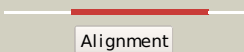

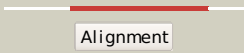







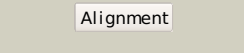
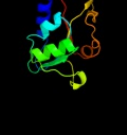
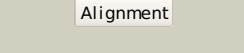

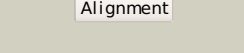



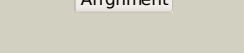

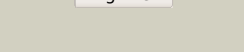




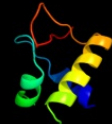
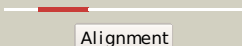



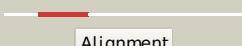

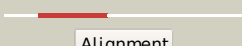

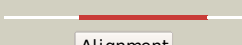









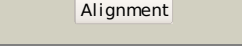

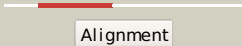



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0A0Q0
Date	Tue Jul 17 17:05:07 BST 2012
Unique Job ID	32d8f343888e9441

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1m0sa1	 Alignment		100.0	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
2	d1lk5a1	 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
3	d1uj4a1	 Alignment		99.9	15	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	21	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	14	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum
6	c1lk5C_	 Alignment		99.8	16	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		99.8	21	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
8	c1m0sA_	 Alignment		99.8	15	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: northeast structural genomics consortium (nesg id ir21)
9	c3l7oB_	 Alignment		99.8	18	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	13	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	23	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	19	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	d1stza1	 Alignment		99.2	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
14	d1j5ya1	 Alignment		99.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
15	c3u7jA_	 Alignment		99.2	18	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
16	d1biaa1	 Alignment		99.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
17	c1j5yA_	 Alignment		99.0	18	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
18	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
19	d1o8bb1	 Alignment		98.7	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
20	d1vb5a_	 Alignment		98.4	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
21	c3cdkD_	 Alignment	not modelled	98.3	15	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
22	c3a11D_	 Alignment	not modelled	98.3	15	PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta subunit; PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
23	c3ecsD_	 Alignment	not modelled	98.2	18	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit PDBTitle: crystal structure of human eif2b alpha
24	d1t9ka_	 Alignment	not modelled	98.2	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
25	d1t5oa_	 Alignment	not modelled	98.2	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
26	c2yvka_	 Alignment	not modelled	98.1	15	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	c2h09A_	 Alignment	not modelled	98.1	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
28	c2vbzA_	 Alignment	not modelled	98.1	15	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	98.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
30	d2d1ha1	Alignment	not modelled	98.0	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
31	c2x4hA	Alignment	not modelled	98.0	21	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
32	c2l4aA	Alignment	not modelled	98.0	18	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
33	d2cfxa1	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
34	c3f8mA	Alignment	not modelled	97.9	27	PDB header: transcription Chain: A: PDB Molecule: gntr-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from mycobacterium smegmatis
35	c1f5tA	Alignment	not modelled	97.9	23	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
36	d1l1ga1	Alignment	not modelled	97.8	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
37	d2cyya1	Alignment	not modelled	97.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
38	d1jhfA1	Alignment	not modelled	97.8	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
39	c2e1cA	Alignment	not modelled	97.8	19	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
40	c2wteB	Alignment	not modelled	97.7	21	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.
41	c3edpB	Alignment	not modelled	97.7	24	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
42	c2it0A	Alignment	not modelled	97.7	22	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
43	c2e7xA	Alignment	not modelled	97.7	17	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
44	c3bwgA	Alignment	not modelled	97.7	21	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
45	c2cg4B	Alignment	not modelled	97.7	16	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
46	c3qlkB	Alignment	not modelled	97.6	15	PDB header: transferase Chain: B: PDB Molecule: coenzyme a transferase; PDBTitle: crystal structure of ripa from yersinia pestis
47	c1stzB	Alignment	not modelled	97.6	22	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
48	c3lmmA	Alignment	not modelled	97.6	16	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
49	d2hs5a1	Alignment	not modelled	97.6	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
50	c2ia0A	Alignment	not modelled	97.6	20	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)
51	c3i4pA	Alignment	not modelled	97.6	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
52	c2p6tH	Alignment	not modelled	97.6	22	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
53	d1z05a1	Alignment	not modelled	97.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

						Family: ROK associated domain
54	c2dbbA	Alignment	not modelled	97.6	20	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
55	c3neuA	Alignment	not modelled	97.6	25	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
56	c3eetA	Alignment	not modelled	97.6	19	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntR-family transcriptional regulator; PDBTitle: crystal structure of putative gntR-family transcriptional2 regulator
57	c2du9A	Alignment	not modelled	97.6	21	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
58	c2cfxD	Alignment	not modelled	97.5	19	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
59	c3cuoB	Alignment	not modelled	97.5	11	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	c1g3wA	Alignment	not modelled	97.5	21	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
61	c2w48D	Alignment	not modelled	97.5	15	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
62	c3c7jA	Alignment	not modelled	97.5	15	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
63	c2hs5A	Alignment	not modelled	97.5	15	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
64	d1ub9a	Alignment	not modelled	97.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
65	c1i1gA	Alignment	not modelled	97.5	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
66	c3eqxB	Alignment	not modelled	97.5	19	PDB header: dna binding protein Chain: B: PDB Molecule: fic domain containing transcriptional regulator; PDBTitle: crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
67	d2ev0a1	Alignment	not modelled	97.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
68	c3by6C	Alignment	not modelled	97.4	22	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
69	d2p4wa1	Alignment	not modelled	97.4	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like
70	c3hruA	Alignment	not modelled	97.4	25	PDB header: transcription Chain: A: PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+
71	c2gqgB	Alignment	not modelled	97.4	19	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
72	d1hwl1a1	Alignment	not modelled	97.4	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
73	d1ooya1	Alignment	not modelled	97.4	15	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
74	d1ulya	Alignment	not modelled	97.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932
75	c2oqgA	Alignment	not modelled	97.4	19	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
76	d1rlua	Alignment	not modelled	97.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
77	c2oasA	Alignment	not modelled	97.4	13	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.
78	d1mkma1	Alignment	not modelled	97.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

						Family: Transcriptional regulator IcIR, N-terminal domain
79	c3f6vA_	Alignment	not modelled	97.3	18	PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family PDBTitle: crystal structure of possible transcriptional regulator for2 arsenical resistance
80	c1fx7C_	Alignment	not modelled	97.3	22	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
81	c3ereD_	Alignment	not modelled	97.3	17	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
82	d2p5ka1	Alignment	not modelled	97.3	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
83	d1sfxa_	Alignment	not modelled	97.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
84	c3gk7A_	Alignment	not modelled	97.3	16	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
85	c1r22B_	Alignment	not modelled	97.2	16	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
86	c3f6oB_	Alignment	not modelled	97.2	13	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
87	c1ooyA_	Alignment	not modelled	97.2	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
88	d3bwga1	Alignment	not modelled	97.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
89	d1g3wa1	Alignment	not modelled	97.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
90	d2htja1	Alignment	not modelled	97.1	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FaeA-like
91	d1r1ta_	Alignment	not modelled	97.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
92	c2qwwB_	Alignment	not modelled	97.1	11	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
93	c1e2xA_	Alignment	not modelled	97.1	27	PDB header: transcriptional regulation Chain: A: PDB Molecule: fatty acid metabolism regulator protein; PDBTitle: fadr, fatty acid responsive transcription factor from e.2 coli
94	c2nyxB_	Alignment	not modelled	97.1	13	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
95	c2di3A_	Alignment	not modelled	97.1	19	PDB header: transcription Chain: A: PDB Molecule: bacterial regulatory proteins, gntR family; PDBTitle: crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
96	d1poib_	Alignment	not modelled	97.1	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
97	d2isya1	Alignment	not modelled	97.0	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
98	c2zkzC_	Alignment	not modelled	97.0	20	PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
99	d1k6da_	Alignment	not modelled	97.0	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
100	c2ev5B_	Alignment	not modelled	97.0	25	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
101	d1lnwa_	Alignment	not modelled	97.0	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
102	d2ahua1	Alignment	not modelled	97.0	10	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
103	c3bj6B_	Alignment	not modelled	97.0	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579 PDB header: dna binding protein

104	c2kkoB	Alignment	not modelled	97.0	20	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.
105	c3eyyA	Alignment	not modelled	97.0	20	PDB header: transport Chain: A: PDB Molecule: putative iron uptake regulatory protein; PDBTitle: structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
106	c3jthA	Alignment	not modelled	97.0	17	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
107	c2lkpB	Alignment	not modelled	97.0	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmr
108	d1v4ra1	Alignment	not modelled	97.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
109	c3bddD	Alignment	not modelled	97.0	22	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
110	c3d3uA	Alignment	not modelled	96.9	23	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
111	d2fxaa1	Alignment	not modelled	96.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
112	c2ewnA	Alignment	not modelled	96.9	14	PDB header: ligase, transcription Chain: A: PDB Molecule: bira bifunctional protein; PDBTitle: ecoli biotin repressor with co-repressor analog
113	c3fmsA	Alignment	not modelled	96.9	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, gntR family; PDBTitle: crystal structure of tm0439, a gntR transcriptional2 regulator
114	c2fa5B	Alignment	not modelled	96.9	10	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator marr/emrr family; PDBTitle: the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
115	c3oopA	Alignment	not modelled	96.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2960 protein; PDBTitle: the structure of a protein with unknown function from listeria innocua2 clip11262
116	d1s3ja	Alignment	not modelled	96.9	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
117	d1okra	Alignment	not modelled	96.9	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
118	c3ihuA	Alignment	not modelled	96.9	21	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
119	c3g3zA	Alignment	not modelled	96.8	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
120	d2etha1	Alignment	not modelled	96.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators