






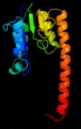






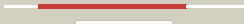
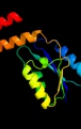








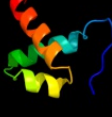








#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2gm4B_</a>	 Alignment		100.0	31	<b>PDB header:</b> recombination, dna <b>Chain:</b> B: <b>PDB Molecule:</b> transposon gamma-delta resolvase; <b>PDBTitle:</b> an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
2	<a href="#">c2r0qF_</a>	 Alignment		100.0	29	<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
3	<a href="#">d1gdta2</a>	 Alignment		99.9	34	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> Resolvase-like <b>Family:</b> gamma,delta resolvase, catalytic domain
4	<a href="#">d2gm4a2</a>	 Alignment		99.9	35	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> Resolvase-like <b>Family:</b> gamma,delta resolvase, catalytic domain
5	<a href="#">c3guvA_</a>	 Alignment		99.9	29	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> site-specific recombinase, resolvase family protein; <b>PDBTitle:</b> crystal structure of a resolvase family site-specific recombinase from2 streptococcus pneumoniae
6	<a href="#">c3g13B_</a>	 Alignment		99.9	26	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> putative conjugative transposon recombinase; <b>PDBTitle:</b> crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
7	<a href="#">c3pkzK_</a>	 Alignment		99.9	29	<b>PDB header:</b> recombination <b>Chain:</b> K: <b>PDB Molecule:</b> recombinase sin; <b>PDBTitle:</b> structural basis for catalytic activation of a serine recombinase
8	<a href="#">c3lhkA_</a>	 Alignment		99.9	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna binding protein mj0014; <b>PDBTitle:</b> crystal structure of putative dna binding protein from2 methanocaldococcus jannaschii.
9	<a href="#">c3ploX_</a>	 Alignment		99.8	42	<b>PDB header:</b> recombination <b>Chain:</b> X: <b>PDB Molecule:</b> dna-invertase; <b>PDBTitle:</b> crystal structure of the fis-independent mutant of gin
10	<a href="#">d2rsla_</a>	 Alignment		99.8	34	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> Resolvase-like <b>Family:</b> gamma,delta resolvase, catalytic domain
11	<a href="#">c3bvpB_</a>	 Alignment		99.8	26	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> tp901-1 integrase; <b>PDBTitle:</b> crystal structure of the n-terminal catalytic domain of tp901-12 integrase

12	<a href="#">c3lhfc_</a>	Alignment		99.8	22	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> serine recombinase; <b>PDBTitle:</b> the crystal structure of a serine recombinase from2 sulfolobus solfataricus to 2.3a
13	<a href="#">d1hx7a_</a>	Alignment		99.8	29	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> Resolvase-like <b>Family:</b> gamma,delta resolvase, catalytic domain
14	<a href="#">d1pdnc_</a>	Alignment		97.7	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
15	<a href="#">c6paxA_</a>	Alignment		97.7	19	<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
16	<a href="#">c1u78A_</a>	Alignment		97.6	17	<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
17	<a href="#">d1k78a1</a>	Alignment		97.5	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
18	<a href="#">d6paxa1</a>	Alignment		97.3	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
19	<a href="#">d2jn6a1</a>	Alignment		97.2	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
20	<a href="#">c2k27A_</a>	Alignment		96.8	19	<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
21	<a href="#">d1ijwc_</a>	Alignment	not modelled	96.6	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
22	<a href="#">c2l4aA_</a>	Alignment	not modelled	96.6	17	<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
23	<a href="#">d1hcra_</a>	Alignment	not modelled	96.6	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
24	<a href="#">c2rn7A_</a>	Alignment	not modelled	96.5	16	<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
25	<a href="#">c2krfB_</a>	Alignment	not modelled	96.4	11	<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
26	<a href="#">d1p4wa_</a>	Alignment	not modelled	96.3	20	<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)
27	<a href="#">c3frwF_</a>	Alignment	not modelled	96.3	21	<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 trpr protein from ruminococcus obeum
28	<a href="#">d1fsea_</a>	Alignment	not modelled	96.3	21	<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)
						<b>PDB header:</b> transcription

29	<a href="#">c1zljE_</a>	Alignment	not modelled	96.3	16	<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
30	<a href="#">d2cg4a1</a>	Alignment	not modelled	96.2	16	<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
31	<a href="#">c3korD_</a>	Alignment	not modelled	96.2	38	<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
32	<a href="#">c3hugA_</a>	Alignment	not modelled	96.2	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
33	<a href="#">d1a04a1</a>	Alignment	not modelled	96.2	16	<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="#">d1trra_</a>	Alignment	not modelled	96.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
35	<a href="#">c3sztB_</a>	Alignment	not modelled	96.1	8	<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
36	<a href="#">d1yioa1</a>	Alignment	not modelled	96.1	19	<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)
37	<a href="#">d2cfxa1</a>	Alignment	not modelled	96.1	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
38	<a href="#">c1x3uA_</a>	Alignment	not modelled	96.1	22	<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
39	<a href="#">c3hefB_</a>	Alignment	not modelled	96.0	21	<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
40	<a href="#">c3mzyA_</a>	Alignment	not modelled	96.0	16	<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
41	<a href="#">d1l3la1</a>	Alignment	not modelled	96.0	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)
42	<a href="#">d1jhga_</a>	Alignment	not modelled	96.0	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
43	<a href="#">c2cfxD_</a>	Alignment	not modelled	96.0	20	<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
44	<a href="#">d1xsva_</a>	Alignment	not modelled	96.0	24	<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
45	<a href="#">d2cyya1</a>	Alignment	not modelled	96.0	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
46	<a href="#">c1h0mD_</a>	Alignment	not modelled	95.9	6	<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
47	<a href="#">c2q0oA_</a>	Alignment	not modelled	95.9	15	<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
48	<a href="#">c2jpcA_</a>	Alignment	not modelled	95.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
49	<a href="#">c2rnjA_</a>	Alignment	not modelled	95.8	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> nmr structure of the s. aureus vvar dna binding domain
50	<a href="#">d1rp3a2</a>	Alignment	not modelled	95.8	22	<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
51	<a href="#">c2oqgA_</a>	Alignment	not modelled	95.7	24	<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
52	<a href="#">d2isya1</a>	Alignment	not modelled	95.6	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
53	<a href="#">d1or7a1</a>	Alignment	not modelled	95.6	19	<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
54	<a href="#">d1rlta_</a>	Alignment	not modelled	95.6	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators

55	<a href="#">dli1ga1</a>	Alignment	not modelled	95.5	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
56	<a href="#">d1r1ua</a>	Alignment	not modelled	95.5	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
57	<a href="#">c3qp5C</a>	Alignment	not modelled	95.4	21	<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)
58	<a href="#">c1r22B</a>	Alignment	not modelled	95.3	11	<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
59	<a href="#">d2d1ha1</a>	Alignment	not modelled	95.3	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
60	<a href="#">c3cloC</a>	Alignment	not modelled	95.3	21	<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
61	<a href="#">c2jscB</a>	Alignment	not modelled	95.3	9	<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
62	<a href="#">c1or7A</a>	Alignment	not modelled	95.3	21	<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
63	<a href="#">c3c3wB</a>	Alignment	not modelled	95.3	16	<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
64	<a href="#">c3pqkD</a>	Alignment	not modelled	95.2	12	<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 fastidiosia
65	<a href="#">d1biaa1</a>	Alignment	not modelled	95.2	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
66	<a href="#">c3f6vA</a>	Alignment	not modelled	95.2	21	<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
67	<a href="#">c2o8xA</a>	Alignment	not modelled	95.2	16	<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
68	<a href="#">c2elha</a>	Alignment	not modelled	95.1	22	<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
69	<a href="#">d2ev0a1</a>	Alignment	not modelled	95.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
70	<a href="#">c3f6oB</a>	Alignment	not modelled	95.1	16	<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
71	<a href="#">d1g3wa1</a>	Alignment	not modelled	95.1	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
72	<a href="#">c3tgnA</a>	Alignment	not modelled	95.1	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr; <b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
73	<a href="#">d1s7oa</a>	Alignment	not modelled	95.0	26	<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
74	<a href="#">d1ulya</a>	Alignment	not modelled	95.0	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
75	<a href="#">d1mkma1</a>	Alignment	not modelled	95.0	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator IclR, N-terminal domain
76	<a href="#">c2h09A</a>	Alignment	not modelled	94.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> crystal structure of diphtheria toxin repressor like protein2 from e. coli
77	<a href="#">c1rp3G</a>	Alignment	not modelled	94.9	25	<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
78	<a href="#">c1f5tA</a>	Alignment	not modelled	94.9	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
79	<a href="#">d1j5ya1</a>	Alignment	not modelled	94.8	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like

80	<a href="#">c3klnC_</a>	Alignment	not modelled	94.8	16	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
81	<a href="#">d1ttya_</a>	Alignment	not modelled	94.7	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> Sigma4 domain
82	<a href="#">c2ev5B_</a>	Alignment	not modelled	94.6	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
83	<a href="#">d1ub9a_</a>	Alignment	not modelled	94.6	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
84	<a href="#">d1smvf2</a>	Alignment	not modelled	94.6	24	<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
85	<a href="#">c2x4hA_</a>	Alignment	not modelled	94.6	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus
86	<a href="#">c2kkoB_</a>	Alignment	not modelled	94.6	14	<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.
87	<a href="#">c1rnlA_</a>	Alignment	not modelled	94.5	16	<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
88	<a href="#">c3by6C_</a>	Alignment	not modelled	94.4	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> predicted transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator from oenococcus oeni
89	<a href="#">c2it0A_</a>	Alignment	not modelled	94.4	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
90	<a href="#">c2wteB_</a>	Alignment	not modelled	94.3	11	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> csa3; <b>PDBTitle:</b> the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
91	<a href="#">c3cuoB_</a>	Alignment	not modelled	94.2	14	<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
92	<a href="#">d1gdta1</a>	Alignment	not modelled	94.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
93	<a href="#">d1hlva1</a>	Alignment	not modelled	94.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
94	<a href="#">c3jthA_</a>	Alignment	not modelled	94.1	16	<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
95	<a href="#">d2fxaa1</a>	Alignment	not modelled	94.0	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
96	<a href="#">c1r71B_</a>	Alignment	not modelled	94.0	23	<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
97	<a href="#">d1sfxa_</a>	Alignment	not modelled	93.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
98	<a href="#">d2etha1</a>	Alignment	not modelled	93.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
99	<a href="#">d1ku3a_</a>	Alignment	not modelled	93.8	19	<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
100	<a href="#">d1hwa1a1</a>	Alignment	not modelled	93.7	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
101	<a href="#">d1r71a_</a>	Alignment	not modelled	93.7	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
102	<a href="#">c3neuA_</a>	Alignment	not modelled	93.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin1836 protein; <b>PDBTitle:</b> the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
103	<a href="#">c3r0aB_</a>	Alignment	not modelled	93.7	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
104	<a href="#">d2p7vb1</a>	Alignment	not modelled	93.7	19	<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



105	<a href="#">d2hs5a1</a>	Alignment	not modelled	93.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
106	<a href="#">d1ku7a_</a>	Alignment	not modelled	93.5	19	<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
107	<a href="#">d2coba1</a>	Alignment	not modelled	93.5	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
108	<a href="#">c3g3zA</a>	Alignment	not modelled	93.4	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
109	<a href="#">c3nqoB_</a>	Alignment	not modelled	93.4	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> marr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
110	<a href="#">c3f3xA</a>	Alignment	not modelled	93.3	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
111	<a href="#">c2rdpA_</a>	Alignment	not modelled	93.1	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr; <b>PDBTitle:</b> the structure of a marr family protein from bacillus2 stearotherophilus
112	<a href="#">d2hr3a1</a>	Alignment	not modelled	93.1	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
113	<a href="#">d1u2wa1</a>	Alignment	not modelled	93.1	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
114	<a href="#">d1jhfa1</a>	Alignment		93.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
115	<a href="#">c1hlvA_</a>	Alignment	not modelled	93.0	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-2 b box dna
116	<a href="#">c2qwwB_</a>	Alignment	not modelled	92.9	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
117	<a href="#">c3hosA_</a>	Alignment	not modelled	92.9	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
118	<a href="#">d1lnwa_</a>	Alignment	not modelled	92.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
119	<a href="#">d1ku9a_</a>	Alignment	not modelled	92.7	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
120	<a href="#">c2fa5B_</a>	Alignment	not modelled	92.6	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator marr/emrr family; <b>PDBTitle:</b> the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris