







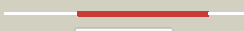















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1m0sa1</a>	 Alignment		100.0	20	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), catalytic domain
2	<a href="#">d1lk5a1</a>	 Alignment		99.9	21	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), catalytic domain
3	<a href="#">d1uj4a1</a>	 Alignment		99.9	16	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), catalytic domain
4	<a href="#">c3hheA_</a>	 Alignment		99.8	15	<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
5	<a href="#">c2f8mB_</a>	 Alignment		99.8	17	<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 falciparum
6	<a href="#">c1lk5C_</a>	 Alignment		99.8	17	<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
7	<a href="#">c1m0sA_</a>	 Alignment		99.8	20	<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)
8	<a href="#">c3kwmC_</a>	 Alignment		99.8	14	<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
9	<a href="#">c1lkzB_</a>	 Alignment		99.8	19	<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 (rpiA)2 from escherichia coli.
10	<a href="#">c3l7oB_</a>	 Alignment		99.8	19	<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
11	<a href="#">c2pjmA_</a>	 Alignment		99.8	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii

12	<a href="#">c1uj6A_</a>	Alignment		99.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
13	<a href="#">d1stza1</a>	Alignment		99.2	20	<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
14	<a href="#">d1j5ya1</a>	Alignment		99.1	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
15	<a href="#">d1biaa1</a>	Alignment		99.1	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
16	<a href="#">c1j5yA_</a>	Alignment		99.0	15	<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
17	<a href="#">c3u7jA_</a>	Alignment		99.0	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 burkholderia2 thailandensis
18	<a href="#">c1xtza_</a>	Alignment		98.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
19	<a href="#">d1o8bb1</a>	Alignment		98.5	20	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), catalytic domain
20	<a href="#">d2d1ha1</a>	Alignment		98.2	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
21	<a href="#">c3f8mA_</a>	Alignment	not modelled	98.1	11	<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
22	<a href="#">c2h09A_</a>	Alignment	not modelled	98.1	16	<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
23	<a href="#">d1vb5a_</a>	Alignment	not modelled	98.1	17	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> IF2B-like
24	<a href="#">c2vbza_</a>	Alignment	not modelled	98.0	23	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
25	<a href="#">d2cg4a1</a>	Alignment	not modelled	98.0	20	<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
26	<a href="#">c2x4hA_</a>	Alignment	not modelled	98.0	18	<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
27	<a href="#">c2l4aA_</a>	Alignment	not modelled	98.0	18	<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
28	<a href="#">c1f5tA_</a>	Alignment	not modelled	98.0	14	<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 <b>PDB header:</b> transcription regulator

29	<a href="#">c3bwgA</a>	Alignment	not modelled	98.0	17	<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
30	<a href="#">d2cfxa1</a>	Alignment	not modelled	97.9	17	<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
31	<a href="#">c2du9A</a>	Alignment	not modelled	97.9	20	<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
32	<a href="#">d1t5oa</a>	Alignment	not modelled	97.9	16	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> IF2B-like
33	<a href="#">d1t9ka</a>	Alignment	not modelled	97.9	16	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> IF2B-like
34	<a href="#">c3edpB</a>	Alignment	not modelled	97.9	13	<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
35	<a href="#">d2hs5a1</a>	Alignment	not modelled	97.9	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
36	<a href="#">c3neuA</a>	Alignment	not modelled	97.9	14	<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
37	<a href="#">d1l1ga1</a>	Alignment	not modelled	97.9	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
38	<a href="#">c3ecsD</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit <b>PDBTitle:</b> crystal structure of human eif2b alpha
39	<a href="#">c3by6C</a>	Alignment	not modelled	97.9	14	<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
40	<a href="#">c2it0A</a>	Alignment	not modelled	97.8	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
41	<a href="#">d2cyya1</a>	Alignment	not modelled	97.8	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
42	<a href="#">c2hs5A</a>	Alignment	not modelled	97.8	12	<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
43	<a href="#">c3c7jA</a>	Alignment	not modelled	97.8	10	<b>PDB header:</b> transcription regulator <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
44	<a href="#">d1jhfa1</a>	Alignment	not modelled	97.8	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
45	<a href="#">c2wteB</a>	Alignment	not modelled	97.8	21	<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 sulfobolus solfataricus at 1.8 angstrom resolution.
46	<a href="#">c3eetA</a>	Alignment	not modelled	97.8	13	<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
47	<a href="#">c2e1cA</a>	Alignment	not modelled	97.8	26	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
48	<a href="#">c3lmmA</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the dip2311 protein from2 corynebacterium diphtheriae, northeast structural genomics3 consortium target cdr35
49	<a href="#">c2e7xA</a>	Alignment	not modelled	97.7	13	<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 sulfobolus tokodaii 7 complexed with its cognate ligand
50	<a href="#">c3a11D</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor eif-2b, delta <b>PDBTitle:</b> crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
51	<a href="#">c2cg4B</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
52	<a href="#">d1hw1a1</a>	Alignment	not modelled	97.7	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
53	<a href="#">c2w48D</a>	Alignment	not modelled	97.7	20	<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>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional

54	<a href="#">c3cuoB</a>	Alignment	not modelled	97.6	13	regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
55	<a href="#">c2ia0A</a>	Alignment	not modelled	97.6	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
56	<a href="#">c2yvka</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylthioribose-1-phosphate isomerase; <b>PDBTitle:</b> crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
57	<a href="#">c2cfxD</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
58	<a href="#">c1stzB</a>	Alignment	not modelled	97.6	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> heat-inducible transcription repressor hrca homolog; <b>PDBTitle:</b> crystal structure of a hypothetical protein at 2.2 a resolution
59	<a href="#">c3i4pA</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
60	<a href="#">c3eqxB</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> fic domain containing transcriptional regulator; <b>PDBTitle:</b> crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
61	<a href="#">c2dbbA</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061
62	<a href="#">c2p6tH</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> transcriptional regulator, lrp/asnc family; <b>PDBTitle:</b> crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
63	<a href="#">dlz05a1</a>	Alignment	not modelled	97.6	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
64	<a href="#">dlv4ra1</a>	Alignment	not modelled	97.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
65	<a href="#">dlub9a</a>	Alignment	not modelled	97.5	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
66	<a href="#">c2oqgA</a>	Alignment	not modelled	97.5	19	<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
67	<a href="#">cle2xA</a>	Alignment	not modelled	97.5	17	<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
68	<a href="#">d2ev0a1</a>	Alignment	not modelled	97.5	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
69	<a href="#">clilgA</a>	Alignment	not modelled	97.5	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
70	<a href="#">dlr1ua</a>	Alignment	not modelled	97.4	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
71	<a href="#">d3bwga1</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> GntR-like transcriptional regulators
72	<a href="#">c3cdkD</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> succinyl-coa:3-ketoacid-coenzyme a transferase <b>PDBTitle:</b> crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
73	<a href="#">dlulya</a>	Alignment	not modelled	97.4	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
74	<a href="#">c2gqgB</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
75	<a href="#">d2p4wa1</a>	Alignment	not modelled	97.4	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
76	<a href="#">c2di3A</a>	Alignment	not modelled	97.4	13	<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
77	<a href="#">c3fmsA</a>	Alignment	not modelled	97.4	16	<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
78	<a href="#">c3f6vA</a>	Alignment	not modelled	97.4	19	<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

79	<a href="#">c1g3wA_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtbr
80	<a href="#">c3hruA_</a>	Alignment	not modelled	97.4	20	<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+
81	<a href="#">c3ihuA_</a>	Alignment	not modelled	97.3	12	<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
82	<a href="#">d1sfxa_</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> TrmB-like
83	<a href="#">d1mkma1</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> Transcriptional regulator lclR, N-terminal domain
84	<a href="#">c1r22B_</a>	Alignment	not modelled	97.3	18	<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
85	<a href="#">c1fx7C_</a>	Alignment	not modelled	97.3	14	<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
86	<a href="#">c3f6oB_</a>	Alignment	not modelled	97.2	19	<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
87	<a href="#">d1r1ta_</a>	Alignment	not modelled	97.2	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
88	<a href="#">d1g3wa1</a>	Alignment	not modelled	97.2	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
89	<a href="#">c3eyyA_</a>	Alignment	not modelled	97.1	24	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative iron uptake regulatory protein; <b>PDBTitle:</b> structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
90	<a href="#">d2htja1</a>	Alignment	not modelled	97.1	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FaeA-like
91	<a href="#">c2qwwB_</a>	Alignment	not modelled	97.1	18	<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
92	<a href="#">c2ev5B_</a>	Alignment	not modelled	97.1	20	<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
93	<a href="#">d2p5ka1</a>	Alignment	not modelled	97.1	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
94	<a href="#">d1lnwa_</a>	Alignment	not modelled	97.1	13	<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="#">c2nyxB_</a>	Alignment	not modelled	97.1	17	<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
96	<a href="#">d1okra_</a>	Alignment	not modelled	97.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
97	<a href="#">c2kkoB_</a>	Alignment	not modelled	97.1	25	<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.
98	<a href="#">c3bj6B_</a>	Alignment	not modelled	97.1	17	<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
99	<a href="#">d2isya1</a>	Alignment	not modelled	97.1	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
100	<a href="#">c2w57A_</a>	Alignment	not modelled	97.0	25	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
101	<a href="#">c2zkzC_</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional repressor pagr; <b>PDBTitle:</b> crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
102	<a href="#">d2fxaa1</a>	Alignment	not modelled	97.0	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
103	<a href="#">c3bddD_</a>	Alignment	not modelled	97.0	27	<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
104	<a href="#">d1k6da_</a>	Alignment	not modelled	97.0	20	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase alpha subunit-like
105	<a href="#">c2dt5A_</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> at-rich dna-binding protein; <b>PDBTitle:</b> crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
106	<a href="#">c2fa5B_</a>	Alignment	not modelled	96.9	17	<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-2 resistance repressor (marr) from xanthomonas campestris
107	<a href="#">c3oopA_</a>	Alignment	not modelled	96.9	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ilin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262
108	<a href="#">c3jthA_</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription activator hlyu; <b>PDBTitle:</b> crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
109	<a href="#">c3g3zA_</a>	Alignment	not modelled	96.9	19	<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
110	<a href="#">c1mkmA_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> iclr transcriptional regulator; <b>PDBTitle:</b> crystal structure of the thermotoga maritima iclr
111	<a href="#">c3s2wB_</a>	Alignment	not modelled	96.9	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1
112	<a href="#">d2etha1</a>	Alignment	not modelled	96.9	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
113	<a href="#">d1s3ja_</a>	Alignment	not modelled	96.9	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
114	<a href="#">c2rdpA_</a>	Alignment	not modelled	96.8	17	<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 stearothermophilus
115	<a href="#">c3r0aB_</a>	Alignment	not modelled	96.8	17	<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)
116	<a href="#">d1ooya1</a>	Alignment	not modelled	96.8	13	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase beta subunit-like
117	<a href="#">c2fxaB_</a>	Alignment	not modelled	96.8	22	<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.
118	<a href="#">c2fe3B_</a>	Alignment	not modelled	96.8	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxide operon regulator; <b>PDBTitle:</b> the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
119	<a href="#">c1o57A_</a>	Alignment	not modelled	96.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pur operon repressor; <b>PDBTitle:</b> crystal structure of the purine operon repressor of2 bacillus subtilis
120	<a href="#">d1ku9a_</a>	Alignment	not modelled	96.8	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