar with bound zn2+
46	<a href="#">d1i5za1</a>	Alignment	not modelled	97.2	20	<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="#">c3k69A_</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
48	<a href="#">c3ctaA_</a>	Alignment	not modelled	97.2	18	<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
49	<a href="#">c2y75F_</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> hth-type transcriptional regulator cymr; <b>PDBTitle:</b> the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
50	<a href="#">c2ewnA_</a>	Alignment	not modelled	97.1	22	<b>PDB header:</b> ligase, transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bira bifunctional protein; <b>PDBTitle:</b> ecoli biotin repressor with co-repressor analog
51	<a href="#">c1g3wA_</a>	Alignment	not modelled	97.0	12	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
52	<a href="#">c3lwfD_</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
53	<a href="#">d1xd7a_</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> Transcriptional regulator Rrf2
54	<a href="#">c3r0aB_</a>	Alignment	not modelled	96.9	29	<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)
55	<a href="#">c2v79B_</a>	Alignment	not modelled	96.8	22	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna replication protein dnad; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad from2

						bacillus subtilis
56	<a href="#">c1ft9A_</a>	Alignment	not modelled	96.7	25	<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
57	<a href="#">d2gaua1</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> CAP C-terminal domain-like
58	<a href="#">d2h6ca1</a>	Alignment	not modelled	96.6	22	<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
59	<a href="#">d2oz6a1</a>	Alignment	not modelled	96.5	25	<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
60	<a href="#">d1ft9a1</a>	Alignment	not modelled	96.5	17	<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
61	<a href="#">c1zybA_</a>	Alignment	not modelled	96.5	11	<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
62	<a href="#">c1fx7C_</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
63	<a href="#">d2coha1</a>	Alignment	not modelled	96.3	25	<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
64	<a href="#">d1ylfa1</a>	Alignment	not modelled	96.3	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator Rrf2
65	<a href="#">d2nwia1</a>	Alignment	not modelled	96.3	14	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> AF1396-like
66	<a href="#">c2gauA_</a>	Alignment	not modelled	96.3	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
67	<a href="#">c3dv8A_</a>	Alignment	not modelled	96.3	19	<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
68	<a href="#">c2oz6A_</a>	Alignment	not modelled	96.3	26	<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
69	<a href="#">c3d0sA_</a>	Alignment	not modelled	96.3	25	<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
70	<a href="#">d2d1ha1</a>	Alignment	not modelled	96.2	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
71	<a href="#">c2x4hA_</a>	Alignment	not modelled	96.2	9	<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 sulfobolus solfataricus
72	<a href="#">c3e97A_</a>	Alignment	not modelled	96.1	27	<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
73	<a href="#">d3e5ua1</a>	Alignment	not modelled	96.1	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
74	<a href="#">c3iwzB_</a>	Alignment	not modelled	96.1	16	<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
75	<a href="#">d2bgca1</a>	Alignment	not modelled	96.1	14	<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
76	<a href="#">c2vn2B_</a>	Alignment	not modelled	96.0	22	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome replication initiation protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
77	<a href="#">c3e6dA_</a>	Alignment	not modelled	96.0	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
78	<a href="#">d2ev0a1</a>	Alignment	not modelled	96.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
79	<a href="#">c3kccA_</a>	Alignment	not modelled	95.9	25	<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
80	<a href="#">c2zy3A_</a>	Alignment	not modelled	95.9	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase

81	<a href="#">d1sfxa_</a>	Alignment	not modelled	95.9	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
82	<a href="#">c2ev5B_</a>	Alignment	not modelled	95.9	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
83	<a href="#">c3f6tA_</a>	Alignment	not modelled	95.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
84	<a href="#">c2zcwA_</a>	Alignment	not modelled	95.8	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, fnr/crp family; <b>PDBTitle:</b> crystal structure of thb1359, a transcriptional regulator,2 crp/fnr family from thermus thermophilus hb8
85	<a href="#">c2fmyB_</a>	Alignment	not modelled	95.8	21	<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 carboxydotherrus2 hydrogenoformans (imidazole-bound form)
86	<a href="#">d2cg4a1</a>	Alignment	not modelled	95.7	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
87	<a href="#">c2zdbA_</a>	Alignment	not modelled	95.7	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp family; <b>PDBTitle:</b> crystal structure of thb099, a transcriptional regulator crp family2 from thermus thermophilus hb8
88	<a href="#">d1ilga1</a>	Alignment	not modelled	95.6	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
89	<a href="#">c3fx3A_</a>	Alignment	not modelled	95.6	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
90	<a href="#">c1zreB_</a>	Alignment	not modelled	95.6	26	<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]cap38 dna
91	<a href="#">c3k2zA_</a>	Alignment	not modelled	95.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> crystal structure of a lexa protein from thermotoga maritima
92	<a href="#">c1r22B_</a>	Alignment	not modelled	95.5	32	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
93	<a href="#">d1rlua_</a>	Alignment	not modelled	95.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
94	<a href="#">d2fxaa1</a>	Alignment	not modelled	95.4	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
95	<a href="#">d2cyya1</a>	Alignment	not modelled	95.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
96	<a href="#">c1dpuA_</a>	Alignment	not modelled	95.4	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a (rpa32) c-terminal domain; <b>PDBTitle:</b> solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
97	<a href="#">d1dpua_</a>	Alignment	not modelled	95.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal domain of RPA32
98	<a href="#">c3dkwB_</a>	Alignment	not modelled	95.4	8	<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.
99	<a href="#">d1pdnc_</a>	Alignment	not modelled	95.4	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
100	<a href="#">c2l4aA_</a>	Alignment	not modelled	95.3	19	<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
101	<a href="#">c3bj6B_</a>	Alignment	not modelled	95.3	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcription regulator sp03579
102	<a href="#">c2oqgA_</a>	Alignment	not modelled	95.3	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1
103	<a href="#">c3f6vA_</a>	Alignment	not modelled	95.3	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for2 arsenical resistance
104	<a href="#">d1ku9a_</a>	Alignment	not modelled	95.3	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
105	<a href="#">c2w48D_</a>	Alignment	not modelled	95.1	28	<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
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle



106	<a href="#">d2bv6a1</a>	Alignment	not modelled	95.1	13	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
107	<a href="#">c3la2A</a>	Alignment	not modelled	95.1	26	<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
108	<a href="#">d2b0la1</a>	Alignment	not modelled	95.1	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CodY HTH domain
109	<a href="#">d3ctaa1</a>	Alignment	not modelled	95.1	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
110	<a href="#">c3tgnA</a>	Alignment	not modelled	95.1	32	<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
111	<a href="#">d2cfxa1</a>	Alignment	not modelled	95.0	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
112	<a href="#">c2qwwB</a>	Alignment	not modelled	95.0	6	<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
113	<a href="#">c2kkoB</a>	Alignment	not modelled	95.0	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulatory protein <b>PDBTitle:</b> 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.
114	<a href="#">c2fxaB</a>	Alignment	not modelled	94.9	14	<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.
115	<a href="#">d3broa1</a>	Alignment	not modelled	94.9	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
116	<a href="#">c6paxA</a>	Alignment	not modelled	94.9	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
117	<a href="#">c2gxgA</a>	Alignment	not modelled	94.9	14	<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="#">c3f6oB</a>	Alignment	not modelled	94.9	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of arsr family transcriptional regulator,2 rha00566
119	<a href="#">d1mkma1</a>	Alignment	not modelled	94.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator lcr, N-terminal domain
120	<a href="#">d2fbha1</a>	Alignment	not modelled	94.8	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