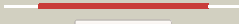



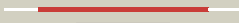
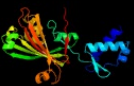


















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0792c_(-)_885840_886649
Date	Fri Jul 26 01:50:37 BST 2019
Unique Job ID	5b0b16c85df6983f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4zs8A_</a>	 Alignment		100.0	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor dasr; <b>PDBTitle:</b> crystal structure of ligand-free, full length dasr
2	<a href="#">c3bwgA_</a>	 Alignment		100.0	19	<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
3	<a href="#">c3f8mA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gntn-family protein transcriptional regulator; <b>PDBTitle:</b> crystal structure of phnf from mycobacterium smegmatis
4	<a href="#">c3edpB_</a>	 Alignment		100.0	20	<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
5	<a href="#">c2wv0H_</a>	 Alignment		100.0	28	<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 gntn-hutc family member yvoa from2 bacillus subtilis
6	<a href="#">c3eetA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative gntn-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative gntn-family transcriptional2 regulator
7	<a href="#">c4zsiA_</a>	 Alignment		99.9	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor dasr; <b>PDBTitle:</b> crystal structure of the effector-binding domain of dasr (dasr-ebd) in2 complex with glucosamine-6-phosphate
8	<a href="#">c4r1hA_</a>	 Alignment		99.9	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0741 protein; <b>PDBTitle:</b> gntn family transcriptional regulator from listeria monocytogenes
9	<a href="#">c4hamA_</a>	 Alignment		99.8	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2241 protein; <b>PDBTitle:</b> crystal structure of transcriptional antiterminator from listeria2 monocytogenes egd-e
10	<a href="#">c3neuA_</a>	 Alignment		99.8	28	<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
11	<a href="#">c3by6C_</a>	 Alignment		99.8	22	<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

12	<a href="#">c2du9A_</a>	Alignment		99.8	26	<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
13	<a href="#">c3f8lC_</a>	Alignment		99.8	22	<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
14	<a href="#">d2fa1a1</a>	Alignment		99.8	20	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
15	<a href="#">d3cnv1</a>	Alignment		99.8	28	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
16	<a href="#">d2p19a1</a>	Alignment		99.8	32	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
17	<a href="#">c4n0bA_</a>	Alignment		99.8	22	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulatory protein gabr; <b>PDBTitle:</b> crystal structure of bacillus subtilis gabr, an autorepressor and d2 transcriptional activator of gabt
18	<a href="#">c4egzA_</a>	Alignment		99.8	36	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> arabinose metabolism transcriptional repressor; <b>PDBTitle:</b> crystal structure of arar(dbd) in complex with operator orr3
19	<a href="#">d2ooia1</a>	Alignment		99.8	17	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
20	<a href="#">c2ra5A_</a>	Alignment		99.8	30	<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
21	<a href="#">d2ra5a1</a>	Alignment	not modelled	99.8	30	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
22	<a href="#">c6az6B_</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> gntr family transcriptional regulator; <b>PDBTitle:</b> streptococcus agalactiae gntr
23	<a href="#">d2ogga1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
24	<a href="#">d1v4ra1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
25	<a href="#">d2ikka1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
26	<a href="#">c3hfiA_</a>	Alignment	not modelled	99.8	16	<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
27	<a href="#">c4p96B_</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from vibrio cholerae
28	<a href="#">d3bwga2</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
29	<a href="#">c2di3A_</a>	Alignment	not modelled	99.8	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory proteins, gntr family;

29	<a href="#">c2u1a_</a>	Alignment	not modelled	99.8	30	<b>PDBTitle:</b> crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum <b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase complex repressor;
30	<a href="#">c5kvrA_</a>	Alignment	not modelled	99.8	36	<b>PDBTitle:</b> x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mcbr;
31	<a href="#">c4p9fA_</a>	Alignment	not modelled	99.8	24	<b>PDBTitle:</b> e. coli mcbr/yncc <b>PDB header:</b> transcriptional regulation <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid metabolism regulator protein;
32	<a href="#">c1e2xA_</a>	Alignment	not modelled	99.8	31	<b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from e.2 coli <b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
33	<a href="#">d2pkha1</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntr family;
34	<a href="#">c3c7jA_</a>	Alignment	not modelled	99.8	30	<b>PDBTitle:</b> crystal structure of transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> lmo0651 protein;
35	<a href="#">c6ep3B_</a>	Alignment	not modelled	99.7	22	<b>PDBTitle:</b> lar controls the expression of the listeria monocytogenes agr system2 and mediates virulence. <b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntr family;
36	<a href="#">c3fmsA_</a>	Alignment	not modelled	99.7	29	<b>PDBTitle:</b> crystal structure of tm0439, a gntr transcriptional regulator <b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntr family;
37	<a href="#">c3ihuA_</a>	Alignment	not modelled	99.7	22	<b>PDBTitle:</b> crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GnTR-like transcriptional regulators
38	<a href="#">d3bwga1</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GnTR-like transcriptional regulators
39	<a href="#">d1hw1a1</a>	Alignment	not modelled	99.7	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GnTR-like transcriptional regulators
40	<a href="#">c3ic7A_</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator;
41	<a href="#">c2hs5A_</a>	Alignment	not modelled	99.7	28	<b>PDBTitle:</b> crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron <b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator gntr;
42	<a href="#">c3lheA_</a>	Alignment	not modelled	99.7	22	<b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1 <b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> gntr family transcriptional regulator;
43	<a href="#">c3tqnC_</a>	Alignment	not modelled	99.7	25	<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 <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, gntr family;
44	<a href="#">d2hs5a1</a>	Alignment	not modelled	99.7	30	<b>PDBTitle:</b> structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii. <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GnTR-like transcriptional regulators
45	<a href="#">d3ddva1</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
46	<a href="#">d1biaa1</a>	Alignment	not modelled	97.9	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
47	<a href="#">c2h09A_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mntr;
48	<a href="#">d1stza1</a>	Alignment	not modelled	97.7	15	<b>PDBTitle:</b> crystal structure of diphtheria toxin repressor like protein2 from e. coli <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
49	<a href="#">c1f5tA_</a>	Alignment	not modelled	97.7	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor;
50	<a href="#">d1jhfa1</a>	Alignment	not modelled	97.6	20	<b>PDBTitle:</b> diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence <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
51	<a href="#">c2it0A_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider;
52	<a href="#">d1j5ya1</a>	Alignment	not modelled	97.4	20	<b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
53	<a href="#">c3rkxA_</a>	Alignment	not modelled	97.3	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin-[acetyl-coa-carboxylase] ligase;
54	<a href="#">c3hruA_</a>	Alignment	not modelled	97.3	16	<b>PDBTitle:</b> structural characterisation of staphylococcus aureus biotin protein2 ligase <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metalloregulator scar;
55	<a href="#">c3ctaA_</a>	Alignment	not modelled	97.2	20	<b>PDBTitle:</b> crystal structure of scar with bound zn2+ <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase;
						<b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma

						acidophilum
56	<a href="#">d1g3wa1</a>	Alignment	not modelled	97.2	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
57	<a href="#">c1j5yA</a>	Alignment	not modelled	97.1	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) from <i>Thermotoga maritima</i> at 2.3 Å resolution
58	<a href="#">c4pqlB</a>	Alignment	not modelled	97.0	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> truncated replication protein repa; <b>PDBTitle:</b> n-terminal domain of dna binding protein
59	<a href="#">d2isya1</a>	Alignment	not modelled	97.0	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
60	<a href="#">c1g3wA</a>	Alignment	not modelled	97.0	21	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
61	<a href="#">d1i5za1</a>	Alignment	not modelled	97.0	19	<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
62	<a href="#">c3lwfD</a>	Alignment	not modelled	96.9	15	<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 <i>Listeria innocua</i> at 2.06 Å resolution
63	<a href="#">c3k69A</a>	Alignment	not modelled	96.9	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator (lp_0360)2 from <i>Lactobacillus plantarum</i> at 1.95 Å resolution
64	<a href="#">c2y75F</a>	Alignment	not modelled	96.9	19	<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 regulator of <i>B. subtilis</i>
65	<a href="#">c3t8tA</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> staphylococcus aureus cymr (oxidized form); <b>PDBTitle:</b> crystal structure of staphylococcus aureus cymr oxidized form
66	<a href="#">c3r0aB</a>	Alignment	not modelled	96.8	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from <i>Methanosarcina mazei go1</i> (gi2_21227196)
67	<a href="#">c2v79B</a>	Alignment	not modelled	96.8	19	<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 from <i>Bacillus subtilis</i>
68	<a href="#">c2ewnA</a>	Alignment	not modelled	96.8	16	<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
69	<a href="#">c4cicB</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, badm/rrf2 family; <b>PDBTitle:</b> t. potens iscr
70	<a href="#">c4hf1B</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator iscr; <b>PDBTitle:</b> crystal structure of iscr bound to its promoter
71	<a href="#">c4o6jA</a>	Alignment	not modelled	96.7	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent transcription repressor related protein; <b>PDBTitle:</b> crystal structure of t. acidophilum ider
72	<a href="#">d1xd7a</a>	Alignment	not modelled	96.5	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator Rrf2
73	<a href="#">c6hsdB</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rrf2 family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the oxidized form of the transcription regulator2 rsrr
74	<a href="#">c1ft9A</a>	Alignment	not modelled	96.4	21	<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 <i>R. rubrum</i>
75	<a href="#">c1fx7C</a>	Alignment	not modelled	96.4	21	<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) from <i>Mycobacterium tuberculosis</i>
76	<a href="#">c5jbrA</a>	Alignment	not modelled	96.3	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bcav_2135; <b>PDBTitle:</b> crystal structure of uncharacterized protein bcav_2135 from <i>Beutenbergia cavernae</i>
77	<a href="#">d1ft9a1</a>	Alignment	not modelled	96.3	21	<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
78	<a href="#">d2h6ca1</a>	Alignment	not modelled	96.2	19	<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
79	<a href="#">c5cviB</a>	Alignment	not modelled	96.2	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
80	<a href="#">c5ey0A</a>	Alignment	not modelled	96.2	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> crystal structure of cody from <i>Staphylococcus aureus</i> with gtp and ile <b>PDB header:</b> transcription regulator

81	<a href="#">c1zybA</a>	Alignment	not modelled	96.2	8	<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
82	<a href="#">d2oz6a1</a>	Alignment	not modelled	96.2	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
83	<a href="#">c2x4hA</a>	Alignment	not modelled	96.1	13	<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
84	<a href="#">c4i2oA</a>	Alignment	not modelled	96.1	25	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> fixk2 protein; <b>PDBTitle:</b> the structure of fixk2 from bradyrhizobium japonicum
85	<a href="#">c3e97A</a>	Alignment	not modelled	96.1	13	<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/fnr family2 (yp_604437.1) from deinococcus geothermaliis dsm 11300 at 1.86 a3 resolution
86	<a href="#">c2oz6A</a>	Alignment	not modelled	96.0	23	<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
87	<a href="#">c6cmvA</a>	Alignment	not modelled	96.0	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrs14-like protein; <b>PDBTitle:</b> crystal structure of archaeal biofilm regulator (abfr2) from2 sulfolobus acidocaldarius
88	<a href="#">d2coha1</a>	Alignment	not modelled	96.0	31	<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
89	<a href="#">d2d1ha1</a>	Alignment	not modelled	96.0	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
90	<a href="#">c3d0sA</a>	Alignment	not modelled	96.0	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
91	<a href="#">c6j0eB</a>	Alignment	not modelled	95.9	30	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> arsenic responsive repressor arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
92	<a href="#">c2h6bA</a>	Alignment	not modelled	95.8	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chlorophenol reduction gene k; <b>PDBTitle:</b> crystal structure of oxidized cpk in complex with o-2 chlorophenolacetic acid
93	<a href="#">d1dpua</a>	Alignment	not modelled	95.8	25	<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
94	<a href="#">c1dpuA</a>	Alignment	not modelled	95.8	25	<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)
95	<a href="#">c3e6dA</a>	Alignment	not modelled	95.7	23	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide-binding protein; <b>PDBTitle:</b> crystal structure of cpk c200s
96	<a href="#">d3e5ua1</a>	Alignment	not modelled	95.7	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
97	<a href="#">c2gauA</a>	Alignment	not modelled	95.7	14	<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
98	<a href="#">c2vn2B</a>	Alignment	not modelled	95.7	25	<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 dna2 protein2 from geobacillus kaustophilus hta426
99	<a href="#">d2gaua1</a>	Alignment	not modelled	95.7	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
100	<a href="#">c4nb5D</a>	Alignment	not modelled	95.7	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
101	<a href="#">c2ev5B</a>	Alignment	not modelled	95.7	14	<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
102	<a href="#">d2bgca1</a>	Alignment	not modelled	95.7	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
103	<a href="#">d1sfxa</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> TrmB-like
104	<a href="#">c2oqgA</a>	Alignment	not modelled	95.6	14	<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
105	<a href="#">c3dv8A</a>	Alignment	not modelled	95.6	12	<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
106	<a href="#">d1r1ua</a>	Alignment	not modelled	95.6	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain



				Family: ArsR-like transcriptional regulators		
107	<a href="#">c5e44A_</a>	Alignment	not modelled	95.6	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fnr regulator; <b>PDBTitle:</b> crystal structure of holo-fnr of a. fischeri
108	<a href="#">c3kccA_</a>	Alignment	not modelled	95.5	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
109	<a href="#">c2zcwA_</a>	Alignment	not modelled	95.5	31	<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
110	<a href="#">c5jlsA_</a>	Alignment	not modelled	95.5	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adhesin competence repressor; <b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
111	<a href="#">c5yszA_</a>	Alignment	not modelled	95.5	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> transcriptional regulator celr-cellobiose complex
112	<a href="#">d1ku9a_</a>	Alignment	not modelled	95.5	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
113	<a href="#">c5w5aB_</a>	Alignment	not modelled	95.4	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator cmr; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis crp-fnr family2 transcription factor cmr (rv1675c)
114	<a href="#">c3f6vA_</a>	Alignment	not modelled	95.4	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for arsenical2 resistance
115	<a href="#">c2zy3A_</a>	Alignment	not modelled	95.4	10	<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
116	<a href="#">c1r22B_</a>	Alignment	not modelled	95.4	23	<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
117	<a href="#">c2fmyB_</a>	Alignment	not modelled	95.4	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 coa from carboxydotherrmus2 hydrogenoformans (imidazole-bound form)
118	<a href="#">c4ev0A_</a>	Alignment	not modelled	95.4	27	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator, crp family; <b>PDBTitle:</b> crystal structure of thermus thermophilus catabolite activator protein
119	<a href="#">c3iwzB_</a>	Alignment	not modelled	95.3	21	<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
120	<a href="#">c2zdbA_</a>	Alignment	not modelled	95.3	22	<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