
































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1vz0B_</a>	 Alignment		100.0	33	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome partitioning protein parb; <b>PDBTitle:</b> chromosome segregation protein spo0j from thermus2 thermophilus
2	<a href="#">dlvk1a_</a>	 Alignment		99.9	17	<b>Fold:</b> ParB/Sulfiredoxin <b>Superfamily:</b> ParB/Sulfiredoxin <b>Family:</b> Hypothetical protein PF0380
3	<a href="#">dlvz0a2</a>	 Alignment		99.9	41	<b>Fold:</b> ParB/Sulfiredoxin <b>Superfamily:</b> ParB/Sulfiredoxin <b>Family:</b> ParB-like nuclease domain
4	<a href="#">dlvz0a1</a>	 Alignment		99.8	25	<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
5	<a href="#">c1r71B_</a>	 Alignment		99.8	21	<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
6	<a href="#">dlr71a_</a>	 Alignment		99.7	21	<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
7	<a href="#">d2b6fa1</a>	 Alignment		99.7	21	<b>Fold:</b> ParB/Sulfiredoxin <b>Superfamily:</b> ParB/Sulfiredoxin <b>Family:</b> Sulfiredoxin-like
8	<a href="#">dlxw3a1</a>	 Alignment		99.7	24	<b>Fold:</b> ParB/Sulfiredoxin <b>Superfamily:</b> ParB/Sulfiredoxin <b>Family:</b> Sulfiredoxin-like
9	<a href="#">c3mkyP_</a>	 Alignment		99.2	15	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> P: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-323)-18mer dna complex, i23 form
10	<a href="#">c3mkzU_</a>	 Alignment		99.1	15	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> U: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-272)-18mer complex, p21 form
11	<a href="#">c1zx4B_</a>	 Alignment		97.3	17	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partition par b protein; <b>PDBTitle:</b> structure of parb bound to dna

12	<a href="#">c1u78A_</a>	Alignment		94.6	15	<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
13	<a href="#">c2w48D_</a>	Alignment		94.5	26	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
14	<a href="#">c2elhA_</a>	Alignment		93.5	17	<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
15	<a href="#">c3sztB_</a>	Alignment		92.5	21	<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
16	<a href="#">d1bw6a_</a>	Alignment		92.1	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
17	<a href="#">c2q0oA_</a>	Alignment		92.0	32	<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
18	<a href="#">d2cg4a1</a>	Alignment		91.8	13	<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
19	<a href="#">d2hwja1</a>	Alignment		91.8	13	<b>Fold:</b> ParB/Sulfiredoxin <b>Superfamily:</b> ParB/Sulfiredoxin <b>Family:</b> Atu1540-like
20	<a href="#">c2e1cA_</a>	Alignment		91.5	10	<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
21	<a href="#">d1fsea_</a>	Alignment	not modelled	91.5	18	<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)
22	<a href="#">c2cg4B_</a>	Alignment	not modelled	91.4	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
23	<a href="#">c2vbzA_</a>	Alignment	not modelled	91.2	21	<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
24	<a href="#">c2ia0A_</a>	Alignment	not modelled	91.2	10	<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)
25	<a href="#">c1zljE_</a>	Alignment	not modelled	91.0	21	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
26	<a href="#">c2dbbA_</a>	Alignment	not modelled	90.7	10	<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
27	<a href="#">c1h0mD_</a>	Alignment	not modelled	90.6	28	<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
28	<a href="#">c2krfB_</a>	Alignment	not modelled	90.6	25	<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

29	<a href="#">d1k78a1</a>	Alignment	not modelled	90.5	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
30	<a href="#">d2cfxa1</a>	Alignment	not modelled	90.2	10	<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="#">c3qp5C</a>	Alignment	not modelled	90.1	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)
32	<a href="#">c2p6tH</a>	Alignment	not modelled	90.0	21	<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
33	<a href="#">c2gm4B</a>	Alignment	not modelled	90.0	15	<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
34	<a href="#">d1hlva1</a>	Alignment	not modelled	90.0	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
35	<a href="#">d1p4wa</a>	Alignment	not modelled	89.9	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)
36	<a href="#">d1lmb3</a>	Alignment	not modelled	89.9	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
37	<a href="#">d1pdnc</a>	Alignment	not modelled	89.7	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
38	<a href="#">d1ilga1</a>	Alignment	not modelled	89.6	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
39	<a href="#">c2x48B</a>	Alignment	not modelled	89.5	35	<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
40	<a href="#">c1rp3G</a>	Alignment	not modelled	89.5	13	<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
41	<a href="#">d1qpza1</a>	Alignment	not modelled	89.4	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
42	<a href="#">d1rp3a2</a>	Alignment	not modelled	89.4	13	<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
43	<a href="#">c2l4aA</a>	Alignment	not modelled	89.3	13	<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
44	<a href="#">c3hugA</a>	Alignment	not modelled	89.2	28	<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
45	<a href="#">c2e7xA</a>	Alignment	not modelled	89.1	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
46	<a href="#">d1a04a1</a>	Alignment	not modelled	88.9	18	<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)
47	<a href="#">d2cyya1</a>	Alignment	not modelled	88.9	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
48	<a href="#">d1yioa1</a>	Alignment	not modelled	88.9	18	<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)
49	<a href="#">d1xsva</a>	Alignment	not modelled	88.8	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> YlxM/p13-like
50	<a href="#">d1l3la1</a>	Alignment	not modelled	88.8	29	<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)
51	<a href="#">c2r0qF</a>	Alignment	not modelled	88.5	17	<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
52	<a href="#">d6paxa1</a>	Alignment	not modelled	88.4	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
53	<a href="#">c3gn5B</a>	Alignment	not modelled	88.1	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa (ygit/b3021); <b>PDBTitle:</b> structure of the e. coli protein mqsa (ygit/b3021)
						<b>PDB header:</b> gene regulation/dna

54	<a href="#">c6paxA</a>	Alignment	not modelled	87.6	24	<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
55	<a href="#">d1rioA</a>	Alignment	not modelled	87.6	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
56	<a href="#">d1nera</a>	Alignment	not modelled	87.5	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
57	<a href="#">c1hlvA</a>	Alignment	not modelled	87.5	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
58	<a href="#">c2cfxD</a>	Alignment	not modelled	87.2	10	<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
59	<a href="#">c3pxpA</a>	Alignment	not modelled	86.9	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> helix-turn-helix domain protein; <b>PDBTitle:</b> crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
60	<a href="#">c2o8xA</a>	Alignment	not modelled	86.8	11	<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 of f2 mycobacterium tuberculosis sigc
61	<a href="#">c3cecA</a>	Alignment	not modelled	86.7	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative antidote protein of plasmid maintenance system; <b>PDBTitle:</b> crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
62	<a href="#">c1or7A</a>	Alignment	not modelled	86.6	13	<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="#">c3mzyA</a>	Alignment	not modelled	85.9	9	<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
64	<a href="#">d1s7oa</a>	Alignment	not modelled	85.6	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> YlxM/p13-like
65	<a href="#">c1x3uA</a>	Alignment	not modelled	85.6	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
66	<a href="#">c3m1eA</a>	Alignment	not modelled	85.4	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of benm_dbd
67	<a href="#">d1hcra</a>	Alignment	not modelled	85.2	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
68	<a href="#">c1i1gA</a>	Alignment	not modelled	85.1	16	<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
69	<a href="#">c2jpcA</a>	Alignment	not modelled	84.9	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
70	<a href="#">d1ijwc</a>	Alignment	not modelled	84.8	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
71	<a href="#">d1l1ib</a>	Alignment	not modelled	84.7	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
72	<a href="#">d2ofya1</a>	Alignment	not modelled	84.6	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
73	<a href="#">c3i4pA</a>	Alignment	not modelled	84.0	17	<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
74	<a href="#">c3h5tA</a>	Alignment	not modelled	83.9	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
75	<a href="#">d1trra</a>	Alignment	not modelled	83.7	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
76	<a href="#">c3cloC</a>	Alignment	not modelled	83.3	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
77	<a href="#">d1or7a1</a>	Alignment	not modelled	83.2	11	<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
78	<a href="#">c1bdhA</a>	Alignment	not modelled	83.0	11	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
79	<a href="#">c3bdnB</a>	Alignment	not modelled	82.9	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> lambda repressor; <b>PDBTitle:</b> crystal structure of the lambda repressor

80	<a href="#">c1umqA</a>	Alignment	not modelled	82.8	15	<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
81	<a href="#">d1umqa</a>	Alignment	not modelled	82.8	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
82	<a href="#">c2rnjA</a>	Alignment	not modelled	82.5	9	<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
83	<a href="#">d1uxca</a>	Alignment	not modelled	82.1	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
84	<a href="#">c2fjrB</a>	Alignment	not modelled	81.8	7	<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
85	<a href="#">d2d1ha1</a>	Alignment	not modelled	81.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
86	<a href="#">c3b73A</a>	Alignment	not modelled	81.7	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phiH1 repressor-like protein; <b>PDBTitle:</b> crystal structure of the phiH1 repressor-like protein from2 haloarcula marismortui
87	<a href="#">c2v79B</a>	Alignment	not modelled	81.7	13	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna replication protein dnad; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
88	<a href="#">d1biaa1</a>	Alignment	not modelled	81.2	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
89	<a href="#">c2vn2B</a>	Alignment	not modelled	80.6	17	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome replication initiation protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
90	<a href="#">d1jhga</a>	Alignment	not modelled	80.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
91	<a href="#">c3c3wB</a>	Alignment	not modelled	80.1	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
92	<a href="#">c3t76A</a>	Alignment	not modelled	79.4	14	<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
93	<a href="#">d1tc3c</a>	Alignment	not modelled	79.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
94	<a href="#">c2gqgB</a>	Alignment	not modelled	78.8	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
95	<a href="#">d1lcda</a>	Alignment	not modelled	78.1	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
96	<a href="#">c1zvva</a>	Alignment	not modelled	78.0	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpa-crh-dna complex
97	<a href="#">d1tlya</a>	Alignment	not modelled	77.8	11	<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
98	<a href="#">c2oqgA</a>	Alignment	not modelled	77.6	8	<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
99	<a href="#">d1ntca</a>	Alignment	not modelled	77.3	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
100	<a href="#">c3trbA</a>	Alignment	not modelled	77.0	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence-associated protein i; <b>PDBTitle:</b> structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
101	<a href="#">d2hsga1</a>	Alignment	not modelled	77.0	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
102	<a href="#">c3omtA</a>	Alignment	not modelled	76.1	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
103	<a href="#">d1r1ua</a>	Alignment	not modelled	76.1	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
104	<a href="#">d2bjca1</a>	Alignment	not modelled	75.7	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
105	<a href="#">c2ivla</a>	Alignment	not modelled	75.7	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> trmbf1;



105	<a href="#">c2jvIA_</a>	Alignment	not modelled	75.7	41	<b>PDBTitle:</b> nmr structure of the c-terminal domain of mbf1 of trichoderma reesei <b>PDB header:</b> antiviral protein
106	<a href="#">c2wteB_</a>	Alignment	not modelled	75.6	12	<b>Chain:</b> B: <b>PDB Molecule:</b> csa3; <b>PDBTitle:</b> the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
107	<a href="#">d2a6ca1</a>	Alignment	not modelled	75.0	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
108	<a href="#">c2zhhA_</a>	Alignment	not modelled	75.0	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensitive transcriptional activator soxr; <b>PDBTitle:</b> crystal structure of soxr
109	<a href="#">c2zkzC_</a>	Alignment	not modelled	74.6	14	<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
110	<a href="#">c2ppxA_</a>	Alignment	not modelled	74.4	4	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1735; <b>PDBTitle:</b> crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
111	<a href="#">d2ppxa1</a>	Alignment	not modelled	74.4	4	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
112	<a href="#">d1uxda_</a>	Alignment	not modelled	74.1	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
113	<a href="#">c2lcvA_</a>	Alignment	not modelled	73.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor cytr; <b>PDBTitle:</b> structure of the cytidine repressor dna-binding domain; an alternate2 calculation
114	<a href="#">d1ku7a_</a>	Alignment	not modelled	73.8	10	<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
115	<a href="#">d1j5ya1</a>	Alignment	not modelled	73.7	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
116	<a href="#">d2p7vb1</a>	Alignment	not modelled	73.1	7	<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
117	<a href="#">d1etob_</a>	Alignment	not modelled	73.0	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
118	<a href="#">c3klnC_</a>	Alignment	not modelled	72.7	22	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
119	<a href="#">c2kpiA_</a>	Alignment	not modelled	72.7	21	<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
120	<a href="#">c3fmyA_</a>	Alignment	not modelled	72.7	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)