

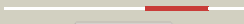






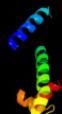












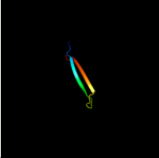
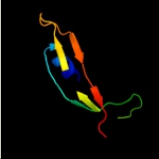
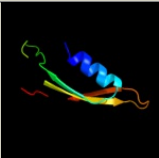




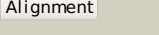
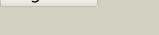




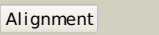
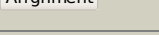
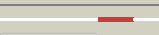

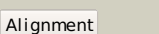
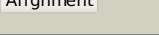


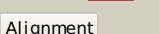
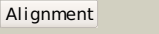
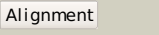
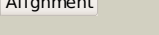



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlj5ya1</a>	 Alignment		96.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
2	<a href="#">dlbtxa_</a>	 Alignment		96.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
3	<a href="#">clu78A_</a>	 Alignment		96.1	11	<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
4	<a href="#">dlbiaa1</a>	 Alignment		96.1	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
5	<a href="#">dlfipa_</a>	 Alignment		96.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
6	<a href="#">c3cloC_</a>	 Alignment		95.7	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
7	<a href="#">clumqA_</a>	 Alignment		95.3	18	<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
8	<a href="#">dlumqa_</a>	 Alignment		95.3	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
9	<a href="#">c2r0qF_</a>	 Alignment		95.1	28	<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
10	<a href="#">dlpdnc_</a>	 Alignment		94.9	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
11	<a href="#">dlrlua_</a>	 Alignment		94.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators

12	<a href="#">c2oqgA_</a>	Alignment		94.6	13	<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
13	<a href="#">d2cg4a1</a>	Alignment		94.5	18	<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
14	<a href="#">c3njaC_</a>	Alignment		94.5	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> probable ggdef family protein; <b>PDBTitle:</b> the crystal structure of the pas domain of a ggdef family protein from2 chromobacterium violaceum atcc 12472.
15	<a href="#">d1etob_</a>	Alignment		94.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
16	<a href="#">d1bywa_</a>	Alignment		94.3	13	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> Flavin-binding PAS domain
17	<a href="#">c2gm4B_</a>	Alignment		94.2	32	<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
18	<a href="#">c3cuoB_</a>	Alignment		94.2	9	<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
19	<a href="#">c3e7lD_</a>	Alignment		94.1	19	<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
20	<a href="#">c2vbzA_</a>	Alignment		94.1	26	<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
21	<a href="#">d2jn6a1</a>	Alignment	not modelled	94.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
22	<a href="#">d1l1ga1</a>	Alignment	not modelled	94.1	18	<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
23	<a href="#">c2p6tH_</a>	Alignment	not modelled	94.0	18	<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
24	<a href="#">d1r1ta_</a>	Alignment	not modelled	94.0	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
25	<a href="#">d1g2ha_</a>	Alignment	not modelled	93.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
26	<a href="#">d1ntca_</a>	Alignment	not modelled	93.8	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
27	<a href="#">d2d1ha1</a>	Alignment	not modelled	93.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
28	<a href="#">c2l4aA_</a>	Alignment	not modelled	93.8	15	<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
						<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulatory protein

29	<a href="#">c2kkoB</a>	Alignment	not modelled	93.7	19	<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.
30	<a href="#">c6paxA</a>	Alignment	not modelled	93.7	16	<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
31	<a href="#">c1r22B</a>	Alignment	not modelled	93.6	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 zn2al pha5-3 form
32	<a href="#">c3jthA</a>	Alignment	not modelled	93.4	13	<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
33	<a href="#">d1a04a1</a>	Alignment	not modelled	93.3	24	<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)
34	<a href="#">c3caxA</a>	Alignment		93.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pf0695; <b>PDBTitle:</b> crystal structure of uncharacterized protein pf0695
35	<a href="#">c2elhA</a>	Alignment	not modelled	93.1	9	<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
36	<a href="#">c3icyB</a>	Alignment		93.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> the crystal structure of sensory box histidine2 kinase/response regulator domain from chlorobium tepidum3 t1s
37	<a href="#">c2e1cA</a>	Alignment	not modelled	92.9	18	<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
38	<a href="#">d2p4wa1</a>	Alignment	not modelled	92.8	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
39	<a href="#">d2cfxa1</a>	Alignment	not modelled	92.8	18	<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
40	<a href="#">c3f6vA</a>	Alignment	not modelled	92.7	17	<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
41	<a href="#">c2qwtA</a>	Alignment	not modelled	92.6	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of the n-terminal domain of diguanylate protein from mycobacterium vanbaalenii
42	<a href="#">c3pqkD</a>	Alignment	not modelled	92.6	15	<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
43	<a href="#">c3iwfA</a>	Alignment	not modelled	92.6	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpri family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpri2 transcriptional regulator from staphylococcus epidermidis to 1.4a
44	<a href="#">c3h9wA</a>	Alignment		92.6	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase with pas/pac sensor; <b>PDBTitle:</b> crystal structure of the n-terminal domain of diguanylate cyclase with2 pas/pac sensor (maqu_2914) from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr66c
45	<a href="#">c1i1gA</a>	Alignment	not modelled	92.4	18	<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
46	<a href="#">c2z6dB</a>	Alignment		92.2	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phototropin-2; <b>PDBTitle:</b> crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana
47	<a href="#">c2nx4A</a>	Alignment	not modelled	91.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family protein; <b>PDBTitle:</b> the crystal structure of the putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
48	<a href="#">c2qkpD</a>	Alignment	not modelled	91.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
49	<a href="#">c2wgbB</a>	Alignment	not modelled	91.9	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional repressor lfrr; <b>PDBTitle:</b> crystal structure of the tetr-like transcriptional2 regulator lfrr from mycobacterium smegmatis

50	<a href="#">c2ia0A_</a>	 Alignment	not modelled	91.9	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 <i>pyrococcus furiosus</i> a2 member of the asnc family (pf0864)
51	<a href="#">c2e7xA_</a>	 Alignment	not modelled	91.9	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from <i>2 sulfolobus tokodaii</i> 7 complexed with its cognate ligand
52	<a href="#">c2pbxB_</a>	 Alignment	not modelled	91.8	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin/protease regulatory protein; <b>PDBTitle:</b> vibrio cholerae hapr
53	<a href="#">d2cyya1</a>	 Alignment	not modelled	91.8	15	<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
54	<a href="#">c3bjbE_</a>	 Alignment	not modelled	91.7	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> E: <b>PDB Molecule:</b> probable transcriptional regulator, tetr family protein; <b>PDBTitle:</b> crystal structure of a tetr transcriptional regulator from <i>rhodococcus</i> 2 sp. rha1
55	<a href="#">d1n9la_</a>	 Alignment	not modelled	91.6	12	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> Flavin-binding PAS domain
56	<a href="#">c3o60A_</a>	 Alignment	not modelled	91.5	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin0861 protein; <b>PDBTitle:</b> the crystal structure of lin0861 from <i>listeria innocua</i> to 2.8a
57	<a href="#">c2jscB_</a>	 Alignment	not modelled	91.5	13	<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 <i>mycobacterium</i> 2 tuberculosis
58	<a href="#">c3f6oB_</a>	 Alignment	not modelled	91.5	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
59	<a href="#">c1r71B_</a>	 Alignment	not modelled	91.4	10	<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
60	<a href="#">c3e7qB_</a>	 Alignment	not modelled	91.3	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the putative transcriptional regulator from <i>2 pseudomonas aeruginosa</i> pao1
61	<a href="#">d1p97a_</a>	 Alignment	not modelled	91.3	21	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> Hypoxia-inducible factor Hif2a, C-terminal domain
62	<a href="#">d2g7ga1</a>	 Alignment	not modelled	91.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
63	<a href="#">c2rekA_</a>	 Alignment	not modelled	91.1	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr-family transcriptional regulator
64	<a href="#">c3luqC_</a>	 Alignment	not modelled	91.0	10	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> the crystal structure of a pas domain from a sensory box2 histidine kinase regulator from <i>geobacter sulfurreducens</i> to3 2.5a
65	<a href="#">d1mzba_</a>	 Alignment	not modelled	90.9	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FUR-like
66	<a href="#">d1r71a_</a>	 Alignment	not modelled	90.8	10	<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
67	<a href="#">d1vz0a1</a>	 Alignment	not modelled	90.7	23	<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
68	<a href="#">c3gziA_</a>	 Alignment	not modelled	90.7	13	<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 <i>shewanella loihica</i> pv-4 at 2.05 a resolution
69	<a href="#">c1hlvA_</a>	 Alignment	not modelled	90.6	17	<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
70	<a href="#">c2cg4B_</a>	 Alignment	not modelled	90.6	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
71	<a href="#">c2kdkA_</a>	 Alignment	not modelled	90.6	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> aryl hydrocarbon receptor nuclear translocator-like protein <b>PDBTitle:</b> structure of human circadian clock protein bmal2 c-terminal pas domain
72	<a href="#">c2raeA_</a>	Alignment	not modelled	90.4	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family protein; <b>PDBTitle:</b> crystal structure of a tetr/acrr family transcriptional regulator from <i>2 rhodococcus</i> sp. rha1
73	<a href="#">c2cfxD_</a>	Alignment	not modelled	90.4	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
		Alignment				<b>PDB header:</b> circadian clock protein

74	<a href="#">c2pdtD_</a>	Alignment	not modelled	90.2	10	<b>Chain:</b> D: <b>PDB Molecule:</b> vivid pas protein vvd; <b>PDBTitle:</b> 2.3 angstrom structure of phosphodiesterase treated vivid
75	<a href="#">c1rnlA_</a>	Alignment	not modelled	90.0	23	<b>PDB header:</b> signal transduction protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite response regulator protein narl; <b>PDBTitle:</b> the nitrate/nitrite response regulator protein narl from narl
76	<a href="#">c2dbbA_</a>	Alignment	not modelled	89.8	24	<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
77	<a href="#">d2ezla_</a>	Alignment	not modelled	89.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
78	<a href="#">d1t33a1</a>	Alignment	not modelled	89.5	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
79	<a href="#">c1h0mD_</a>	Alignment	not modelled	89.4	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional activator protein trar; <b>PDBTitle:</b> three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
80	<a href="#">d2hkua1</a>	Alignment	not modelled	89.4	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
81	<a href="#">c3eqxB_</a>	Alignment	not modelled	89.4	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> fic domain containing transcriptional regulator; <b>PDBTitle:</b> crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
82	<a href="#">c3i4pA_</a>	Alignment	not modelled	89.3	21	<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
83	<a href="#">c3c3wB_</a>	Alignment	not modelled	89.0	25	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulatory protein devr; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
84	<a href="#">c2o7tA_</a>	Alignment	not modelled	88.7	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tet family transcriptional regulator2 (ncgl1578, cgl1640) from corynebacterium glutamicum at 2.10 a3 resolution
85	<a href="#">d1ulya_</a>	Alignment	not modelled	88.7	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
86	<a href="#">c2rn7A_</a>	Alignment	not modelled	88.6	17	<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
87	<a href="#">c2zkzC_</a>	Alignment	not modelled	88.6	20	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional repressor pagr; <b>PDBTitle:</b> crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
88	<a href="#">c2fe3B_</a>	Alignment	not modelled	88.6	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 bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
89	<a href="#">c2i4rA_</a>	Alignment	not modelled	88.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 2; <b>PDBTitle:</b> nmr solution structure of the n-terminal pas domain of herg
90	<a href="#">d1jnua_</a>	Alignment	not modelled	88.2	13	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> Flavin-binding PAS domain
91	<a href="#">c3qp5C_</a>	Alignment	not modelled	88.2	23	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> cvir transcriptional regulator; <b>PDBTitle:</b> crystal structure of cvir bound to antagonist chlorolactone (cl)
92	<a href="#">d2vkea1</a>	Alignment	not modelled	88.2	21	<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="#">c2of7A_</a>	Alignment	not modelled	88.2	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
94	<a href="#">d2isya1</a>	Alignment	not modelled	87.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
95	<a href="#">d1k78a1</a>	Alignment	not modelled	87.9	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
96	<a href="#">d1v7ba1</a>	Alignment	not modelled	87.7	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
97	<a href="#">c2x48B_</a>	Alignment	not modelled	87.6	22	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> cag38821; <b>PDBTitle:</b> orf 55 from sulfolobus islandicus rudivirus 1
98	<a href="#">d2vkva1</a>	Alignment	not modelled	87.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
						<b>PDB header:</b> transcription



99	<a href="#">c3lyxA</a>	Alignment	not modelled	87.5	14	<b>Chain:</b> A: <b>PDB Molecule:</b> sensory box/ggdef domain protein; <b>PDBTitle:</b> crystal structure of the pas domain of the protein cps_12912 from colwellia psychrerythraea. northeast structural3 genomics consortium target id csr222b
100	<a href="#">c3ljIB</a>	Alignment	not modelled	87.5	5	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator luxt; <b>PDBTitle:</b> the crystal structure of the full-length transcriptional regulator2 luxt from vibrio parahaemolyticus rimd 2210633.
101	<a href="#">c3mvpA</a>	Alignment	not modelled	87.5	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr/acrr transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a tetr/acrr transcriptional regulator from2 streptococcus mutans to 1.85a
102	<a href="#">c3eyyA</a>	Alignment	not modelled	87.4	13	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative iron uptake regulatory protein; <b>PDBTitle:</b> structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
103	<a href="#">d2o7ta1</a>	Alignment	not modelled	87.4	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
104	<a href="#">c2iu5A</a>	Alignment	not modelled	87.3	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type dhaklm operon transcriptional activator dhas; <b>PDBTitle:</b> dihydroxyacetone kinase operon activator dhas
105	<a href="#">d2esna1</a>	Alignment	not modelled	87.3	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
106	<a href="#">d1mkma1</a>	Alignment	not modelled	87.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator lclR, N-terminal domain
107	<a href="#">c3szTB</a>	Alignment	not modelled	87.2	12	<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
108	<a href="#">d2id6a1</a>	Alignment	not modelled	87.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
109	<a href="#">c2q0oA</a>	Alignment	not modelled	87.0	19	<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
110	<a href="#">d1u2wa1</a>	Alignment	not modelled	86.8	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
111	<a href="#">d1t56a1</a>	Alignment	not modelled	86.7	32	<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="#">c2fu4B</a>	Alignment	not modelled	86.6	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
113	<a href="#">d2gena1</a>	Alignment	not modelled	86.6	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
114	<a href="#">d2i10a1</a>	Alignment	not modelled	86.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
115	<a href="#">c3eehA</a>	Alignment	not modelled	86.6	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative light and redox sensing histidine kinase; <b>PDBTitle:</b> the crystal structure of the domain of the putative light and redox2 sensing histidine kinase from haloarcula marismortui
116	<a href="#">d1g3wa1</a>	Alignment	not modelled	86.6	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
117	<a href="#">d2iu5a1</a>	Alignment	not modelled	86.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
118	<a href="#">c3pasA</a>	Alignment	not modelled	86.3	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcription regulator; <b>PDBTitle:</b> crystal structure of a tetr family transcription regulator (maqu_1417)2 from marinobacter aquaeolei vt8 at 1.90 a resolution
119	<a href="#">d1lrza</a>	Alignment	not modelled	86.2	32	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
120	<a href="#">d1ui5a1</a>	Alignment	not modelled	86.2	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain