

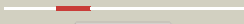








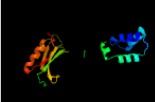



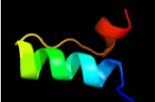





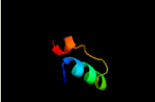


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1199c_(-)_1341364_1342611
Date	Wed Jul 31 22:05:28 BST 2019
Unique Job ID	a89f9a938832665a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k78a1	 Alignment		94.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
2	d6paxa1	 Alignment		93.7	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
3	d1pdnc_	 Alignment		93.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
4	c6paxA_	 Alignment		92.4	10	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
5	c1u78A_	 Alignment		87.8	20	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
6	c4fcyA_	 Alignment		84.1	20	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
7	c2k27A_	 Alignment		83.1	13	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
8	d1e3oc2	 Alignment		82.5	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
9	c2r0qF_	 Alignment		82.3	16	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
10	c2m8eA_	 Alignment		82.3	17	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
11	d1au7a2	 Alignment		81.9	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain

12	d1jhga_	Alignment		79.4	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
13	c3l1pA_	Alignment		78.3	22	PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex
14	c1au7B_	Alignment		77.4	11	PDB header: transcription/dna Chain: B: PDB Molecule: protein pit-1; PDBTitle: pit-1 mutant/dna complex
15	d1xsva_	Alignment		76.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
16	c3frwF_	Alignment		75.5	21	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
17	c1zljE_	Alignment		74.6	10	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
18	c2gm4B_	Alignment		72.8	15	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
19	c3korD_	Alignment		72.8	21	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
20	c3izbO_	Alignment		72.7	9	PDB header: ribosome Chain: O: PDB Molecule: 40s ribosomal protein rps13 (s15p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
21	c3zeyG_	Alignment	not modelled	72.0	14	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
22	c1rp3G_	Alignment	not modelled	71.3	17	PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (flia); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm
23	c3u5cN_	Alignment	not modelled	70.2	7	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s13; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
24	c2xzmO_	Alignment	not modelled	69.8	7	PDB header: ribosome Chain: O: PDB Molecule: rps13e; PDBTitle: 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
25	d1l3la1	Alignment	not modelled	68.6	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
26	c3d1nK_	Alignment	not modelled	68.4	20	PDB header: transcription regulator/dna Chain: K: PDB Molecule: pou domain, class 6, transcription factor 1; PDBTitle: structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
27	c1iufA_	Alignment	not modelled	68.2	8	PDB header: dna binding protein Chain: A: PDB Molecule: centromere abp1 protein; PDBTitle: low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
						PDB header: transcription

28	c3sztB	Alignment	not modelled	68.0	5	Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
29	c1hf0A	Alignment	not modelled	67.8	15	PDB header: transcription Chain: A: PDB Molecule: octamer-binding transcription factor 1; PDBTitle: crystal structure of the dna-binding domain of oct-1 bound to dna as a2 dimer
30	d1bcoa2	Alignment	not modelled	67.8	24	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
31	c3mzyA	Alignment	not modelled	66.9	13	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
32	d1fsea	Alignment	not modelled	66.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
33	c2jpcA	Alignment	not modelled	65.5	15	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
34	d1trra	Alignment	not modelled	65.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
35	c1x3uA	Alignment	not modelled	65.0	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
36	c6jqsA	Alignment	not modelled	64.5	11	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
37	c3cloC	Alignment	not modelled	63.8	14	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: 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
38	c6jnyA	Alignment	not modelled	63.3	15	PDB header: transcription Chain: A: PDB Molecule: antiterminator q protein; PDBTitle: crystal structure of bacteriophage 21 q protein
39	c2rnjA	Alignment	not modelled	63.1	8	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
40	d1yioa1	Alignment	not modelled	61.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
41	c2krfB	Alignment	not modelled	59.3	10	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
42	d1yb3a1	Alignment	not modelled	57.2	13	Fold: YktB/PF0168-like Superfamily: YktB/PF0168-like Family: PF0168-like
43	d1a04a1	Alignment	not modelled	56.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
44	c3j20Q	Alignment	not modelled	54.0	13	PDB header: ribosome Chain: Q: PDB Molecule: 30s ribosomal protein s15p/s13e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
45	c2lvsA	Alignment	not modelled	53.3	20	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
46	d1p4wa	Alignment	not modelled	52.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
47	c2xsdC	Alignment	not modelled	52.5	15	PDB header: transcription/dna Chain: C: PDB Molecule: pou domain, class 3, transcription factor 1; PDBTitle: crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
48	c3c3wB	Alignment	not modelled	49.4	10	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
49	c3hosA	Alignment	not modelled	49.1	13	PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg
50	d2p5ka1	Alignment	not modelled	47.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
51	d1s7oa	Alignment	not modelled	45.4	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
52	c4kisA	Alignment	not modelled	45.0	10	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex
53	d1smyf2	Alignment	not modelled	44.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors

						Family: Sigma4 domain
54	c2q0oA	Alignment	not modelled	42.0	10	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
55	d1iufa1	Alignment	not modelled	41.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
56	c5ipmF	Alignment	not modelled	41.7	14	PDB header: transcription, transferase/dna/rna Chain: F: PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
57	d2bw3a2	Alignment	not modelled	41.7	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Hermes transposase-like
58	c5f64C	Alignment	not modelled	41.6	21	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
59	d1f9na1	Alignment	not modelled	41.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
60	c2bw3A	Alignment	not modelled	41.2	14	PDB header: dna recombination Chain: A: PDB Molecule: transposase; PDBTitle: three-dimensional structure of the hermes dna transposase
61	c1bcoA	Alignment	not modelled	41.1	24	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
62	c4ifuA	Alignment	not modelled	39.6	10	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
63	c1h0mD	Alignment	not modelled	39.3	10	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
64	d1b4aa1	Alignment	not modelled	39.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
65	c3klnC	Alignment	not modelled	38.9	13	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
66	c3qyxD	Alignment	not modelled	35.5	5	PDB header: transcription/dna Chain: D: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
67	c5o8yG	Alignment	not modelled	33.7	17	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
68	c5xyiN	Alignment	not modelled	33.1	8	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
69	d1aoya	Alignment	not modelled	30.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
70	c3qp5C	Alignment	not modelled	29.7	8	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
71	c6ideA	Alignment	not modelled	29.0	21	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
72	c1b4aA	Alignment	not modelled	27.3	14	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
73	c5hevC	Alignment	not modelled	24.9	8	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium
74	c4if4A	Alignment	not modelled	24.9	6	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vvar2 from staphylococcus aureus
75	c2vbzA	Alignment	not modelled	24.8	15	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
76	c2w48D	Alignment	not modelled	23.2	18	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
77	c3ereD	Alignment	not modelled	22.8	18	PDB header: dna binding protein/dna Chain: D: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
78	d2g9wa1	Alignment	not modelled	22.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
79	c3hugA	Alignment	not modelled	21.7	15	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of

						sigl
80	c3v4gA_	Alignment	not modelled	20.5	18	PDB header: dna binding protein Chain: A: PDB Molecule: arginine repressor; PDBTitle: 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
81	c5uxxC_	Alignment	not modelled	20.3	6	PDB header: dna binding protein/unknown function Chain: C: PDB Molecule: rna polymerase sigma factor; PDBTitle: co-crystal structure of the sigma factor rpoE in complex with the2 anti-sigma factor nepr from bartonella quintana
82	c2mqkA_	Alignment	not modelled	19.9	10	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
83	d1stza1	Alignment	not modelled	19.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
84	c3vepA_	Alignment	not modelled	19.5	10	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
85	c4go1A_	Alignment	not modelled	19.4	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
86	d1z6ra1	Alignment	not modelled	19.4	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
87	d2fcja1	Alignment	not modelled	19.3	15	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
88	c6cy1B_	Alignment	not modelled	19.2	13	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
89	c5u1cD_	Alignment	not modelled	19.1	26	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
90	d1or7a1	Alignment	not modelled	19.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
91	c5zx3F_	Alignment	not modelled	18.8	6	PDB header: transcription Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
92	c3jugA_	Alignment	not modelled	18.2	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-mannanase; PDBTitle: crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
93	c4yn8A_	Alignment	not modelled	17.8	15	PDB header: dna binding protein Chain: A: PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system
94	c3nf9A_	Alignment	not modelled	17.8	27	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: integrase; PDBTitle: structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
95	c3c65A_	Alignment	not modelled	17.6	18	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearothermophilus uvrC 5' endonuclease2 domain
96	d2jn6a1	Alignment	not modelled	17.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
97	d2fnaa1	Alignment	not modelled	16.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
98	c2e7xA_	Alignment	not modelled	16.7	18	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
99	c3iwfA_	Alignment	not modelled	16.4	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a