

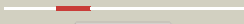










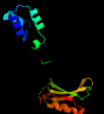








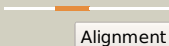

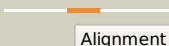

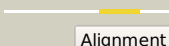

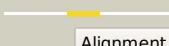

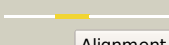

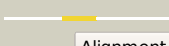

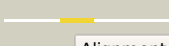

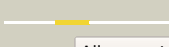



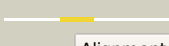
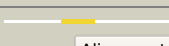
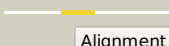
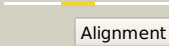

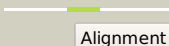

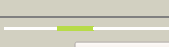


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3023c_(-)_3381386_3382633
Date	Thu Aug 8 16:20:19 BST 2019
Unique Job ID	3c6a978a06fc81cc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1k78a1</a>	 Alignment		92.9	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
2	<a href="#">d1pdnc_</a>	 Alignment		92.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
3	<a href="#">d6paxa1</a>	 Alignment		92.0	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
4	<a href="#">c6paxA_</a>	 Alignment		90.7	10	<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
5	<a href="#">d1au7a2</a>	 Alignment		89.0	10	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
6	<a href="#">d1e3oc2</a>	 Alignment		88.9	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
7	<a href="#">c4fcyA_</a>	 Alignment		88.5	19	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposase; <b>PDBTitle:</b> crystal structure of the bacteriophage mu transposome
8	<a href="#">c2m8eA_</a>	 Alignment		86.2	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sleeping beauty transposase; <b>PDBTitle:</b> nmr structure of the pai subdomain of sleeping beauty transposase
9	<a href="#">c1u78A_</a>	 Alignment		85.7	21	<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
10	<a href="#">c1au7B_</a>	 Alignment		85.4	11	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> protein pit-1; <b>PDBTitle:</b> pit-1 mutant/dna complex
11	<a href="#">c2r0qF_</a>	 Alignment		82.3	16	<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

12	<a href="#">c2k27A_</a>	 Alignment		80.8	13	<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
13	<a href="#">c1hf0A_</a>	 Alignment		80.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> octamer-binding transcription factor 1; <b>PDBTitle:</b> crystal structure of the dna-binding domain of oct-1 bound to dna as a2 dimer
14	<a href="#">d1bcoa2</a>	 Alignment		79.9	28	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> mu transposase, core domain
15	<a href="#">c3d1nK_</a>	 Alignment		79.5	18	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> K: <b>PDB Molecule:</b> pou domain, class 6, transcription factor 1; <b>PDBTitle:</b> structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
16	<a href="#">c3zeyG_</a>	 Alignment		78.1	14	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 40s ribosomal protein s13, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
17	<a href="#">c1rp3G_</a>	 Alignment		77.8	20	<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-sigma complex, sigma-2 28/flgm
18	<a href="#">c3l1pA_</a>	 Alignment		77.7	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> pou domain, class 5, transcription factor 1; <b>PDBTitle:</b> pou protein:dna complex
19	<a href="#">c2xzmO_</a>	 Alignment		76.2	6	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> rps13e; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
20	<a href="#">c3u5cN_</a>	 Alignment		76.0	6	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 40s ribosomal protein s13; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
21	<a href="#">c3izbO_</a>	 Alignment	not modelled	75.4	7	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 40s ribosomal protein rps13 (s15p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
22	<a href="#">c2gm4B_</a>	 Alignment	not modelled	74.0	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
23	<a href="#">c3frwF_</a>	 Alignment	not modelled	72.6	22	<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
24	<a href="#">c3korD_</a>	 Alignment	not modelled	70.5	21	<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
25	<a href="#">c1iufA_</a>	 Alignment	not modelled	69.2	8	<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
26	<a href="#">c2xsdC_</a>	 Alignment	not modelled	68.5	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> pou domain, class 3, transcription factor 1; <b>PDBTitle:</b> crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
27	<a href="#">d1jhga_</a>	 Alignment	not modelled	68.1	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
28	<a href="#">c6jnyA_</a>	 Alignment	not modelled	62.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> antiterminator q protein; <b>PDBTitle:</b> crystal structure of bacteriophage 21 q protein

29	<a href="#">d1xsva_</a>	Alignment	not modelled	62.6	15	<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
30	<a href="#">d1trra_</a>	Alignment	not modelled	61.3	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
31	<a href="#">c1zljE_</a>	Alignment	not modelled	60.7	10	<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
32	<a href="#">d1yb3a1</a>	Alignment	not modelled	59.5	13	<b>Fold:</b> YktB/PF0168-like <b>Superfamily:</b> YktB/PF0168-like <b>Family:</b> PF0168-like
33	<a href="#">d1yioa1</a>	Alignment	not modelled	57.9	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)
34	<a href="#">c3hosA_</a>	Alignment	not modelled	57.4	13	<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
35	<a href="#">d1l3la1</a>	Alignment	not modelled	56.0	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)
36	<a href="#">c3j20Q_</a>	Alignment	not modelled	53.5	14	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 30s ribosomal protein s15p/s13e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
37	<a href="#">c2jpcA_</a>	Alignment	not modelled	50.3	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
38	<a href="#">c3mzyA_</a>	Alignment	not modelled	49.4	13	<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
39	<a href="#">c2rnjA_</a>	Alignment	not modelled	49.1	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vrar; <b>PDBTitle:</b> nmr structure of the s. aureus vrar dna binding domain
40	<a href="#">c1x3uA_</a>	Alignment	not modelled	47.7	10	<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
41	<a href="#">d1fsea_</a>	Alignment	not modelled	47.6	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)
42	<a href="#">c3sztB_</a>	Alignment	not modelled	46.5	5	<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
43	<a href="#">d1iufa1</a>	Alignment	not modelled	46.0	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
44	<a href="#">c5xyiN_</a>	Alignment	not modelled	45.9	11	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 40s ribosomal protein s13, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
45	<a href="#">c6jqsA_</a>	Alignment	not modelled	45.6	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> structure of transcription factor, gere
46	<a href="#">c3cloC_</a>	Alignment	not modelled	42.9	14	<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
47	<a href="#">c3c3wB_</a>	Alignment	not modelled	42.7	10	<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
48	<a href="#">c5ipmF_</a>	Alignment	not modelled	42.6	12	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor rpos; <b>PDBTitle:</b> sigmas-transcription initiation complex with 4-nt nascent rna
49	<a href="#">c1bcoA_</a>	Alignment	not modelled	42.1	24	<b>PDB header:</b> transposase <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophage mu transposase; <b>PDBTitle:</b> bacteriophage mu transposase core domain
50	<a href="#">d1a04a1</a>	Alignment	not modelled	40.7	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)
51	<a href="#">c2lvsA_</a>	Alignment	not modelled	40.4	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of a crispr repeat binding protein
52	<a href="#">d2bw3a2</a>	Alignment	not modelled	38.8	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Hermes transposase-like
53	<a href="#">d1p4wa_</a>	Alignment	not modelled	38.2	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)
54	<a href="#">c2krfB_</a>	Alignment	not modelled	38.2	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma;

54	<a href="#">c2k1tD</a>	Alignment	not modelled	38.2	11	<b>PDBTitle:</b> nmr solution structure of the dna binding domain of competence protein2 a <b>PDB header:</b> transcription regulator
55	<a href="#">c5f64C</a>	Alignment	not modelled	37.4	21	<b>Chain:</b> C; <b>PDB Molecule:</b> positive transcription regulator evga; <b>PDBTitle:</b> putative positive transcription regulator (sensor evgs) from shigella2 flexneri
56	<a href="#">c4kisA</a>	Alignment	not modelled	37.0	10	<b>PDB header:</b> recombination/dna <b>Chain:</b> A; <b>PDB Molecule:</b> putative integrase [bacteriophage a118]; <b>PDBTitle:</b> crystal structure of a lsr-dna complex
57	<a href="#">c3qyxD</a>	Alignment	not modelled	36.3	5	<b>PDB header:</b> transcription/dna <b>Chain:</b> D; <b>PDB Molecule:</b> esx-1 secretion-associated regulator espr; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
58	<a href="#">c3kinC</a>	Alignment	not modelled	34.0	13	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
59	<a href="#">c2mqkA</a>	Alignment	not modelled	33.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent target dna activator b; <b>PDBTitle:</b> solution structure of n terminal domain of the mub aaa+ atpase
60	<a href="#">d2p5ka1</a>	Alignment	not modelled	31.9	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
61	<a href="#">c2m0nA</a>	Alignment	not modelled	31.9	26	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c, seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
62	<a href="#">c1e1cA</a>	Alignment	not modelled	29.1	18	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> methylmalonyl-coa mutase alpha chain; <b>PDBTitle:</b> methylmalonyl-coa mutase h244a mutant
63	<a href="#">d1s7oa</a>	Alignment	not modelled	27.6	17	<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
64	<a href="#">c5o8yG</a>	Alignment	not modelled	27.2	17	<b>PDB header:</b> transcription <b>Chain:</b> G; <b>PDB Molecule:</b> transcriptional regulatory protein rcsb; <b>PDBTitle:</b> conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
65	<a href="#">c5nwtM</a>	Alignment	not modelled	27.0	11	<b>PDB header:</b> transferase <b>Chain:</b> M; <b>PDB Molecule:</b> rna polymerase sigma-54 factor,rna polymerase sigma-54 <b>PDBTitle:</b> crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
66	<a href="#">c3nf9A</a>	Alignment	not modelled	26.9	28	<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
67	<a href="#">c5u1cD</a>	Alignment	not modelled	26.7	22	<b>PDB header:</b> viral protein <b>Chain:</b> D; <b>PDB Molecule:</b> hiv-1 integrase, sso7d chimera; <b>PDBTitle:</b> structure of tetrameric hiv-1 strand transfer complex intasome
68	<a href="#">d1f9na1</a>	Alignment	not modelled	26.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
69	<a href="#">d1pbua</a>	Alignment	not modelled	25.6	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eEF1-gamma domain <b>Family:</b> eEF1-gamma domain
70	<a href="#">c2vzbA</a>	Alignment	not modelled	24.9	15	<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
71	<a href="#">c4go1A</a>	Alignment	not modelled	24.5	19	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator lsr;rr; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsr from e.2 coli.
72	<a href="#">c6cy1B</a>	Alignment	not modelled	24.1	13	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
73	<a href="#">c4if4A</a>	Alignment	not modelled	24.0	8	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the magnesium and berylliofluoride-activated vvar2 from staphylococcus aureus
74	<a href="#">d1stza1</a>	Alignment	not modelled	23.9	20	<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
75	<a href="#">d1b4aa1</a>	Alignment	not modelled	23.7	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
76	<a href="#">d2fnaa1</a>	Alignment	not modelled	23.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Helicase DNA-binding domain
77	<a href="#">c5z7iC</a>	Alignment	not modelled	22.1	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C; <b>PDB Molecule:</b> cell cycle regulatory protein gcra; <b>PDBTitle:</b> caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
78	<a href="#">c5zx3F</a>	Alignment	not modelled	21.5	7	<b>PDB header:</b> transcription <b>Chain:</b> F; <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigh; <b>PDBTitle:</b> mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
79	<a href="#">c6ideA</a>	Alignment	not modelled	21.3	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator luxr family; <b>PDBTitle:</b> crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design

80	<a href="#">c5hevC</a>	Alignment	not modelled	20.8	10	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> response regulator protein vrrar; <b>PDBTitle:</b> crystal structure of the beryllofluoride-activated liar from2 enterococcus faecium
81	<a href="#">c2khqA</a>	Alignment	not modelled	20.6	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
82	<a href="#">c5cz1B</a>	Alignment	not modelled	20.4	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the catalytic core domain of mmtv integrase
83	<a href="#">d1z6ra1</a>	Alignment	not modelled	19.8	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
84	<a href="#">c2q0oA</a>	Alignment	not modelled	19.6	10	<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
85	<a href="#">c2bw3A</a>	Alignment	not modelled	19.2	14	<b>PDB header:</b> dna recombination <b>Chain:</b> A: <b>PDB Molecule:</b> transposase; <b>PDBTitle:</b> three-dimensional structure of the hermes dna transposase
86	<a href="#">c1h0mD</a>	Alignment	not modelled	18.7	10	<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 protein trar bound2 to its autoinducer and to its target dna
87	<a href="#">d2ch5a2</a>	Alignment	not modelled	18.6	25	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
88	<a href="#">c3c65A</a>	Alignment	not modelled	18.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein c; <b>PDBTitle:</b> crystal structure of bacillus stearothermophilus uvrC 5' endonuclease2 domain
89	<a href="#">c1r6uB</a>	Alignment	not modelled	18.1	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
90	<a href="#">c4lfuA</a>	Alignment	not modelled	17.3	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> crystal structure of escherichia coli sdia in the space group c2
91	<a href="#">c5uxxC</a>	Alignment	not modelled	17.2	6	<b>PDB header:</b> dna binding protein/unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> co-crystal structure of the sigma factor rpoe in complex with the2 anti-sigma factor nepr from bartonella quintana
92	<a href="#">d1g3wa1</a>	Alignment	not modelled	17.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
93	<a href="#">c2gqgB</a>	Alignment	not modelled	16.9	17	<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)
94	<a href="#">c2e7xA</a>	Alignment	not modelled	16.8	18	<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
95	<a href="#">d1ku3a</a>	Alignment	not modelled	15.9	5	<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
96	<a href="#">c4yn8A</a>	Alignment	not modelled	15.9	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator chra; <b>PDBTitle:</b> crystal structure of response regulator chra in heme-sensing two2 component system
97	<a href="#">c2hteB</a>	Alignment	not modelled	15.9	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> the crystal structure of spermidine synthase from p. falciparum in2 complex with 5'-methylthioadenosine
98	<a href="#">c4n1vA</a>	Alignment	not modelled	15.7	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein hu-beta; <b>PDBTitle:</b> structure of dna-binding protein hu from micoplasma spiroplasma2 melliferum
99	<a href="#">d2isya1</a>	Alignment	not modelled	15.6	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein