































# Phyre2

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Description	P39410
Date	Thu Jan 5 12:00:47 GMT 2012
Unique Job ID	daa35e288fb3a8a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dntB_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein hipa; <b>PDBTitle:</b> structures of mdt proteins
2	<a href="#">c3akjB_</a>	 Alignment		99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ctka; <b>PDBTitle:</b> crystal structure of a helicobacter pylori proinflammatory kinase ctkA
3	<a href="#">c2oqgA_</a>	 Alignment		96.7	26	<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
4	<a href="#">c2jscB_</a>	 Alignment		96.7	23	<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
5	<a href="#">c2zkzC_</a>	 Alignment		96.6	19	<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
6	<a href="#">d1r1ua_</a>	 Alignment		96.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
7	<a href="#">d1r1ta_</a>	 Alignment		96.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
8	<a href="#">d1u2wa1</a>	 Alignment		96.3	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
9	<a href="#">c3pqkD_</a>	 Alignment		96.3	26	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> biofilm growth-associated repressor; <b>PDBTitle:</b> crystal structure of the transcriptional repressor bigr from xylella2 fastidiosA
10	<a href="#">c1r22B_</a>	 Alignment		96.3	23	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
11	<a href="#">c3f6vA_</a>	 Alignment		96.2	21	<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

12	<a href="#">d2d1ha1</a>	Alignment		96.2	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
13	<a href="#">c3f6oB_</a>	Alignment		96.2	15	<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
14	<a href="#">c1z6rC_</a>	Alignment		96.1	19	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> mlc protein; <b>PDBTitle:</b> crystal structure of mlc from escherichia coli
15	<a href="#">c3jthA_</a>	Alignment		96.1	26	<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
16	<a href="#">c2hoeA_</a>	Alignment		95.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine kinase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
17	<a href="#">c3cuoB_</a>	Alignment		95.9	23	<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
18	<a href="#">d1z05a1</a>	Alignment		95.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
19	<a href="#">c2kkoB_</a>	Alignment		95.7	21	<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.
20	<a href="#">c1z05A_</a>	Alignment		95.3	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rok family; <b>PDBTitle:</b> crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
21	<a href="#">c2w48D_</a>	Alignment	not modelled	94.7	22	<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
22	<a href="#">d2p4wa1</a>	Alignment	not modelled	94.6	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
23	<a href="#">d1z6ra1</a>	Alignment	not modelled	94.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
24	<a href="#">d1ub9a_</a>	Alignment	not modelled	94.1	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
25	<a href="#">d2cg4a1</a>	Alignment	not modelled	93.8	23	<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="#">c3ctaA_</a>	Alignment	not modelled	93.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma2 acidophilum
27	<a href="#">d1biaa1</a>	Alignment	not modelled	93.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
28	<a href="#">d1b4aa1</a>	Alignment	not modelled	93.2	24	<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
29	<a href="#">c2guvB_</a>	Alignment	not modelled	93.2	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor pf0095;

29	<a href="#">c2qub_</a>	Alignment	not modelled	93.2	15	<b>PDBTitle:</b> crystal structure of transcription factor axxa-pf0095 from <i>pyrococcus2 furiosus</i>
30	<a href="#">d1cjaa_</a>	Alignment	not modelled	93.0	23	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Actin-fragmin kinase, catalytic domain
31	<a href="#">c2dbbA_</a>	Alignment	not modelled	92.7	16	<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
32	<a href="#">c2ia0A_</a>	Alignment	not modelled	92.4	19	<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 <i>pyrococcus furiosus</i> a2 member of the asnc family (pf0864)
33	<a href="#">d3ctaa1</a>	Alignment	not modelled	92.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
34	<a href="#">d2etha1</a>	Alignment	not modelled	92.4	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
35	<a href="#">c2nyxB_</a>	Alignment	not modelled	92.3	24	<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 <i>mycobacterium tuberculosis</i>
36	<a href="#">d2ev0a1</a>	Alignment	not modelled	92.3	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
37	<a href="#">d1ilga1</a>	Alignment	not modelled	92.3	23	<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="#">d2p5ka1</a>	Alignment	not modelled	92.3	22	<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
39	<a href="#">d1ulya_</a>	Alignment	not modelled	92.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
40	<a href="#">d2cfxa1</a>	Alignment	not modelled	91.9	19	<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
41	<a href="#">c3k0lA_</a>	Alignment	not modelled	91.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein; <b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from <i>acinetobacter</i> sp. adp
42	<a href="#">c2bnoA_</a>	Alignment	not modelled	91.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase2 from <i>s. wedmorensis</i> .
43	<a href="#">c1j5yA_</a>	Alignment	not modelled	91.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, biotin repressor family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (tm1602) from <i>2 thermotoga maritima</i> at 2.3 a resolution
44	<a href="#">d1g3wa1</a>	Alignment	not modelled	91.8	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
45	<a href="#">c2cfxD_</a>	Alignment	not modelled	91.7	19	<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
46	<a href="#">d1j5ya1</a>	Alignment	not modelled	91.7	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
47	<a href="#">d2cyya1</a>	Alignment	not modelled	91.5	13	<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
48	<a href="#">d1ku9a_</a>	Alignment	not modelled	91.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
49	<a href="#">c1y9qA_</a>	Alignment	not modelled	91.5	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from <i>vibrio cholerae</i>
50	<a href="#">c3bpxB_</a>	Alignment	not modelled	91.5	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
51	<a href="#">c2e7xA_</a>	Alignment	not modelled	91.5	23	<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 from <i>2 sulfobolus tokodaii</i> 7 complexed with its cognate ligand
52	<a href="#">c3frwF_</a>	Alignment	not modelled	91.4	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trpR protein from <i>ruminococcus obeum</i>
53	<a href="#">d2isya1</a>	Alignment	not modelled	91.4	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
54	<a href="#">c1b4aA_</a>	Alignment	not modelled	91.4	24	<b>PDB header:</b> repressor <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> structure of the arginine repressor from <i>bacillus stearothermophilus</i>
						<b>PDB header:</b> dna-binding protein

55	<a href="#">c2vzbA_</a>	Alignment	not modelled	91.4	23	<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
56	<a href="#">c2rdpA_</a>	Alignment	not modelled	91.3	29	<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 steartothermophilus
57	<a href="#">c2cg4B_</a>	Alignment	not modelled	91.3	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
58	<a href="#">d2a61a1</a>	Alignment	not modelled	91.1	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
59	<a href="#">c3g3zA_</a>	Alignment	not modelled	91.1	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
60	<a href="#">c1ilgA_</a>	Alignment	not modelled	91.1	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrp; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
61	<a href="#">c3bddD_</a>	Alignment	not modelled	91.1	33	<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
62	<a href="#">d1sfxa_</a>	Alignment	not modelled	91.0	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
63	<a href="#">c1bdhA_</a>	Alignment	not modelled	90.9	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
64	<a href="#">c2nnnB_</a>	Alignment	not modelled	90.9	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
65	<a href="#">c3i4pA_</a>	Alignment	not modelled	90.8	16	<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
66	<a href="#">c2h09A_</a>	Alignment	not modelled	90.7	19	<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
67	<a href="#">c2x4hA_</a>	Alignment	not modelled	90.6	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
68	<a href="#">c2o38A_</a>	Alignment	not modelled	90.6	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative xre family transcriptional regulator
69	<a href="#">d2o38a1</a>	Alignment	not modelled	90.6	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
70	<a href="#">c3e6mD_</a>	Alignment	not modelled	90.5	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
71	<a href="#">c2e1cA_</a>	Alignment	not modelled	90.5	13	<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
72	<a href="#">d2a6ca1</a>	Alignment	not modelled	90.5	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
73	<a href="#">d1jhga_</a>	Alignment	not modelled	90.4	34	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
74	<a href="#">c2l4aA_</a>	Alignment	not modelled	90.3	29	<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
75	<a href="#">c3korD_</a>	Alignment	not modelled	90.2	29	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
76	<a href="#">c3fzjC_</a>	Alignment	not modelled	90.2	34	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> lysr type regulator of tsambcd; <b>PDBTitle:</b> tsar low resolution crystal structure, tetragonal form
77	<a href="#">c2wteB_</a>	Alignment	not modelled	90.1	26	<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.
78	<a href="#">c1zvva_</a>	Alignment	not modelled	90.1	29	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpa-crh-dna complex
79	<a href="#">d2hr3a1</a>	Alignment	not modelled	90.1	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
80	<a href="#">d1lnwa_</a>	Alignment	not modelled	89.9	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
81	<a href="#">c3b5fA_</a>	Alignment	not modelled	89.8	25	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family;

81	<a href="#">c3b9A_</a>	Alignment	not modelled	89.8	23	<b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
82	<a href="#">c1b9nA_</a>	Alignment	not modelled	89.8	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein (mode); <b>PDBTitle:</b> regulator from escherichia coli
83	<a href="#">d1trra_</a>	Alignment	not modelled	89.7	34	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
84	<a href="#">c3r0aB_</a>	Alignment	not modelled	89.6	18	<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)
85	<a href="#">d1aoya_</a>	Alignment	not modelled	89.6	22	<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
86	<a href="#">c3kxD_</a>	Alignment	not modelled	89.6	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
87	<a href="#">c2ppxA_</a>	Alignment	not modelled	89.5	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1735; <b>PDBTitle:</b> crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
88	<a href="#">d2ppxa1</a>	Alignment	not modelled	89.5	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
89	<a href="#">c2p6tH_</a>	Alignment	not modelled	89.5	29	<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
90	<a href="#">c2fa5B_</a>	Alignment	not modelled	89.3	39	<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
91	<a href="#">c3cjnA_</a>	Alignment	not modelled	89.1	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
92	<a href="#">c2gxgA_</a>	Alignment	not modelled	89.1	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
93	<a href="#">c3fmyA_</a>	Alignment	not modelled	89.0	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli protein2 mqsa (ygi/b3021)
94	<a href="#">d1s3ja_</a>	Alignment	not modelled	89.0	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
95	<a href="#">d2fbia1</a>	Alignment	not modelled	88.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
96	<a href="#">c3bj6B_</a>	Alignment	not modelled	88.7	30	<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
97	<a href="#">c2kpiA_</a>	Alignment	not modelled	88.6	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
98	<a href="#">c2y75F_</a>	Alignment	not modelled	88.3	24	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> hth-type transcriptional regulator cymr; <b>PDBTitle:</b> the structure of cymr (yrcz) the global cysteine regulator2 of b. subtilis
99	<a href="#">c3bs3A_</a>	Alignment	not modelled	88.1	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of a putative dna-binding protein from bacteroides2 fragilis
100	<a href="#">c3nqoB_</a>	Alignment	not modelled	87.8	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> marr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
101	<a href="#">c3eqxB_</a>	Alignment	not modelled	87.7	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
102	<a href="#">c1r71B_</a>	Alignment	not modelled	87.7	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor protein korb; <b>PDBTitle:</b> crystal structure of the dna binding domain of korb in2 complex with the operator dna
103	<a href="#">c2qwwB_</a>	Alignment	not modelled	87.7	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
104	<a href="#">d1lcda_</a>	Alignment	not modelled	87.5	25	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
105	<a href="#">d1mkma1</a>	Alignment	not modelled	87.5	16	<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



106	<a href="#">d2fbha1</a>	Alignment	not modelled	87.4	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
107	<a href="#">c3lwfD</a>	Alignment	not modelled	87.4	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
108	<a href="#">c2pexA</a>	Alignment	not modelled	87.4	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator ohrr; <b>PDBTitle:</b> structure of reduced c22s ohrr from xanthomonas campestris
109	<a href="#">c3nrvC</a>	Alignment	not modelled	87.4	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> putative transcriptional regulator (marr/emrr family); <b>PDBTitle:</b> crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
110	<a href="#">d2bv6a1</a>	Alignment	not modelled	87.3	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
111	<a href="#">d1xd7a</a>	Alignment	not modelled	87.3	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator Rrf2
112	<a href="#">d1qpza1</a>	Alignment	not modelled	87.3	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
113	<a href="#">d1lj9a</a>	Alignment	not modelled	87.1	10	<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="#">c3tgnA</a>	Alignment	not modelled	86.7	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr; <b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
115	<a href="#">c2it0A</a>	Alignment	not modelled	86.7	26	<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
116	<a href="#">d1utxa</a>	Alignment	not modelled	86.5	25	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
117	<a href="#">c3cdhB</a>	Alignment	not modelled	86.1	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3
118	<a href="#">c2fxaB</a>	Alignment	not modelled	86.1	13	<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.
119	<a href="#">c3hhgF</a>	Alignment	not modelled	86.0	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
120	<a href="#">d1i5za1</a>	Alignment	not modelled	85.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like