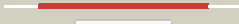



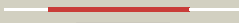



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2896c (- )_3205275_3206444
Date	Thu Aug 8 16:20:05 BST 2019
Unique Job ID	b7f6c7a22043a21e

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3majA_</a>	 Alignment		100.0	35	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna processing chain a; <b>PDBTitle:</b> crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
2	<a href="#">c3uqzB_</a>	 Alignment		100.0	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna processing protein dpra; <b>PDBTitle:</b> x-ray structure of dna processing protein a (dpra) from streptococcus pneumoniae
3	<a href="#">c4ljkA_</a>	 Alignment		100.0	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna processing chain a (dpra); <b>PDBTitle:</b> structural insights into the unique single-stranded dna binding mode2 of dna processing protein a from helicobacter pylori
4	<a href="#">c2iz6A_</a>	 Alignment		99.9	21	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum cofactor carrier protein; <b>PDBTitle:</b> structure of the chlamydomonas reinhardtii moco carrier2 protein
5	<a href="#">d1weka_</a>	 Alignment		99.9	19	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
6	<a href="#">c3sbxC_</a>	 Alignment		99.9	21	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium marinum bound to adenosine 5'-monophosphate amp
7	<a href="#">d1rcua_</a>	 Alignment		99.9	19	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
8	<a href="#">c1rcuB_</a>	 Alignment		99.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein vt76; <b>PDBTitle:</b> x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
9	<a href="#">d2nx2a1</a>	 Alignment		99.9	10	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> YpsA-like
10	<a href="#">d1weha_</a>	 Alignment		99.8	18	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
11	<a href="#">c3quaA_</a>	 Alignment		99.8	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis

12	<a href="#">c5wq3A_</a>	Alignment		99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytokinin riboside 5'-monophosphate phosphoribohydrolase; <b>PDBTitle:</b> crystal strcuture of type-ii log from corynebacterium glutamicum
13	<a href="#">c5zi9B_</a>	Alignment		99.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cytokinin riboside 5'-monophosphate phosphoribohydrolase; <b>PDBTitle:</b> crystal strcuture of type-ii log from streptomyces coelicolor a3
14	<a href="#">d1t35a_</a>	Alignment		99.1	15	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
15	<a href="#">c5zbjA_</a>	Alignment		99.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytokinin riboside 5'-monophosphate <b>PDBTitle:</b> crystal strcuture of type-i log from pseudomonas aeruginosa pao1
16	<a href="#">c5itsD_</a>	Alignment		99.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cytokinin riboside 5'-monophosphate phosphoribohydrolase; <b>PDBTitle:</b> crystal strcuture of log from corynebacterium glutamicum
17	<a href="#">d2q4oa1</a>	Alignment		99.1	20	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
18	<a href="#">c2q4oA_</a>	Alignment		99.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein at2g37210/t2n18.3; <b>PDBTitle:</b> ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
19	<a href="#">c2q4dB_</a>	Alignment		99.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lysine decarboxylase-like protein at5g11950; <b>PDBTitle:</b> ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
20	<a href="#">d1ydhA_</a>	Alignment		99.0	18	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
21	<a href="#">c5ajtA_</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribohydrolase lonely guy; <b>PDBTitle:</b> crystal structure of ligand-free phosphoribohydrolase lonely guy from2 claviceps purpurea
22	<a href="#">c6gfmA_</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine/purine nucleotide 5'-monophosphate nucleosidase; <b>PDBTitle:</b> crystal structure of the escherichia coli nucleosidase ppnn (ppgpp-2 form)
23	<a href="#">c3bq9A_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted rossmann fold nucleotide-binding domain- <b>PDBTitle:</b> crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
24	<a href="#">c3gh1A_</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted nucleotide-binding protein; <b>PDBTitle:</b> crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
25	<a href="#">c3imkA_</a>	Alignment	not modelled	97.7	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
26	<a href="#">c5bqtC_</a>	Alignment	not modelled	97.2	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative hth-type transcriptional regulator trmb12; <b>PDBTitle:</b> structure of trmb12, an archaeal chromatin protein, shows a novel mode2 of dna binding.
27	<a href="#">c5yhxH_</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> zinc transport transcriptional regulator; <b>PDBTitle:</b> structure of lactococcus lactis zitr, wild type
28	<a href="#">d1sfxA_</a>	Alignment	not modelled	96.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain

						Family:TrmB-like
29	<a href="#">d2d1ha1</a>	Alignment	not modelled	96.7	17	<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="#">c2rdpA</a>	Alignment	not modelled	96.7	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr; <b>PDBTitle:</b> the structure of a marr family protein from bacillus2 stearothermophilus
31	<a href="#">c3r0aB</a>	Alignment	not modelled	96.6	16	<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)
32	<a href="#">c6cmvA</a>	Alignment	not modelled	96.5	27	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrs14-like protein; <b>PDBTitle:</b> crystal structure of archaeal biofilm regulator (abfr2) from2 sulfobolus acidocaldarius
33	<a href="#">c3bj6B</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcription regulator sp03579
34	<a href="#">c4nb5D</a>	Alignment	not modelled	96.4	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
35	<a href="#">d1mkma1</a>	Alignment	not modelled	96.4	13	<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
36	<a href="#">c5zc2B</a>	Alignment	not modelled	96.2	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
37	<a href="#">d1okra</a>	Alignment	not modelled	96.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
38	<a href="#">c2g7uB</a>	Alignment	not modelled	96.2	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
39	<a href="#">c1mkmA</a>	Alignment	not modelled	96.2	14	<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
40	<a href="#">d1jhfa1</a>	Alignment	not modelled	96.2	26	<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
41	<a href="#">d1lnwa</a>	Alignment	not modelled	96.2	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
42	<a href="#">c5jbrA</a>	Alignment	not modelled	96.1	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bcav_2135; <b>PDBTitle:</b> crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
43	<a href="#">d2dk5a1</a>	Alignment	not modelled	96.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> RPO3F domain-like
44	<a href="#">c2wteB</a>	Alignment	not modelled	96.1	17	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> csa3; <b>PDBTitle:</b> the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
45	<a href="#">c2l4aA</a>	Alignment	not modelled	96.1	20	<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
46	<a href="#">c4ijaA</a>	Alignment	not modelled	96.1	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> xylyr protein; <b>PDBTitle:</b> structure of s. aureus methicillin resistance factor mecR2
47	<a href="#">c6jbxB</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid biosynthesis transcriptional regulator; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae fabt in complex with dna
48	<a href="#">d1ku9a</a>	Alignment	not modelled	96.0	23	<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="#">d2etha1</a>	Alignment	not modelled	96.0	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
50	<a href="#">c4yifE</a>	Alignment	not modelled	95.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> marr family protein rv0880; <b>PDBTitle:</b> crystal structure of rv0880
51	<a href="#">c5h1aC</a>	Alignment	not modelled	95.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> iclR transcription factor homolog; <b>PDBTitle:</b> crystal structure of an iclR homolog from microbacterium sp. strain2 hm58-2
52	<a href="#">c5w1eA</a>	Alignment	not modelled	95.9	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> pobr in complex with phb
53	<a href="#">c2nyxB</a>	Alignment	not modelled	95.9	15	<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
54	<a href="#">d1biaa1</a>	Alignment	not modelled	95.8	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like

55	<a href="#">c3g3zA_</a>	Alignment	not modelled	95.8	26	<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
56	<a href="#">c3bjaA_</a>	Alignment	not modelled	95.8	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
57	<a href="#">c3tgnA_</a>	Alignment	not modelled	95.8	18	<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
58	<a href="#">c2h09A_</a>	Alignment	not modelled	95.8	23	<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
59	<a href="#">c2x4hA_</a>	Alignment	not modelled	95.8	25	<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 sulfobolus solfataricus
60	<a href="#">c2it0A_</a>	Alignment	not modelled	95.8	19	<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
61	<a href="#">d2cyya1</a>	Alignment	not modelled	95.8	22	<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
62	<a href="#">d2cg4a1</a>	Alignment	not modelled	95.7	22	<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
63	<a href="#">d2a61a1</a>	Alignment	not modelled	95.7	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
64	<a href="#">d2hr3a1</a>	Alignment	not modelled	95.7	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
65	<a href="#">c4fhtA_</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pcav transcriptional regulator; <b>PDBTitle:</b> crystal structure of the pcav transcriptional regulator from2 streptomyces coelicolor in complex with its natural ligand
66	<a href="#">c2fa5B_</a>	Alignment	not modelled	95.6	16	<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
67	<a href="#">d1lj9a_</a>	Alignment	not modelled	95.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
68	<a href="#">c5tjA_</a>	Alignment	not modelled	95.6	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of iclr transcriptional regulator from2 alicyclobacillus acidocaldarius
69	<a href="#">d2cfxa1</a>	Alignment	not modelled	95.6	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
70	<a href="#">d1s3ja_</a>	Alignment	not modelled	95.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
71	<a href="#">c3cjnA_</a>	Alignment	not modelled	95.6	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
72	<a href="#">c2qwwB_</a>	Alignment	not modelled	95.6	8	<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
73	<a href="#">c4xrfA_</a>	Alignment	not modelled	95.5	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of mepr like protein complexed with pseudoligands
74	<a href="#">d1tw3a1</a>	Alignment	not modelled	95.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain
75	<a href="#">c6c28C_</a>	Alignment	not modelled	95.5	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> transcriptional repressor, cour, bound to p-coumaroyl-coa
76	<a href="#">c3hrmA_</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator sarz; <b>PDBTitle:</b> crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
77	<a href="#">d1p6ra_</a>	Alignment	not modelled	95.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
78	<a href="#">c1f5tA_</a>	Alignment	not modelled	95.4	21	<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
79	<a href="#">c3nrVC_</a>	Alignment	not modelled	95.4	19	<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
						<b>PDB header:</b> transcription

80	<a href="#">c5jlsA</a>	Alignment	not modelled	95.4	13	<b>Chain:</b> A: <b>PDB Molecule:</b> adhesin competence repressor; <b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from <i>Streptococcus pyogenes</i> (C-terminally His tagged)
81	<a href="#">c3r4kD</a>	Alignment	not modelled	95.4	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from <i>Silicibacter</i> sp. tm1040 at 2.46 Å resolution
82	<a href="#">d1ilga1</a>	Alignment	not modelled	95.4	24	<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
83	<a href="#">c2yu3A</a>	Alignment	not modelled	95.3	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase iii 39 kda <b>PDBTitle:</b> solution structure of the domain swapped wingedhelix in dna-2 directed rna polymerase iii 39 kda polypeptide
84	<a href="#">c2gxgA</a>	Alignment	not modelled	95.3	21	<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 <i>Sulfolobus tokodaii</i> strain7
85	<a href="#">d2fbia1</a>	Alignment	not modelled	95.3	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
86	<a href="#">d2fxaa1</a>	Alignment	not modelled	95.3	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
87	<a href="#">c2nnnB</a>	Alignment	not modelled	95.3	15	<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 from <i>Pseudomonas aeruginosa</i>
88	<a href="#">c3cuoB</a>	Alignment	not modelled	95.3	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygv; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from <i>E. coli</i>
89	<a href="#">c3bddD</a>	Alignment	not modelled	95.2	15	<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 <i>Streptococcus suis</i> 89/1591 at 2.20 Å resolution
90	<a href="#">c3oopA</a>	Alignment	not modelled	95.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from <i>Listeria innocua</i> 2 clip11262
91	<a href="#">d2bv6a1</a>	Alignment	not modelled	95.2	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
92	<a href="#">d1sd4a</a>	Alignment	not modelled	95.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
93	<a href="#">c4q77B</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator rot; <b>PDBTitle:</b> crystal structure of rot, a global regulator of virulence genes in <i>Staphylococcus aureus</i>
94	<a href="#">c4mnuA</a>	Alignment	not modelled	95.2	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> slya-like transcription regulator; <b>PDBTitle:</b> crystal structure of uncharacterized slya-like transcription regulator2 from <i>Listeria monocytogenes</i>
95	<a href="#">c2xroE</a>	Alignment	not modelled	95.2	23	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> hth-type transcriptional regulator ttgv; <b>PDBTitle:</b> crystal structure of ttgv in complex with its dna operator
96	<a href="#">c3bpxB</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
97	<a href="#">c2o0yB</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from <i>Rhodococcus</i> sp.
98	<a href="#">d3broa1</a>	Alignment	not modelled	95.2	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
99	<a href="#">c5aiqD</a>	Alignment	not modelled	95.2	21	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of ligand-free nadr
100	<a href="#">c3k0A</a>	Alignment	not modelled	95.1	17	<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
101	<a href="#">c2vzbA</a>	Alignment	not modelled	95.1	28	<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 <i>M. tuberculosis</i> complexed with L-tryptophan
102	<a href="#">d1stza1</a>	Alignment	not modelled	95.1	15	<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
103	<a href="#">c2fxaB</a>	Alignment	not modelled	95.0	19	<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 from <i>Bacillus subtilis</i> .
104	<a href="#">c3s2wB</a>	Alignment	not modelled	95.0	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the crystal structure of a marr transcriptional regulator from <i>Methanosarcina mazei</i> go1
						<b>PDB header:</b> transcription

105	<a href="#">c5eriA_</a>	Alignment	not modelled	95.0	12	<b>Chain:</b> A: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> marr protein from peptoclostridium difficile da00132
106	<a href="#">d2p4wa1</a>	Alignment	not modelled	95.0	34	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
107	<a href="#">c3nqoB_</a>	Alignment	not modelled	95.0	17	<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
108	<a href="#">c2pexA_</a>	Alignment	not modelled	95.0	21	<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="#">c3i53A_</a>	Alignment	not modelled	95.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
110	<a href="#">c3e6mD_</a>	Alignment	not modelled	94.9	17	<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.
111	<a href="#">c5dukA_</a>	Alignment	not modelled	94.9	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna binding protein; <b>PDBTitle:</b> n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
112	<a href="#">c5whmB_</a>	Alignment	not modelled	94.9	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> iclr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of iclr family transcriptional regulator from2 brucella abortus
113	<a href="#">c4em1A_</a>	Alignment	not modelled	94.9	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator sar2349; <b>PDBTitle:</b> staphylococcus aureus marr native
114	<a href="#">c4b8xB_</a>	Alignment	not modelled	94.9	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> possible marr-transcriptional regulator; <b>PDBTitle:</b> near atomic resolution crystal structure of sco5413, a marr family2 transcriptional regulator from streptomyces coelicolor
115	<a href="#">d1j5ya1</a>	Alignment	not modelled	94.9	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
116	<a href="#">c2dbbA_</a>	Alignment	not modelled	94.9	15	<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
117	<a href="#">c3pqkD_</a>	Alignment	not modelled	94.9	17	<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
118	<a href="#">d2fbha1</a>	Alignment	not modelled	94.8	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
119	<a href="#">c3zmdD_</a>	Alignment	not modelled	94.8	11	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor
120	<a href="#">c1fx7C_</a>	Alignment	not modelled	94.8	19	<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) from2 mycobacterium tuberculosis