



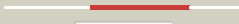









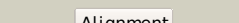

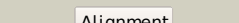



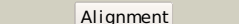





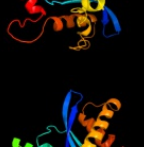
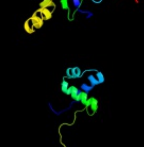
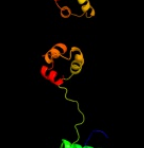

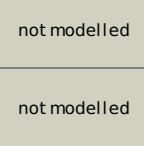


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1bcoA_</a>	 Alignment		99.9	17	<b>PDB header:</b> transposase <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophage mu transposase; <b>PDBTitle:</b> bacteriophage mu transposase core domain
2	<a href="#">d1bcoa2</a>	 Alignment		99.9	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> mu transposase, core domain
3	<a href="#">c3f9kV_</a>	 Alignment		99.8	18	<b>PDB header:</b> viral protein, recombination <b>Chain:</b> V: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> two domain fragment of hiv-2 integrase in complex with ledgf ibd
4	<a href="#">d1c0ma2</a>	 Alignment		99.8	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
5	<a href="#">c1c0mA_</a>	 Alignment		99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (integrase); <b>PDBTitle:</b> crystal structure of rsv two-domain integrase
6	<a href="#">d1asua_</a>	 Alignment		99.7	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
7	<a href="#">c3nf9A_</a>	 Alignment		99.7	21	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
8	<a href="#">d1exqa_</a>	 Alignment		99.6	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
9	<a href="#">c1ex4A_</a>	 Alignment		99.6	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> hiv-1 integrase catalytic core and c-terminal domain
10	<a href="#">d1cxqa_</a>	 Alignment		99.6	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
11	<a href="#">c3hosA_</a>	 Alignment		99.6	15	<b>PDB header:</b> transferase, dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element mariner, complete cds; <b>PDBTitle:</b> crystal structure of the mariner mos1 paired end complex with mg

12	<a href="#">c3kksB_</a>	Alignment		99.6	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of catalytic core domain of biv integrase in crystal2 form ii
13	<a href="#">c3hpgC_</a>	Alignment		99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
14	<a href="#">c3l2tB_</a>	Alignment		99.5	20	<b>PDB header:</b> recombination/dna <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
15	<a href="#">d1hyva_</a>	Alignment		99.5	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
16	<a href="#">d1c6va_</a>	Alignment		99.5	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
17	<a href="#">c1k6yB_</a>	Alignment		99.5	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of a two-domain fragment of hiv-1 integrase
18	<a href="#">c6paxA_</a>	Alignment		99.3	18	<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
19	<a href="#">d1pdnc_</a>	Alignment		99.3	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
20	<a href="#">c3dlrA_</a>	Alignment		99.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the catalytic core domain from pfv2 integrase
21	<a href="#">c2k27A_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
22	<a href="#">c1u78A_</a>	Alignment	not modelled	98.9	16	<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
23	<a href="#">d2jn6a1</a>	Alignment	not modelled	98.3	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
24	<a href="#">d1k78a1</a>	Alignment	not modelled	98.0	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
25	<a href="#">c1hlvA_</a>	Alignment	not modelled	98.0	13	<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
26	<a href="#">d6paxa1</a>	Alignment	not modelled	97.9	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
27	<a href="#">c2rn7A_</a>	Alignment	not modelled	97.9	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
28	<a href="#">c2elhA_</a>	Alignment	not modelled	97.4	19	<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
						<b>PDB header:</b> transcription

29	<a href="#">c2w48D_</a>	Alignment	not modelled	97.3	18	<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
30	<a href="#">d1bcoa1</a>	Alignment	not modelled	97.2	9	<b>Fold:</b> mu transposase, C-terminal domain <b>Superfamily:</b> mu transposase, C-terminal domain <b>Family:</b> mu transposase, C-terminal domain
31	<a href="#">d1hlva1</a>	Alignment	not modelled	97.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
32	<a href="#">c3e7lD_</a>	Alignment	not modelled	97.2	6	<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
33	<a href="#">d1ntca_</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
34	<a href="#">c1umqA_</a>	Alignment	not modelled	97.0	14	<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
35	<a href="#">d1umqa_</a>	Alignment	not modelled	97.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
36	<a href="#">c3hefB_</a>	Alignment	not modelled	97.0	18	<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
37	<a href="#">d1fipa_</a>	Alignment	not modelled	96.8	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
38	<a href="#">d1bw6a_</a>	Alignment	not modelled	96.8	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
39	<a href="#">d1jhga_</a>	Alignment	not modelled	96.8	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
40	<a href="#">c2f7tA_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mos1 transposase; <b>PDBTitle:</b> crystal structure of the catalytic domain of mos1 mariner2 transposase
41	<a href="#">d1trra_</a>	Alignment	not modelled	96.7	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
42	<a href="#">d1etxa_</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
43	<a href="#">c3sztB_</a>	Alignment	not modelled	96.4	11	<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
44	<a href="#">d1etob_</a>	Alignment	not modelled	96.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
45	<a href="#">c3frwF_</a>	Alignment	not modelled	96.3	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trp protein from ruminococcus obeum
46	<a href="#">c2q0oA_</a>	Alignment	not modelled	96.3	17	<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
47	<a href="#">d1rlua_</a>	Alignment	not modelled	96.3	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
48	<a href="#">c1h0mD_</a>	Alignment	not modelled	96.2	9	<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
49	<a href="#">c3korD_</a>	Alignment	not modelled	96.2	18	<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
50	<a href="#">c1zljE_</a>	Alignment	not modelled	96.2	13	<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
51	<a href="#">d1g2ha_</a>	Alignment	not modelled	96.1	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
52	<a href="#">d1rlta_</a>	Alignment	not modelled	96.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
53	<a href="#">d1j5ya1</a>	Alignment	not modelled	96.1	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
54	<a href="#">c1r22B_</a>	Alignment	not modelled	96.0	17	<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
						<b>PDB header:</b> transcription

55	<a href="#">c3jthA_</a>	Alignment	not modelled	96.0	14	<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
56	<a href="#">c3f2kB_</a>	Alignment	not modelled	96.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histone-lysine n-methyltransferase setmar; <b>PDBTitle:</b> structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
57	<a href="#">d1biaa1</a>	Alignment	not modelled	95.9	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
58	<a href="#">c2oqgA_</a>	Alignment	not modelled	95.9	22	<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
59	<a href="#">c2ia0A_</a>	Alignment	not modelled	95.9	13	<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)
60	<a href="#">d1a04a1</a>	Alignment	not modelled	95.9	15	<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)
61	<a href="#">c2jscB_</a>	Alignment	not modelled	95.8	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="#">c1iufA_</a>	Alignment	not modelled	95.8	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> centromere abp1 protein; <b>PDBTitle:</b> low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
63	<a href="#">c2krfB_</a>	Alignment	not modelled	95.8	14	<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
64	<a href="#">c2cg4B_</a>	Alignment	not modelled	95.8	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
65	<a href="#">d2coba1</a>	Alignment	not modelled	95.7	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
66	<a href="#">c2vbzA_</a>	Alignment	not modelled	95.7	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
67	<a href="#">d1p4wa_</a>	Alignment	not modelled	95.7	12	<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)
68	<a href="#">c3cuoB_</a>	Alignment	not modelled	95.6	17	<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
69	<a href="#">c3c3wB_</a>	Alignment	not modelled	95.6	11	<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
70	<a href="#">c2cfxD_</a>	Alignment	not modelled	95.6	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
71	<a href="#">c3qp5C_</a>	Alignment	not modelled	95.6	14	<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)
72	<a href="#">c1j5yA_</a>	Alignment	not modelled	95.6	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, biotin repressor family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
73	<a href="#">c3i4pA_</a>	Alignment	not modelled	95.6	15	<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="#">c1x3uA_</a>	Alignment	not modelled	95.4	26	<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
75	<a href="#">c1rnlA_</a>	Alignment	not modelled	95.4	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
76	<a href="#">c3pqkD_</a>	Alignment	not modelled	95.4	16	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> biofilm growth-associated repressor; <b>PDBTitle:</b> crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
77	<a href="#">c2p6tH_</a>	Alignment	not modelled	95.3	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
78	<a href="#">c2e7xA_</a>	Alignment	not modelled	95.3	10	<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
79	<a href="#">c2f07A</a>	Alignment	not modelled	95.3	19 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yvdt; <b>PDBTitle:</b> crystal structure of yvdt from bacillus subtilis
80	<a href="#">c2kkoB</a>	Alignment	not modelled	95.3	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.
81	<a href="#">dlq06a</a>	Alignment	not modelled	95.3	13 <b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
82	<a href="#">clor7A</a>	Alignment	not modelled	95.2	10 <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
83	<a href="#">c3f6oB</a>	Alignment	not modelled	95.1	17 <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
84	<a href="#">d2d1ha1</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> TrmB-like
85	<a href="#">dlvioa1</a>	Alignment	not modelled	95.1	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)
86	<a href="#">dlfsea</a>	Alignment	not modelled	95.1	13 <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)
87	<a href="#">dl13la1</a>	Alignment	not modelled	95.1	10 <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)
88	<a href="#">clr71B</a>	Alignment	not modelled	95.1	17 <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
89	<a href="#">c2zhA</a>	Alignment	not modelled	95.0	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
90	<a href="#">d2p4wa1</a>	Alignment	not modelled	95.0	14 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
91	<a href="#">c2kpiA</a>	Alignment	not modelled	95.0	19 <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
92	<a href="#">d2ezla</a>	Alignment	not modelled	95.0	13 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
93	<a href="#">dlxsva</a>	Alignment	not modelled	94.9	20 <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
94	<a href="#">dlulya</a>	Alignment	not modelled	94.9	19 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
95	<a href="#">clz4hA</a>	Alignment	not modelled	94.9	11 <b>PDB header:</b> protein binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tor inhibition protein; <b>PDBTitle:</b> the response regulator tori belongs to a new family of2 atypical excisionase
96	<a href="#">c2vz4A</a>	Alignment	not modelled	94.8	17 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> the n-terminal domain of merr-like protein tipal bound to2 promoter dna
97	<a href="#">clilgA</a>	Alignment	not modelled	94.8	15 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
98	<a href="#">dlr8da</a>	Alignment	not modelled	94.8	15 <b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
99	<a href="#">dlvz0a1</a>	Alignment	not modelled	94.8	17 <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
100	<a href="#">c2e1cA</a>	Alignment	not modelled	94.8	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
101	<a href="#">c3mzyA</a>	Alignment	not modelled	94.8	15 <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
102	<a href="#">c2dbbA</a>	Alignment	not modelled	94.7	13 <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



103	<a href="#">c3f6vA</a>	 Alignment	not modelled	94.7	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
104	<a href="#">d1i1ga1</a>	 Alignment	not modelled	94.7	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
105	<a href="#">c3by6C</a>	 Alignment	not modelled	94.7	11	<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
106	<a href="#">c3klnC</a>	 Alignment	not modelled	94.6	13	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
107	<a href="#">d2cg4a1</a>	 Alignment	not modelled	94.6	22	<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
108	<a href="#">c3gpvA</a>	 Alignment	not modelled	94.6	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
109	<a href="#">d1r71a</a>	 Alignment	not modelled	94.6	17	<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
110	<a href="#">c2zkzC</a>	 Alignment	not modelled	94.6	9	<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
111	<a href="#">c3cloC</a>	 Alignment	not modelled	94.5	19	<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
112	<a href="#">d1s7oa</a>	 Alignment	not modelled	94.5	20	<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
113	<a href="#">c3hugA</a>	 Alignment	not modelled	94.4	13	<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
114	<a href="#">c3hh0C</a>	 Alignment	not modelled	94.4	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr family2 from bacillus cereus
115	<a href="#">d1stza1</a>	 Alignment	not modelled	94.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
116	<a href="#">c2ewnA</a>	 Alignment	not modelled	94.3	17	<b>PDB header:</b> ligase, transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bira bifunctional protein; <b>PDBTitle:</b> ecoli biotin repressor with co-repressor analog
117	<a href="#">c2jpcA</a>	 Alignment	not modelled	94.3	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
118	<a href="#">d1u2wa1</a>	 Alignment	not modelled	94.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
119	<a href="#">c2l4aA</a>	 Alignment	not modelled	94.2	21	<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
120	<a href="#">c2rnjA</a>	 Alignment	not modelled	94.2	12	<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