

# Phyre<sup>2</sup>

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Description	Q79E92
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Detailed template information

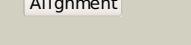
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2jn6a1</a>			99.8	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
2	<a href="#">c2rn7A_</a>			99.8	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> iS629 orfa; <b>PDBTitle:</b> nmr solution structure of tpe protein from shigella2 flexneri. northeast structural genomics target sfr125
3	<a href="#">c1hlvA_</a>			98.1	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-b box dna
4	<a href="#">c6paxA_</a>			98.0	12	<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
5	<a href="#">d1pdnc</a>			97.9	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
6	<a href="#">c2elhA_</a>			97.9	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
7	<a href="#">d6paxa1</a>			97.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
8	<a href="#">c1u78A_</a>			97.7	9	<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
9	<a href="#">d1k78a1</a>			97.7	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
10	<a href="#">d1bw6a_</a>			97.5	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
11	<a href="#">d2cba1</a>			97.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain

12	<a href="#">d1hlva1</a>			97.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
13	<a href="#">c2w48D</a>			96.9	14	<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
14	<a href="#">c3hefB</a>			96.8	16	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gene 1 protein; <b>PDBTitle:</b> crystal structure of the bacteriophage sf6 terminase small2 subunit
15	<a href="#">c2gloA</a>			96.8	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> brinker cg9653-pa; <b>PDBTitle:</b> solution structure of the brinker dna binding domain in2 complex with the omb enhancer
16	<a href="#">c2k27A</a>			96.6	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
17	<a href="#">d2ao9a1</a>			95.1	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
18	<a href="#">d1ntca</a>			94.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
19	<a href="#">c1iufA</a>			94.6	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> centromere abp1 protein; <b>PDBTitle:</b> low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
20	<a href="#">c3e7ID</a>			94.4	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
21	<a href="#">c2r0qF</a>		not modelled	94.4	18	<b>PDB header:</b> recombination/dna <b>Chain:</b> F: <b>PDB Molecule:</b> putative transposon tn552 dna-invertase bin3; <b>PDBTitle:</b> crystal structure of a serine recombinase- dna regulatory2 complex
22	<a href="#">c3hosA</a>		not modelled	94.2	15	<b>PDB header:</b> transferase, dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element mariner, complete cds; <b>PDBTitle:</b> crystal structure of the mariner mos1 paired end complex with mg
23	<a href="#">c2kpjA</a>		not modelled	93.9	11	<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
24	<a href="#">d1umqa</a>		not modelled	93.9	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
25	<a href="#">c1umqa</a>		not modelled	93.9	16	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prrA(rega) from r. sphaeroides:3 insights into dna binding specificity
26	<a href="#">d1ijwc</a>		not modelled	93.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
27	<a href="#">c2o8xA</a>		not modelled	93.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter

						recognition domain of2 mycobacterium tuberculosis sigc
28	<a href="#">d1rp3a2</a>	Alignment	not modelled	93.6	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
29	<a href="#">d1fipa</a>	Alignment	not modelled	93.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
30	<a href="#">c1or7A</a>	Alignment	not modelled	93.5	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-e factor; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
31	<a href="#">d1etxa</a>	Alignment	not modelled	93.4	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
32	<a href="#">c2cg4B</a>	Alignment	not modelled	93.4	7	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
33	<a href="#">d1hcra</a>	Alignment	not modelled	93.4	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
34	<a href="#">c210kA</a>	Alignment	not modelled	93.3	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein d; <b>PDBTitle:</b> nmr solution structure of a transcription factor spoiid in complex2 with dna
35	<a href="#">c3mzyA</a>	Alignment	not modelled	93.3	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
36	<a href="#">c2gm4B</a>	Alignment	not modelled	93.2	18	<b>PDB header:</b> recombination, dna <b>Chain:</b> B: <b>PDB Molecule:</b> transposon gamma-delta resolvase; <b>PDBTitle:</b> an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
37	<a href="#">d1or7a1</a>	Alignment	not modelled	93.2	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
38	<a href="#">c2zhhA</a>	Alignment	not modelled	93.0	13	<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
39	<a href="#">c3hugA</a>	Alignment	not modelled	93.0	17	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsl42 in complex with -35 promoter binding domain of sigl
40	<a href="#">d1xsva</a>	Alignment	not modelled	92.4	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Y1xm/p13-like
41	<a href="#">c2vz4A</a>	Alignment	not modelled	92.3	16	<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 to2 promoter dna
42	<a href="#">d1jhga</a>	Alignment	not modelled	92.2	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
43	<a href="#">d2ezla</a>	Alignment	not modelled	92.2	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
44	<a href="#">d1tra</a>	Alignment	not modelled	92.1	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
45	<a href="#">c2e7xA</a>	Alignment	not modelled	92.1	26	<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 from2 sulfolobus tokodaii 7 complexed with its cognate ligand
46	<a href="#">d1rlua</a>	Alignment	not modelled	91.9	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
47	<a href="#">c3i4pA</a>	Alignment	not modelled	91.8	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
48	<a href="#">c2ia0A</a>	Alignment	not modelled	91.8	9	<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 pyrococcus furiosus a2 member of the asnc family (pf0864)
49	<a href="#">d1q06a</a>	Alignment	not modelled	91.8	18	<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
50	<a href="#">c2cfxD</a>	Alignment	not modelled	91.6	5	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrp; <b>PDBTitle:</b> structure of b.subtilis lrp
51	<a href="#">c3gp4B</a>	Alignment	not modelled	91.5	6	<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
52	<a href="#">c1rp3G</a>	Alignment	not modelled	91.4	12	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> rna polymerase sigma factor sigma-28 (flia); <b>PDBTitle:</b> cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm <b>PDB header:</b> transcription

53	<a href="#">c2oqgA</a>	Alignment	not modelled	91.2	18	<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
54	<a href="#">c3frwF</a>	Alignment	not modelled	91.2	7	<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 trp repressor protein from rumicoccus obaeum
55	<a href="#">d1ulya</a>	Alignment	not modelled	91.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
56	<a href="#">c1r71B</a>	Alignment	not modelled	91.1	5	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor korb; <b>PDBTitle:</b> crystal structure of the dna binding domain of korb in2 complex with the operator dna
57	<a href="#">c1r22B</a>	Alignment	not modelled	91.0	7	<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
58	<a href="#">c3op9A</a>	Alignment	not modelled	91.0	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 listeria innocua
59	<a href="#">d1g2ha</a>	Alignment	not modelled	90.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
60	<a href="#">d1r71a</a>	Alignment	not modelled	90.9	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
61	<a href="#">d1r8da</a>	Alignment	not modelled	90.7	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
62	<a href="#">d1s7oa</a>	Alignment	not modelled	90.7	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Y1xm/p13-like
63	<a href="#">d1r1ta</a>	Alignment	not modelled	90.6	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
64	<a href="#">c2vbzA</a>	Alignment	not modelled	90.5	12	<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
65	<a href="#">c3b7hA</a>	Alignment	not modelled	90.5	12	<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
66	<a href="#">c2p6tH</a>	Alignment	not modelled	90.3	5	<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
67	<a href="#">c3gpvA</a>	Alignment	not modelled	90.3	13	<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
68	<a href="#">d1rzsa</a>	Alignment	not modelled	90.3	25	<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="#">c3korD</a>	Alignment	not modelled	90.2	12	<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
70	<a href="#">d2b5aa1</a>	Alignment	not modelled	90.1	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
71	<a href="#">c3t76A</a>	Alignment	not modelled	90.0	9	<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
72	<a href="#">c3f6oB</a>	Alignment	not modelled	89.8	11	<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
73	<a href="#">d1y9qa1</a>	Alignment	not modelled	89.8	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Probable transcriptional regulator VC1968, N-terminal domain
74	<a href="#">d1x57a1</a>	Alignment	not modelled	89.8	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
75	<a href="#">c3sztB</a>	Alignment	not modelled	89.7	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
76	<a href="#">d1etob</a>	Alignment	not modelled	89.7	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
77	<a href="#">d2cg4a1</a>	Alignment	not modelled	89.7	7	<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
78	<a href="#">d1y7ya1</a>	Alignment	not modelled	89.2	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like

79	<a href="#">d1vz0a1</a>	Alignment	not modelled	89.2	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
80	<a href="#">d1ku7a_</a>	Alignment	not modelled	89.1	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
81	<a href="#">c2dbbA_</a>	Alignment	not modelled	88.6	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
82	<a href="#">c2jmlA_</a>	Alignment	not modelled	88.6	16	<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
83	<a href="#">c3jthA_</a>	Alignment	not modelled	88.4	14	<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
84	<a href="#">c2pbxB_</a>	Alignment	not modelled	88.2	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin/protease regulatory protein; <b>PDBTitle:</b> vibrio cholerae hapr
85	<a href="#">c2jscB_</a>	Alignment	not modelled	88.2	9	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator rv1994c/mtb2050; <b>PDBTitle:</b> nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
86	<a href="#">c1zljE_</a>	Alignment	not modelled	88.1	9	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
87	<a href="#">c3f6vA_</a>	Alignment	not modelled	88.1	9	<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
88	<a href="#">d1l3la1</a>	Alignment	not modelled	88.0	11	<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)
89	<a href="#">d1a04a1</a>	Alignment	not modelled	87.9	23	<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)
90	<a href="#">c3pkD_</a>	Alignment	not modelled	87.8	14	<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
91	<a href="#">c3bs3A_</a>	Alignment	not modelled	87.8	7	<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
92	<a href="#">d1adra_</a>	Alignment	not modelled	87.8	9	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
93	<a href="#">c3gziA_</a>	Alignment	not modelled	87.8	5	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
94	<a href="#">d1biaa1</a>	Alignment	not modelled	87.8	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
95	<a href="#">d1sq8a_</a>	Alignment	not modelled	87.8	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
96	<a href="#">c2kk0B_</a>	Alignment	not modelled	87.7	9	<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.
97	<a href="#">c1i1gA_</a>	Alignment	not modelled	87.6	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
98	<a href="#">d1r69a_</a>	Alignment	not modelled	87.5	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
99	<a href="#">d1r8ea1</a>	Alignment	not modelled	87.4	21	<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
100	<a href="#">c2krfB_</a>	Alignment	not modelled	87.4	17	<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
101	<a href="#">c1rnIA_</a>	Alignment	not modelled	87.3	22	<b>PDB header:</b> signal transduction protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite response regulator protein narI; <b>PDBTitle:</b> the nitrate/nitrite response regulator protein narI from narI
102	<a href="#">d1b0na2</a>	Alignment	not modelled	87.3	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SimR domain-like

103	<a href="#">d1yioa1</a>		Alignment	not modelled	87.2	17	<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)
104	<a href="#">c3omtA_</a>		Alignment	not modelled	87.1	15	<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 xre family from2 prevotella buccae.
105	<a href="#">c2qo0A_</a>		Alignment	not modelled	87.0	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional activator protein trar; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
106	<a href="#">d1utxa_</a>		Alignment	not modelled	87.0	10	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
107	<a href="#">d1p4wa_</a>		Alignment	not modelled	86.9	18	<b>PDB header:</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)
108	<a href="#">c2jpcA_</a>		Alignment	not modelled	86.8	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
109	<a href="#">c3qaoA_</a>		Alignment	not modelled	86.8	14	<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 merrilike2 transcriptional regulator from listeria monocytogenes egd-e
110	<a href="#">c2l4aA_</a>		Alignment	not modelled	86.8	7	<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 Irp
111	<a href="#">c2e1ca_</a>		Alignment	not modelled	86.8	12	<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
112	<a href="#">c2w7nA_</a>		Alignment	not modelled	86.8	22	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation
113	<a href="#">d1wh5a_</a>		Alignment	not modelled	86.8	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
114	<a href="#">d1fsea_</a>		Alignment	not modelled	86.7	14	<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)
115	<a href="#">c2ao9H_</a>		Alignment	not modelled	86.6	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> phage protein; <b>PDBTitle:</b> structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
116	<a href="#">d2cyya1</a>		Alignment	not modelled	86.5	12	<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
117	<a href="#">d1ttya_</a>		Alignment	not modelled	86.5	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
118	<a href="#">c2ewtA_</a>		Alignment	not modelled	86.3	10	<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 the dna-binding domain of bldd
119	<a href="#">c3cuoB_</a>		Alignment	not modelled	86.2	5	<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
120	<a href="#">c2xcjB_</a>		Alignment	not modelled	85.9	11	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> c protein; <b>PDBTitle:</b> crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2