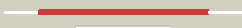
































# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1828 (-) _2073088_2073831
Date	Fri Aug 2 13:30:44 BST 2019
Unique Job ID	abe70cce3942acd5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2dg6A_</a>	 Alignment		99.8	14	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
2	<a href="#">c3gp4B_</a>	 Alignment		99.7	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
3	<a href="#">c3hh0C_</a>	 Alignment		99.7	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
4	<a href="#">c3qaoA_</a>	 Alignment		99.7	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> merr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
5	<a href="#">c3d6zA_</a>	 Alignment		99.7	19	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug-efflux transporter 1 regulator; <b>PDBTitle:</b> crystal structure of r275e mutant of bmrr bound to dna and rhodamine
6	<a href="#">c2zhhA_</a>	 Alignment		99.7	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensitive transcriptional activator soxr; <b>PDBTitle:</b> crystal structure of soxr
7	<a href="#">c3gpvA_</a>	 Alignment		99.7	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
8	<a href="#">c5ydcA_</a>	 Alignment		99.7	100	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv1828; <b>PDBTitle:</b> crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis
9	<a href="#">d1q06a_</a>	 Alignment		99.7	25	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
10	<a href="#">c5xqlA_</a>	 Alignment		99.7	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug-efflux transporter 1 regulator; <b>PDBTitle:</b> crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
11	<a href="#">c4r4eA_</a>	 Alignment		99.7	24	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator glnr; <b>PDBTitle:</b> structure of glnr-dna complex

12	<a href="#">d1r8da_</a>	Alignment		99.7	20	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
13	<a href="#">c2vz4A_</a>	Alignment		99.7	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> the n-terminal domain of merr-like protein tipal bound to promoter dna
14	<a href="#">c5c8eC_</a>	Alignment		99.7	20	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> light-dependent transcriptional regulator carh; <b>PDBTitle:</b> crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
15	<a href="#">c4r24B_</a>	Alignment		99.7	27	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator tnra; <b>PDBTitle:</b> complete dissection of b. subtilis nitrogen homeostatic circuitry
16	<a href="#">d1r8ea1</a>	Alignment		99.7	19	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
17	<a href="#">c5gpeB_</a>	Alignment		99.7	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, merr-family; <b>PDBTitle:</b> crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
18	<a href="#">c5af3A_</a>	Alignment		99.6	13	<b>PDB header:</b> dna binding <b>Chain:</b> A: <b>PDB Molecule:</b> vapbc49; <b>PDBTitle:</b> x-ray crystal structure of rv2018 from mycobacterium tuberculosis
19	<a href="#">c5i44E_</a>	Alignment		99.6	20	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> chromosome-anchoring protein raca; <b>PDBTitle:</b> structure of raca-dna complex; p21 form
20	<a href="#">c2jmlA_</a>	Alignment		99.6	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding domain/transcriptional regulator; <b>PDBTitle:</b> solution structure of the n-terminal domain of cara repressor
21	<a href="#">c3ucsB_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone-modulator protein cbpm; <b>PDBTitle:</b> crystal structure of the complex between cbpa j-domain and cbpm
22	<a href="#">c5crlA_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric resistance operon regulatory protein; <b>PDBTitle:</b> crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
23	<a href="#">c4ua2B_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of dual function transcriptional regulator merr from2 bacillus megaterium mb1
24	<a href="#">c6amaO_</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> O: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
25	<a href="#">c2ev2B_</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cylcase rv1264, at ph 8.5
26	<a href="#">c4j2nB_</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
27	<a href="#">c4j2nA_</a>	Alignment	not modelled	97.3	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
28	<a href="#">d1q08a_</a>	Alignment	not modelled	95.9	20	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators

29	<a href="#">c3ezfA</a>	Alignment	not modelled	94.9	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> para; <b>PDBTitle:</b> partition protein
30	<a href="#">c1z4hA</a>	Alignment	not modelled	92.7	11	<b>PDB header:</b> protein binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tor inhibition protein; <b>PDBTitle:</b> the response regulator tori belongs to a new family of 2 atypical excisionase
31	<a href="#">c2kfsA</a>	Alignment	not modelled	91.8	20	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical regulatory protein; <b>PDBTitle:</b> nmr structure of rv2175c
32	<a href="#">d1j5ya1</a>	Alignment	not modelled	89.2	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
33	<a href="#">d1biaa1</a>	Alignment	not modelled	88.0	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
34	<a href="#">c3fmyA</a>	Alignment	not modelled	87.5	10	<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 (ygit/b3021)
35	<a href="#">c5dukA</a>	Alignment	not modelled	86.6	19	<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 from 2 thermoplasmatales archaeon scgc ab-539-n05
36	<a href="#">c4k05B</a>	Alignment	not modelled	85.3	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical exported protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0371) from 2 bacteroides fragilis nctc 9343 at 1.65 a resolution
37	<a href="#">c5j9iH</a>	Alignment	not modelled	84.0	26	<b>PDB header:</b> antitoxin <b>Chain:</b> H: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higa2 antitoxin c-terminal domain
38	<a href="#">c3cuoB</a>	Alignment	not modelled	83.8	19	<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
39	<a href="#">c1u78A</a>	Alignment	not modelled	83.5	12	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
40	<a href="#">c5chhA</a>	Alignment	not modelled	80.9	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arac family transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
41	<a href="#">c2wusR</a>	Alignment	not modelled	80.4	13	<b>PDB header:</b> structural protein <b>Chain:</b> R: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> bacterial actin mreB assembles in complex with cell shape protein rodz
42	<a href="#">d2ppxa1</a>	Alignment	not modelled	80.3	7	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
43	<a href="#">c2ppxA</a>	Alignment	not modelled	80.3	7	<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
44	<a href="#">c6j05B</a>	Alignment	not modelled	79.8	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for 2 the mechanism of derepression
45	<a href="#">d2jn6a1</a>	Alignment	not modelled	79.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
46	<a href="#">c5jaaB</a>	Alignment	not modelled	79.5	20	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higa2 toxin-antitoxin complex
47	<a href="#">c5wayB</a>	Alignment	not modelled	78.3	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional activator; <b>PDBTitle:</b> mgaspn protein, mga regulator from streptococcus pneumoniae
48	<a href="#">d1j9ia</a>	Alignment	not modelled	77.7	23	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Terminase gpNU1 subunit domain
49	<a href="#">d1stza1</a>	Alignment	not modelled	77.2	26	<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
50	<a href="#">c2ebyA</a>	Alignment	not modelled	76.6	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybaq; <b>PDBTitle:</b> crystal structure of a hypothetical protein from e. coli
51	<a href="#">c4r6iA</a>	Alignment	not modelled	76.6	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> anthrax toxin expression trans-acting positive regulator; <b>PDBTitle:</b> atxa protein, a virulence regulator from bacillus anthracis.
52	<a href="#">c3zeyU</a>	Alignment	not modelled	76.2	22	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 40s ribosomal protein s25, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
53	<a href="#">c3bs3A</a>	Alignment	not modelled	76.1	4	<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
54	<a href="#">c3jthA</a>	Alignment	not modelled	76.0	20	<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 from 2 vibrio vulnificus cmcp6
						<b>PDB header:</b> structural genomics, unknown function

55	<a href="#">c4jjaA</a>	Alignment	not modelled	75.6	18	<b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0379) from <i>Bacteroides fragilis</i> nctc 9343 at 1.30 Å resolution
56	<a href="#">c1stzB</a>	Alignment	not modelled	75.5	29	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> heat-inducible transcription repressor hrca homolog; <b>PDBTitle:</b> crystal structure of a hypothetical protein at 2.2 Å resolution
57	<a href="#">c3f6vA</a>	Alignment	not modelled	75.4	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for arsenical2 resistance
58	<a href="#">c6paxA</a>	Alignment	not modelled	75.4	18	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
59	<a href="#">c4omzG</a>	Alignment	not modelled	75.2	12	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from <i>Sinorhizobium fredii</i>
60	<a href="#">c4nb5D</a>	Alignment	not modelled	74.2	14	<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
61	<a href="#">c2xzm8</a>	Alignment	not modelled	73.9	15	<b>PDB header:</b> ribosome <b>Chain:</b> 8: <b>PDB Molecule:</b> rps25e,; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
62	<a href="#">c3izbV</a>	Alignment	not modelled	73.8	28	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein rps25 (s25e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 Å cryo-em map of <i>Saccharomyces cerevisiae</i> translating 80s ribosome
63	<a href="#">c3j3aZ</a>	Alignment	not modelled	72.4	17	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 40s ribosomal protein s25; <b>PDBTitle:</b> structure of the human 40s ribosomal proteins
64	<a href="#">d2d1ha1</a>	Alignment	not modelled	72.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
65	<a href="#">c3fymA</a>	Alignment	not modelled	71.5	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the 1a structure of yfmf, a putative dna-binding membrane2 protein from <i>Staphylococcus aureus</i>
66	<a href="#">c2bnoA</a>	Alignment	not modelled	71.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase from <i>S. wedmorensis</i> .
67	<a href="#">c3omtA</a>	Alignment	not modelled	71.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> putative antitoxin component, chu_2935 protein, from <i>Xre</i> family from <i>Prevotella buccae</i> .
68	<a href="#">d1adra</a>	Alignment	not modelled	71.1	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
69	<a href="#">c3sqnA</a>	Alignment	not modelled	71.0	5	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> putative mga family transcriptional regulator from <i>Enterococcus faecalis</i>
70	<a href="#">d1pdnc</a>	Alignment	not modelled	70.3	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
71	<a href="#">d1r69a</a>	Alignment	not modelled	70.1	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
72	<a href="#">c6j0eB</a>	Alignment	not modelled	70.0	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> arsenic responsive repressor arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
73	<a href="#">c2fe3B</a>	Alignment	not modelled	69.9	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxide operon regulator; <b>PDBTitle:</b> the crystal structure of <i>Bacillus subtilis</i> per-zn reveals a novel2 zn(cys)4 structural redox switch
74	<a href="#">d1ku9a</a>	Alignment	not modelled	69.8	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
75	<a href="#">c1zljE</a>	Alignment	not modelled	69.8	10	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the <i>Mycobacterium tuberculosis</i> hypoxic2 response regulator dosr c-terminal domain
76	<a href="#">c3bd1B</a>	Alignment	not modelled	69.4	34	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cro protein; <b>PDBTitle:</b> structure of the cro protein from putative prophage element xfaso 1 in2 <i>Xylella fastidiosa</i> strain ann-1
77	<a href="#">c3op9A</a>	Alignment	not modelled	69.2	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> pli0006 protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator from <i>Listeria innocua</i>
78	<a href="#">c4razB</a>	Alignment	not modelled	69.1	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding transcriptional dual regulator of siderophore <b>PDBTitle:</b> crystal structure of <i>Magnetospirillum gryphiswaldense</i> msr-1 holo-fur
79	<a href="#">c2mezA</a>	Alignment	not modelled	69.1	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> multi-protein bridging factor (mbp-like); <b>PDBTitle:</b> flexible anchoring of archaeal mbf1 on ribosomes suggests role as2 recruitment factor
						<b>PDB header:</b> transcription repressor

80	<a href="#">c1r22B_</a>	Alignment	not modelled	68.7	16	<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
81	<a href="#">c2lkbB_</a>	Alignment	not modelled	68.5	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, arsr family; <b>PDBTitle:</b> solution structure of apo-nmtr
82	<a href="#">c2kpiA_</a>	Alignment	not modelled	68.4	6	<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
83	<a href="#">c5woqA_</a>	Alignment	not modelled	68.3	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator clgr; <b>PDBTitle:</b> crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
84	<a href="#">d2ofya1</a>	Alignment	not modelled	68.2	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
85	<a href="#">c3f52A_</a>	Alignment	not modelled	68.2	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> clp gene regulator (clgr); <b>PDBTitle:</b> crystal structure of the clp gene regulator clgr from c. glutamicum
86	<a href="#">d1jt6a1</a>	Alignment	not modelled	67.7	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
87	<a href="#">c3vk0B_</a>	Alignment	not modelled	67.3	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of hypothetical transcription factor nhtf from2 heisseria
88	<a href="#">c2ef8A_</a>	Alignment	not modelled	66.9	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription factor; <b>PDBTitle:</b> crystal structure of c.ecot38is
89	<a href="#">c5whmB_</a>	Alignment	not modelled	66.7	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> iclcr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of iclr family transcriptional regulator from2 brucella abortus
90	<a href="#">c3b7hA_</a>	Alignment	not modelled	66.4	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
91	<a href="#">d2hsqa1</a>	Alignment	not modelled	66.3	15	<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
92	<a href="#">d1t56a1</a>	Alignment	not modelled	65.7	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
93	<a href="#">c1y9qA_</a>	Alignment	not modelled	65.4	26	<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 vibrio cholerae
94	<a href="#">d1yioa1</a>	Alignment	not modelled	65.3	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
95	<a href="#">c3i4pA_</a>	Alignment	not modelled	65.3	0	<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
96	<a href="#">c1efaA_</a>	Alignment	not modelled	64.9	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> lac repressor; <b>PDBTitle:</b> crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
97	<a href="#">c3f6wE_</a>	Alignment	not modelled	64.8	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> xre-family like protein; <b>PDBTitle:</b> xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
98	<a href="#">d2o7ta1</a>	Alignment	not modelled	64.7	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
99	<a href="#">d2b5aa1</a>	Alignment	not modelled	64.7	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
100	<a href="#">d1luxca_</a>	Alignment	not modelled	64.7	15	<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
101	<a href="#">d1fsea_</a>	Alignment	not modelled	64.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
102	<a href="#">c1x3uA_</a>	Alignment	not modelled	64.5	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein fixj; <b>PDBTitle:</b> solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
103	<a href="#">c3clcC_</a>	Alignment	not modelled	64.4	17	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
104	<a href="#">c2dg7A_</a>	Alignment	not modelled	64.2	5	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
105	<a href="#">c3trbA_</a>	Alignment	not modelled	64.1	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence-associated protein i; <b>PDBTitle:</b> structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii

106	<a href="#">d1uxda_</a>	Alignment	not modelled	64.1	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GaIR/LacI-like bacterial regulator
107	<a href="#">d1r1ua_</a>	Alignment	not modelled	64.0	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
108	<a href="#">c2vbzA_</a>	Alignment	not modelled	63.8	5	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
109	<a href="#">d2r1j1_</a>	Alignment	not modelled	63.5	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
110	<a href="#">d2icta1_</a>	Alignment	not modelled	63.5	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
111	<a href="#">d2fbqa1_</a>	Alignment	not modelled	63.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
112	<a href="#">c5d50_</a>	Alignment	not modelled	63.4	3	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> repressor; <b>PDBTitle:</b> crystal structure of rep-ant complex from salmonella-temperate phage
113	<a href="#">c3t76A_</a>	Alignment	not modelled	63.3	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator vanug; <b>PDBTitle:</b> crystal structure of transcriptional regulator vanug, form ii
114	<a href="#">c6f8sA_</a>	Alignment	not modelled	63.3	22	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> xre family transcriptional regulator; <b>PDBTitle:</b> toxin-antitoxin complex grata
115	<a href="#">c1bjzA_</a>	Alignment	not modelled	63.3	5	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline repressor; <b>PDBTitle:</b> tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction
116	<a href="#">c6ideA_</a>	Alignment	not modelled	63.2	10	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator luxr family; <b>PDBTitle:</b> crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
117	<a href="#">c2d6yA_</a>	Alignment	not modelled	63.2	14	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr family regulatory protein; <b>PDBTitle:</b> crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)
118	<a href="#">c1bdhA_</a>	Alignment	not modelled	62.9	15	<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
119	<a href="#">c4cgrA_</a>	Alignment	not modelled	62.8	5	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> structure of regulator protein sco3201 from streptomyces coelicolor
120	<a href="#">c2krfB_</a>	Alignment	not modelled	62.6	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma; <b>PDBTitle:</b> nmr solution structure of the dna binding domain of competence protein2 a