

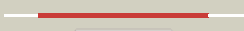
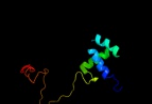











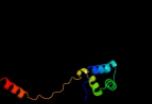








#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2jn6a1</a>	 Alignment		99.7	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
2	<a href="#">c2rn7A_</a>	 Alignment		99.6	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfa; <b>PDBTitle:</b> nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
3	<a href="#">c6paxA_</a>	 Alignment		98.4	13	<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
4	<a href="#">c1hlvA_</a>	 Alignment		98.4	34	<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-2 b box dna
5	<a href="#">c2elhA_</a>	 Alignment		98.4	35	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cgl1849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cgl1849-pa
6	<a href="#">d1pdnc_</a>	 Alignment		98.3	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
7	<a href="#">d1hlva1</a>	 Alignment		98.1	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
8	<a href="#">c1u78A_</a>	 Alignment		98.1	5	<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="#">d1bw6a_</a>	 Alignment		98.0	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
10	<a href="#">d6paxa1</a>	 Alignment		97.9	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
11	<a href="#">d1k78a1</a>	 Alignment		97.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain

12	<a href="#">c2gloA_</a>	Alignment		97.8	18	<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
13	<a href="#">d2coba1</a>	Alignment		97.7	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
14	<a href="#">c2k27A_</a>	Alignment		97.3	16	<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
15	<a href="#">c3hefB_</a>	Alignment		96.9	17	<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
16	<a href="#">c1iufA_</a>	Alignment		96.6	19	<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
17	<a href="#">c3hosA_</a>	Alignment		96.5	10	<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
18	<a href="#">c2w48D_</a>	Alignment		96.3	24	<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
19	<a href="#">d2ao9a1</a>	Alignment		96.1	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
20	<a href="#">d2oa4a1</a>	Alignment		96.0	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> SPO1678-like
21	<a href="#">c2jrtA_</a>	Alignment	not modelled	95.7	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
22	<a href="#">d1ntca_</a>	Alignment	not modelled	95.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
23	<a href="#">d1fipa_</a>	Alignment	not modelled	95.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
24	<a href="#">c1umqA_</a>	Alignment	not modelled	95.1	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
25	<a href="#">d1umqa_</a>	Alignment	not modelled	95.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
26	<a href="#">d1etxa_</a>	Alignment	not modelled	95.0	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
27	<a href="#">c3e7ID_</a>	Alignment	not modelled	95.0	27	<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
						<b>PDB header:</b> recombination/dna <b>Chain:</b> F: <b>PDB Molecule:</b> putative transposon tn552 dna-invertase

28	<a href="#">c2r0qF_</a>	Alignment	not modelled	94.9	13	bin3; <b>PDBTitle:</b> crystal structure of a serine recombinase- dna regulatory2 complex
29	<a href="#">dlijwc_</a>	Alignment	not modelled	94.1	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
30	<a href="#">d1hcra_</a>	Alignment	not modelled	93.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
31	<a href="#">c2gm4B_</a>	Alignment	not modelled	93.4	13	<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
32	<a href="#">c2cg4B_</a>	Alignment	not modelled	93.3	12	<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="#">c1or7A_</a>	Alignment	not modelled	93.3	9	<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
34	<a href="#">d1rp3a2</a>	Alignment	not modelled	93.2	16	<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
35	<a href="#">c3hugA_</a>	Alignment	not modelled	93.0	19	<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 rslA2 in complex with -35 promoter binding domain of sigl
36	<a href="#">c2o8xA_</a>	Alignment	not modelled	93.0	10	<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
37	<a href="#">c2oqgA_</a>	Alignment	not modelled	92.7	12	<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
38	<a href="#">c2kpiA_</a>	Alignment	not modelled	92.7	17	<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
39	<a href="#">c2e7xA_</a>	Alignment	not modelled	92.1	14	<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 sulfobolus tokodaii 7 complexed with its cognate ligand
40	<a href="#">d1rlua_</a>	Alignment	not modelled	92.0	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
41	<a href="#">d1xsva_</a>	Alignment	not modelled	91.9	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
42	<a href="#">d1r71a_</a>	Alignment	not modelled	91.9	14	<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
43	<a href="#">d1x57a1</a>	Alignment	not modelled	91.8	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
44	<a href="#">c210kA_</a>	Alignment	not modelled	91.8	24	<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 spoiiiid in complex2 with dna
45	<a href="#">c1r71B_</a>	Alignment	not modelled	91.7	14	<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
46	<a href="#">c1rr7A_</a>	Alignment	not modelled	91.7	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> middle operon regulator; <b>PDBTitle:</b> crystal structure of the middle operon regulator protein of2 bacteriophage mu
47	<a href="#">d1rr7a_</a>	Alignment	not modelled	91.7	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Middle operon regulator, Mor
48	<a href="#">d2ezla_</a>	Alignment	not modelled	91.6	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
49	<a href="#">d1etob_</a>	Alignment	not modelled	91.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
50	<a href="#">d1ulya_</a>	Alignment	not modelled	91.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
51	<a href="#">c2vz4A_</a>	Alignment	not modelled	91.6	21	<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
52	<a href="#">d1or7a1</a>	Alignment	not modelled	91.5	8	<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
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

53	<a href="#">d2ecba1</a>	Alignment	not modelled	91.5	13	<b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
54	<a href="#">c3i4pA</a>	Alignment	not modelled	91.5	13	<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
55	<a href="#">c1rp3G</a>	Alignment	not modelled	91.4	16	<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
56	<a href="#">d1ahdp</a>	Alignment	not modelled	91.3	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
57	<a href="#">c2pbxB</a>	Alignment	not modelled	91.3	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin/protease regulatory protein; <b>PDBTitle:</b> vibrio cholerae hapr
58	<a href="#">c3t76A</a>	Alignment	not modelled	91.2	13	<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
59	<a href="#">c2p6tH</a>	Alignment	not modelled	91.2	19	<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
60	<a href="#">c2cfxD</a>	Alignment	not modelled	91.2	9	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrp;c <b>PDBTitle:</b> structure of b.subtilis lrp
61	<a href="#">c2ao9H</a>	Alignment	not modelled	91.1	27	<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
62	<a href="#">d1wh5a</a>	Alignment	not modelled	91.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
63	<a href="#">d1lrza</a>	Alignment	not modelled	91.0	29	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
64	<a href="#">c2ia0A</a>	Alignment	not modelled	91.0	18	<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)
65	<a href="#">c1r22B</a>	Alignment	not modelled	90.9	13	<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
66	<a href="#">d1q06a</a>	Alignment	not modelled	90.8	15	<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
67	<a href="#">d1nera</a>	Alignment	not modelled	90.7	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
68	<a href="#">c3b7hA</a>	Alignment	not modelled	90.5	14	<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
69	<a href="#">c3op9A</a>	Alignment	not modelled	90.4	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
70	<a href="#">d1r1ta</a>	Alignment	not modelled	90.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
71	<a href="#">d2craa1</a>	Alignment	not modelled	90.1	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
72	<a href="#">d1jhga</a>	Alignment	not modelled	90.1	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
73	<a href="#">d2b5aa1</a>	Alignment	not modelled	89.8	8	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
74	<a href="#">c3narA</a>	Alignment	not modelled	89.7	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc fingers and homeoboxes protein 1; <b>PDBTitle:</b> crystal structure of zhx1 hd4 (zinc-fingers and homeoboxes protein 1,2 homeodomain 4)
75	<a href="#">c2vbzA</a>	Alignment	not modelled	89.6	14	<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
76	<a href="#">d1y9qa1</a>	Alignment	not modelled	89.6	16	<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
77	<a href="#">c2jscB</a>	Alignment	not modelled	89.5	11	<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
78	<a href="#">c3mzyA</a>	Alignment	not modelled	89.5	8	<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

79	<a href="#">d1trra_</a>	Alignment	not modelled	89.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
80	<a href="#">c1i1gA_</a>	Alignment	not modelled	89.2	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator Irpa; <b>PDBTitle:</b> crystal structure of the Irp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
81	<a href="#">d2cuea1</a>	Alignment	not modelled	89.1	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
82	<a href="#">d1g2ha_</a>	Alignment	not modelled	89.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
83	<a href="#">d2cg4a1</a>	Alignment	not modelled	88.6	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
84	<a href="#">d2e1oa1</a>	Alignment	not modelled	88.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
85	<a href="#">d1e3oc1</a>	Alignment	not modelled	88.5	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
86	<a href="#">d1r69a_</a>	Alignment	not modelled	88.4	9	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
87	<a href="#">d1vz0a1</a>	Alignment	not modelled	88.4	29	<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
88	<a href="#">d1y7ya1</a>	Alignment	not modelled	88.3	11	<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="#">d1le8b_</a>	Alignment	not modelled	88.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
90	<a href="#">c3f6oB_</a>	Alignment	not modelled	88.1	9	<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
91	<a href="#">c2kkoB_</a>	Alignment	not modelled	88.1	13	<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.
92	<a href="#">c2e1cA_</a>	Alignment	not modelled	88.1	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
93	<a href="#">c2dmpA_</a>	Alignment	not modelled	88.0	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc fingers and homeoboxes protein 2; <b>PDBTitle:</b> solution structure of the third homeobox domain of zinc2 fingers and homeoboxes protein 2
94	<a href="#">c2da4A_</a>	Alignment	not modelled	87.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein dkfzp686k21156; <b>PDBTitle:</b> solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
95	<a href="#">c2dg7A_</a>	Alignment	not modelled	87.7	21	<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)
96	<a href="#">c2fjrB_</a>	Alignment	not modelled	87.5	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of bacteriophage 186
97	<a href="#">c2da5A_</a>	Alignment	not modelled	87.5	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc fingers and homeoboxes protein 3; <b>PDBTitle:</b> solution structure of the second homeobox domain of zinc2 fingers and homeoboxes protein 3 (triple homeobox 13 protein)
98	<a href="#">d1p7ia_</a>	Alignment	not modelled	87.4	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
99	<a href="#">c3jthA_</a>	Alignment	not modelled	87.4	11	<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
100	<a href="#">d1sq8a_</a>	Alignment	not modelled	87.2	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
101	<a href="#">c2ewtA_</a>	Alignment	not modelled	87.2	13	<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
102	<a href="#">d1b0na2</a>	Alignment	not modelled	87.2	31	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
103	<a href="#">d1gt0c1</a>	Alignment	not modelled	87.2	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
						<b>Fold:</b> lambda repressor-like DNA-binding domains

104	<a href="#">d1adra_</a>	Alignment	not modelled	87.2	11	<b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
105	<a href="#">d1bw5a_</a>	Alignment	not modelled	87.1	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
106	<a href="#">c3cuoB_</a>	Alignment	not modelled	87.1	15	<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
107	<a href="#">c3bs3A_</a>	Alignment	not modelled	87.1	21	<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
108	<a href="#">c2xcjB_</a>	Alignment	not modelled	87.0	16	<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
109	<a href="#">d1s7oa_</a>	Alignment	not modelled	86.9	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> YlxM/p13-like
110	<a href="#">c2da1A_</a>	Alignment	not modelled	86.8	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-fetoprotein enhancer binding protein; <b>PDBTitle:</b> solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
111	<a href="#">c3f6vA_</a>	Alignment	not modelled	86.7	18	<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
112	<a href="#">d1biaa1</a>	Alignment	not modelled	86.6	2	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
113	<a href="#">c2l9rA_</a>	Alignment	not modelled	86.5	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein nkx-3.1; <b>PDBTitle:</b> solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
114	<a href="#">c2w7nA_</a>	Alignment	not modelled	86.5	14	<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
115	<a href="#">d2cyya1</a>	Alignment	not modelled	86.4	11	<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
116	<a href="#">c2dbbA_</a>	Alignment	not modelled	86.4	9	<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="#">c3bd1B_</a>	Alignment	not modelled	86.4	25	<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 xylella fastidiosa strain ann-1
118	<a href="#">d1b8ia_</a>	Alignment	not modelled	86.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
119	<a href="#">c3pqkD_</a>	Alignment	not modelled	86.3	16	<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
120	<a href="#">d1yrnb_</a>	Alignment	not modelled	86.2	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain