























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1m0sa1</a>	 Alignment		100.0	15	<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		100.0	17	<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	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
4	<a href="#">c3hheA_</a>	 Alignment		99.9	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 bartonella2 henselae
5	<a href="#">c2f8mB_</a>	 Alignment		99.8	13	<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	16	<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="#">c3kwmC_</a>	 Alignment		99.8	16	<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
8	<a href="#">c1m0sA_</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> northeast structural genomics consortium (nesg id ir21)
9	<a href="#">c3l7oB_</a>	 Alignment		99.8	14	<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
10	<a href="#">c1lkzB_</a>	 Alignment		99.8	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 (rpiA)2 from escherichia coli.
11	<a href="#">c2pjmA_</a>	 Alignment		99.8	17	<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="#">c3u7jA_</a>	Alignment		99.0	16	<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
14	<a href="#">d1j5ya1</a>	Alignment		99.0	15	<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="#">c1j5yA_</a>	Alignment		99.0	13	<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
16	<a href="#">d1stza1</a>	Alignment		98.9	18	<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
17	<a href="#">d1biaa1</a>	Alignment		98.9	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
18	<a href="#">c1xtza_</a>	Alignment		98.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
19	<a href="#">c2w48D_</a>	Alignment		98.6	17	<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
20	<a href="#">d1o8bb1</a>	Alignment		98.5	15	<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
21	<a href="#">d1vb5a_</a>	Alignment	not modelled	98.1	22	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> IF2B-like
22	<a href="#">d1t5oa_</a>	Alignment	not modelled	98.0	17	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> IF2B-like
23	<a href="#">d1t9ka_</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> IF2B-like
24	<a href="#">c1f5tA_</a>	Alignment	not modelled	97.9	6	<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
25	<a href="#">c2yvka_</a>	Alignment	not modelled	97.9	19	<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
26	<a href="#">c3cdkD_</a>	Alignment	not modelled	97.9	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
27	<a href="#">c2h09A_</a>	Alignment	not modelled	97.9	7	<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
28	<a href="#">c3a11D_</a>	Alignment	not modelled	97.8	16	<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

29	<a href="#">d2dlha1</a>	Alignment	not modelled	97.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
30	<a href="#">c3f8mA</a>	Alignment	not modelled	97.8	17	<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
31	<a href="#">c2it0A</a>	Alignment	not modelled	97.7	8	<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
32	<a href="#">c3neuA</a>	Alignment	not modelled	97.7	13	<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
33	<a href="#">c2vbzA</a>	Alignment	not modelled	97.7	7	<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
34	<a href="#">c2du9A</a>	Alignment	not modelled	97.7	10	<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
35	<a href="#">d2hs5a1</a>	Alignment	not modelled	97.7	17	<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="#">c3edpB</a>	Alignment	not modelled	97.7	10	<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
37	<a href="#">c3bwgA</a>	Alignment	not modelled	97.6	12	<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
38	<a href="#">c3ecsD</a>	Alignment	not modelled	97.6	22	<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="#">d2cg4a1</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> Lrp/AsnC-like transcriptional regulator N-terminal domain
40	<a href="#">c2e1cA</a>	Alignment	not modelled	97.5	11	<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
41	<a href="#">c2l4aA</a>	Alignment	not modelled	97.5	11	<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
42	<a href="#">c2hs5A</a>	Alignment	not modelled	97.5	16	<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="#">c2x4hA</a>	Alignment	not modelled	97.5	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 sulfolobus solfataricus
44	<a href="#">c3ereD</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
45	<a href="#">c3eetA</a>	Alignment	not modelled	97.5	12	<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
46	<a href="#">d2cfxa1</a>	Alignment	not modelled	97.4	9	<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
47	<a href="#">c3by6C</a>	Alignment	not modelled	97.4	13	<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
48	<a href="#">dli1ga1</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> Lrp/AsnC-like transcriptional regulator N-terminal domain
49	<a href="#">d2cyva1</a>	Alignment	not modelled	97.4	14	<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
50	<a href="#">c3c7jA</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 transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000
51	<a href="#">c2cg4B</a>	Alignment	not modelled	97.4	12	<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="#">d2p5ka1</a>	Alignment	not modelled	97.4	11	<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
53	<a href="#">dlooya1</a>	Alignment	not modelled	97.4	19	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase beta subunit-like
54	<a href="#">d1hw1a1</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> GntR-like transcriptional regulators

55	<a href="#">c2cfxD</a>	Alignment	not modelled	97.3	11	<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
56	<a href="#">c2dbbA</a>	Alignment	not modelled	97.3	10	<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
57	<a href="#">c1fx7C</a>	Alignment	not modelled	97.3	8	<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
58	<a href="#">c3cuoB</a>	Alignment	not modelled	97.3	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
59	<a href="#">c1stzB</a>	Alignment	not modelled	97.3	19	<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
60	<a href="#">c2wteB</a>	Alignment	not modelled	97.3	8	<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.
61	<a href="#">c1ilgA</a>	Alignment	not modelled	97.2	12	<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
62	<a href="#">c2e7xA</a>	Alignment	not modelled	97.2	10	<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
63	<a href="#">c1b4aA</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> repressor <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> structure of the arginine repressor from bacillus stearothermophilus
64	<a href="#">d1b4aa1</a>	Alignment	not modelled	97.2	13	<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
65	<a href="#">c2ia0A</a>	Alignment	not modelled	97.2	14	<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)
66	<a href="#">c2p6tH</a>	Alignment	not modelled	97.2	13	<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
67	<a href="#">d1k6da</a>	Alignment	not modelled	97.2	15	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase alpha subunit-like
68	<a href="#">c1e2xA</a>	Alignment	not modelled	97.2	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
69	<a href="#">c3lmmA</a>	Alignment	not modelled	97.2	12	<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
70	<a href="#">c2oqgA</a>	Alignment	not modelled	97.2	8	<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
71	<a href="#">c3eqxB</a>	Alignment	not modelled	97.2	8	<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
72	<a href="#">d1z05a1</a>	Alignment	not modelled	97.2	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
73	<a href="#">c2di3A</a>	Alignment	not modelled	97.2	9	<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
74	<a href="#">c3i4pA</a>	Alignment	not modelled	97.1	14	<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
75	<a href="#">d2gnpa1</a>	Alignment	not modelled	97.1	14	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
76	<a href="#">c1g3wA</a>	Alignment	not modelled	97.1	7	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
77	<a href="#">c3fmsA</a>	Alignment	not modelled	97.1	11	<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="#">d1v4ra1</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> Gntr-like transcriptional regulators
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

79	<a href="#">d1g3wa1</a>	Alignment	not modelled	97.1	7	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
80	<a href="#">c2qqqB</a>	Alignment	not modelled	97.1	12	<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)
81	<a href="#">d3bwga1</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> GntR-like transcriptional regulators
82	<a href="#">d2isyA1</a>	Alignment	not modelled	97.0	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
83	<a href="#">c3hruA</a>	Alignment	not modelled	97.0	11	<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+
84	<a href="#">c3ihuA</a>	Alignment	not modelled	97.0	13	<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
85	<a href="#">d1jhfa1</a>	Alignment	not modelled	96.9	5	<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
86	<a href="#">c3v4gA</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
87	<a href="#">d1rlua</a>	Alignment	not modelled	96.9	8	<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="#">c3f6vA</a>	Alignment	not modelled	96.9	8	<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
89	<a href="#">c3cdkA</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <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
90	<a href="#">d2p4wa1</a>	Alignment	not modelled	96.9	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
91	<a href="#">d2ev0a1</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
92	<a href="#">d1ulya</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
93	<a href="#">d1ub9a</a>	Alignment	not modelled	96.9	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
94	<a href="#">c3f6oB</a>	Alignment	not modelled	96.9	10	<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
95	<a href="#">c1r22B</a>	Alignment	not modelled	96.8	16	<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
96	<a href="#">c3nzeB</a>	Alignment	not modelled	96.8	11	<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.
97	<a href="#">d1f9na1</a>	Alignment	not modelled	96.7	11	<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
98	<a href="#">c2zkzC</a>	Alignment	not modelled	96.7	14	<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
99	<a href="#">c3kv1A</a>	Alignment	not modelled	96.6	9	<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
100	<a href="#">d1sfxa</a>	Alignment	not modelled	96.6	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
101	<a href="#">c3rrlC</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; <b>PDBTitle:</b> complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
102	<a href="#">c2kkoB</a>	Alignment	not modelled	96.6	18	<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.
103	<a href="#">d1rlta</a>	Alignment	not modelled	96.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators

104	<a href="#">c3eh7A_</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxybutyrate coa-transferase; <b>PDBTitle:</b> the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
105	<a href="#">c2dt5A_</a>	Alignment	not modelled	96.5	15	<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 tha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
106	<a href="#">c3jthA_</a>	Alignment	not modelled	96.5	13	<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
107	<a href="#">d1mkma1</a>	Alignment	not modelled	96.4	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator IclR, N-terminal domain
108	<a href="#">d2htja1</a>	Alignment	not modelled	96.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FaeA-like
109	<a href="#">c2ev5B_</a>	Alignment	not modelled	96.3	13	<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
110	<a href="#">c2ahvC_</a>	Alignment	not modelled	96.3	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative enzyme ydif; <b>PDBTitle:</b> crystal structure of acyl-coa transferase from e. coli o157:h7 (ydif)-2 thioester complex with coa- 1
111	<a href="#">d1okra_</a>	Alignment	not modelled	96.3	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
112	<a href="#">c1mkmA_</a>	Alignment	not modelled	96.2	8	<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
113	<a href="#">c2nyxB_</a>	Alignment	not modelled	96.2	16	<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
114	<a href="#">d3efba1</a>	Alignment	not modelled	96.1	14	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
115	<a href="#">c2qwwB_</a>	Alignment	not modelled	96.1	2	<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
116	<a href="#">c2jscB_</a>	Alignment	not modelled	96.1	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator rv1994c/mt2050; <b>PDBTitle:</b> nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
117	<a href="#">d2okga1</a>	Alignment	not modelled	96.1	13	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
118	<a href="#">c3eyyA_</a>	Alignment	not modelled	96.0	14	<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
119	<a href="#">c3bj6B_</a>	Alignment	not modelled	96.0	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
120	<a href="#">d2fxaa1</a>	Alignment	not modelled	96.0	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators