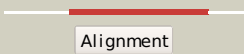



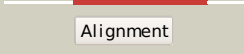





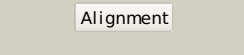

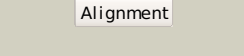

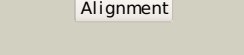

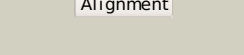

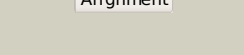

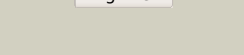




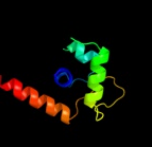








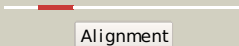
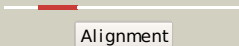
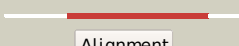

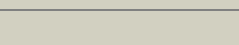
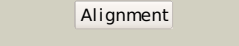
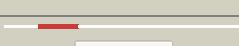
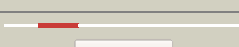



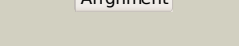
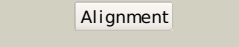
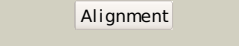
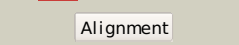

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1m0sa1	 Alignment		100.0	23	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
2	d1lk5a1	 Alignment		100.0	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
3	d1uj4a1	 Alignment		99.9	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
4	c3hheA_	 Alignment		99.9	20	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
5	c2f8mB_	 Alignment		99.9	19	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum
6	c1lk5C_	 Alignment		99.9	24	PDB header: isomerase Chain: C: PDB Molecule: d-ribose-5-phosphate isomerase; PDBTitle: structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
7	c3kwmC_	 Alignment		99.9	26	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
8	c1m0sA_	 Alignment		99.9	24	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: northeast structural genomics consortium (nesg id ir21)
9	c3l7oB_	 Alignment		99.9	24	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
10	c1lkzB_	 Alignment		99.8	21	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA)2 from escherichia coli.
11	c2pjmA_	 Alignment		99.8	22	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii

12	c1uj6A_	Alignment		99.8	16	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
13	c3u7jA_	Alignment		99.1	25	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
14	c1xtzA_	Alignment		99.0	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
15	d1stza1	Alignment		98.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
16	d1biaa1	Alignment		98.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
17	d1j5ya1	Alignment		98.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
18	c1j5yA_	Alignment		98.7	25	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, biotin repressor family; PDBTitle: crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
19	d1o8bb1	Alignment		98.6	22	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
20	c2w48D_	Alignment		98.5	13	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
21	d1vb5a_	Alignment	not modelled	98.3	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
22	d1t9ka_	Alignment	not modelled	98.2	12	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
23	d1t5oa_	Alignment	not modelled	98.2	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
24	c3cdkD_	Alignment	not modelled	98.2	13	PDB header: transferase Chain: D: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase PDBTitle: crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
25	c3ecsD_	Alignment	not modelled	98.1	13	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit PDBTitle: crystal structure of human eif2b alpha
26	c2yvka_	Alignment	not modelled	98.1	12	PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
27	c3a11D_	Alignment	not modelled	98.0	10	PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
28	c2vbza_	Alignment	not modelled	97.9	19	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan

29	d2cg4a1	Alignment	not modelled	97.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
30	d1ooya1	Alignment	not modelled	97.9	15	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
31	d2cfxa1	Alignment	not modelled	97.8	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
32	d2cyya1	Alignment	not modelled	97.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
33	c2l4aA	Alignment	not modelled	97.8	13	PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
34	dlilga1	Alignment	not modelled	97.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
35	c2e1cA	Alignment	not modelled	97.7	17	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
36	d2d1ha1	Alignment	not modelled	97.7	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
37	c2cfxD	Alignment	not modelled	97.6	9	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpC; PDBTitle: structure of b.subtilis lrpC
38	c1f5tA	Alignment	not modelled	97.6	9	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
39	c2e7xA	Alignment	not modelled	97.6	19	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
40	c2cg4B	Alignment	not modelled	97.6	20	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
41	c2ia0A	Alignment	not modelled	97.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
42	c2p6tH	Alignment	not modelled	97.6	16	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
43	c2dbbA	Alignment	not modelled	97.6	17	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
44	c2x4hA	Alignment	not modelled	97.6	6	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
45	c3i4pA	Alignment	not modelled	97.5	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
46	c2it0A	Alignment	not modelled	97.5	11	PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii
47	c2h09A	Alignment	not modelled	97.5	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
48	c1stzB	Alignment	not modelled	97.5	13	PDB header: transcription Chain: B: PDB Molecule: heat-inducible transcription repressor hrca homolog; PDBTitle: crystal structure of a hypothetical protein at 2.2 a resolution
49	d2ev0a1	Alignment	not modelled	97.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
50	c1i1gA	Alignment	not modelled	97.4	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
51	c2dt5A	Alignment	not modelled	97.4	18	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
52	c2wteB	Alignment	not modelled	97.4	19	PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
53	c2gqgB	Alignment	not modelled	97.4	15	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
						Fold: NagB/RpiA/CoA transferase-like

54	d1k6da_	Alignment	not modelled	97.3	15	Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
55	d1z05a1	Alignment	not modelled	97.3	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
56	c3by6C_	Alignment	not modelled	97.3	15	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
57	c3lmmA_	Alignment	not modelled	97.2	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the dip2311 protein from2 corynebacterium diphtheriae, northeast structural genomics3 consortium target cdr35
58	c3neuA_	Alignment	not modelled	97.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
59	c3cuoB_	Alignment	not modelled	97.1	13	PDB header: transcription regulator Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator ygav; PDBTitle: crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
60	c3cdkA_	Alignment	not modelled	97.1	16	PDB header: transferase Chain: A: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase PDBTitle: crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
61	c3f8mA_	Alignment	not modelled	97.1	17	PDB header: transcription Chain: A: PDB Molecule: gntr-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from mycobacterium smegmatis
62	d2p5ka1	Alignment	not modelled	97.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
63	d1jhfa1	Alignment	not modelled	97.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
64	d2p4wa1	Alignment	not modelled	97.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like
65	d1ub9a_	Alignment	not modelled	97.0	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
66	c1ooyA_	Alignment	not modelled	97.0	13	PDB header: transferase Chain: A: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase, PDBTitle: succinyl-coa:3-ketoacid coa transferase from pig heart
67	c1g3wA_	Alignment	not modelled	97.0	13	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
68	d1g3wa1	Alignment	not modelled	96.9	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
69	c1fx7C_	Alignment	not modelled	96.9	16	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
70	c2ev5B_	Alignment	not modelled	96.9	18	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
71	c3ereD_	Alignment	not modelled	96.9	28	PDB header: dna binding protein/dna Chain: D: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
72	d1b4aa1	Alignment	not modelled	96.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
73	d1ulya_	Alignment	not modelled	96.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932
74	c2oqgA_	Alignment	not modelled	96.8	28	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
75	d2isya1	Alignment	not modelled	96.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
76	c3eetA_	Alignment	not modelled	96.8	17	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntr-family transcriptional regulator; PDBTitle: crystal structure of putative gntr-family transcriptional2 regulator
77	c2du9A_	Alignment	not modelled	96.8	14	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c. glutamicum
78	c3rrlC_	Alignment	not modelled	96.8	15	PDB header: transferase Chain: C: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; PDBTitle: complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695 PDB header: dna binding protein Chain: B: PDB Molecule: fic domain containingq transcriptional

79	c3eqxB_	Alignment	not modelled	96.7	11	regulator; PDBTitle: crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
80	d1rlua_	Alignment	not modelled	96.7	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
81	c1b4aA_	Alignment	not modelled	96.7	21	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
82	c1r22B_	Alignment	not modelled	96.7	20	PDB header: transcription repressor Chain: B: PDB Molecule: transcriptional repressor smtb; PDBTitle: crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
83	c3ketA_	Alignment	not modelled	96.7	16	PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
84	d1u2wa1	Alignment	not modelled	96.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
85	c3f6vA_	Alignment	not modelled	96.6	22	PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family PDBTitle: crystal structure of possible transcriptional regulator for2 arsenical resistance
86	c3c7jA_	Alignment	not modelled	96.6	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, gntr family; PDBTitle: crystal structure of transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000
87	d2hs5a1	Alignment	not modelled	96.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GnTR-like transcriptional regulators
88	d2htja1	Alignment	not modelled	96.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FaeA-like
89	d1mkma1	Alignment	not modelled	96.5	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
90	d1sfxa_	Alignment	not modelled	96.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
91	c3v4gA_	Alignment	not modelled	96.5	12	PDB header: dna binding protein Chain: A: PDB Molecule: arginine repressor; PDBTitle: 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
92	c2nyxB_	Alignment	not modelled	96.4	17	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
93	d1v4ra1	Alignment	not modelled	96.4	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GnTR-like transcriptional regulators
94	c3hruA_	Alignment	not modelled	96.4	23	PDB header: transcription Chain: A: PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+
95	c3f6oB_	Alignment	not modelled	96.4	6	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
96	c3bwgA_	Alignment	not modelled	96.4	20	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator yydk; PDBTitle: the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
97	c2hs5A_	Alignment	not modelled	96.4	20	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator gntr; PDBTitle: structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
98	d2gnpa1	Alignment	not modelled	96.4	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
99	c3fmsA_	Alignment	not modelled	96.4	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, gntr family; PDBTitle: crystal structure of tm0439, a gntr transcriptional2 regulator
100	c2zkzC_	Alignment	not modelled	96.4	17	PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
101	c3bj6B_	Alignment	not modelled	96.3	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579
102	c2qwwB_	Alignment	not modelled	96.3	4	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
103	d1hw1a1	Alignment	not modelled	96.3	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GnTR-like transcriptional regulators

104	c2ahvC	 Alignment	not modelled	96.3	21	PDB header: transferase Chain: C: PDB Molecule: putative enzyme ydif; PDBTitle: crystal structure of acyl-coa transferase from e. coli o157:h7 (ydif)-2 thioester complex with coa- 1
105	c3edpB	 Alignment	not modelled	96.3	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin2111 protein; PDBTitle: the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
106	d2dt5a1	 Alignment	not modelled	96.3	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional repressor Rex, N-terminal domain
107	c3nzeB	 Alignment	not modelled	96.3	10	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator, sugar-binding family; PDBTitle: the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aureescens tc1.
108	d1lnwa	 Alignment	not modelled	96.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
109	c2kkoB	 Alignment	not modelled	96.2	17	PDB header: dna binding protein Chain: B: PDB Molecule: possible transcriptional regulatory protein PDBTitle: 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.
110	d1r1ta	 Alignment	not modelled	96.2	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
111	c3jthA	 Alignment	not modelled	96.2	22	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
112	c3gk7A	 Alignment	not modelled	96.1	17	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
113	c2ewnA	 Alignment	not modelled	96.0	14	PDB header: ligase, transcription Chain: A: PDB Molecule: bira bifunctional protein; PDBTitle: ecoli biotin repressor with co-repressor analog
114	c2oasA	 Alignment	not modelled	96.0	11	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coenzyme a transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
115	d1f9na1	 Alignment	not modelled	95.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
116	c3e6mD	 Alignment	not modelled	95.9	19	PDB header: transcription regulator Chain: D: PDB Molecule: marr family transcriptional regulator; PDBTitle: the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
117	c3bddD	 Alignment	not modelled	95.9	18	PDB header: transcription Chain: D: PDB Molecule: regulatory protein marr; PDBTitle: crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
118	d1lj9a	 Alignment	not modelled	95.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
119	c3ihuA	 Alignment	not modelled	95.9	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, gntr family; PDBTitle: crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution
120	c2o0mA	 Alignment	not modelled	95.8	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, sorc family; PDBTitle: the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis