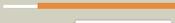
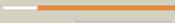
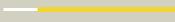
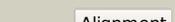
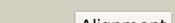
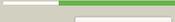
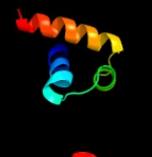
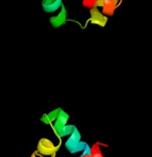
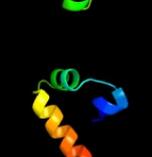


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1473A (-) _1662387_1662578
Date	Fri Aug 2 13:30:05 BST 2019
Unique Job ID	f2ddc9d52950bd00

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r0qF_	 Alignment		88.9	12	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
2	c1u78A_	 Alignment		83.9	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
3	c6paxA_	 Alignment		75.8	21	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
4	d1k78a1	 Alignment		75.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
5	c2gm4B_	 Alignment		73.5	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
6	d1rr7a_	 Alignment		69.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Middle operon regulator, Mor
7	c1rr7A_	 Alignment		69.4	13	PDB header: transcription Chain: A: PDB Molecule: middle operon regulator; PDBTitle: crystal structure of the middle operon regulator protein of2 bacteriophage mu
8	d6paxa1	 Alignment		69.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
9	d1pdnc_	 Alignment		64.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
10	c2o8xA_	 Alignment		56.8	24	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
11	d1or7a1	 Alignment		55.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain

12	d1nera_	Alignment		48.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
13	c6dvdF_	Alignment		45.2	20	PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigI; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
14	c3mzyA_	Alignment		44.8	17	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
15	c3hugA_	Alignment		44.0	24	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 sigI
16	c2bnoA_	Alignment		44.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
17	c4hf1B_	Alignment		43.4	16	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator iscr; PDBTitle: crystal structure of iscr bound to its promoter
18	d1xsva_	Alignment		43.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
19	d1s7oa_	Alignment		42.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
20	c3t8tA_	Alignment		42.0	24	PDB header: unknown function Chain: A: PDB Molecule: staphylococcus aureus cymr (oxidized form); PDBTitle: crystal structure of staphylococcus aureus cymr oxidized form
21	c3hefB_	Alignment	not modelled	41.4	11	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
22	c6j0eB_	Alignment	not modelled	41.2	27	PDB header: transcription Chain: B: PDB Molecule: arsenic responsive repressor arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
23	d1rp3a2	Alignment	not modelled	40.5	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
24	c6hsdB_	Alignment	not modelled	39.3	13	PDB header: transcription Chain: B: PDB Molecule: rrf2 family transcriptional regulator; PDBTitle: crystal structure of the oxidized form of the transcription regulator2 rsrr
25	c2lfwA_	Alignment	not modelled	37.7	11	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
26	c3t0yA_	Alignment	not modelled	36.1	8	PDB header: transcription regulator/protein binding Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
27	d1r71a_	Alignment	not modelled	35.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
28	d2g7ga1	Alignment	not modelled	35.0	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain PDB header: transcription/dna

29	c1r71B_	Alignment	not modelled	34.7	15	Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in complex with2 the operator dna
30	c1y9qA_	Alignment	not modelled	33.9	26	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
31	c3lsgD_	Alignment	not modelled	33.8	11	PDB header: transcription regulator Chain: D: PDB Molecule: two-component response regulator yesn; PDBTitle: the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
32	c2k27A_	Alignment	not modelled	32.9	16	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
33	d1ku3a_	Alignment	not modelled	32.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
34	d1ttya_	Alignment	not modelled	32.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
35	c3vepA_	Alignment	not modelled	31.4	19	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
36	c4go1A_	Alignment	not modelled	31.2	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
37	d1vz0a1	Alignment	not modelled	31.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
38	c5wurB_	Alignment	not modelled	30.7	11	PDB header: metal binding protein Chain: B: PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
39	c4cicB_	Alignment	not modelled	30.1	20	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, badm/rrf2 family; PDBTitle: t. potens iscr
40	d2p7vb1	Alignment	not modelled	28.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
41	c3vdoA_	Alignment	not modelled	27.2	21	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: rna polymerase sigma factor sigk; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
42	c5z7iC_	Alignment	not modelled	26.2	24	PDB header: dna binding protein/dna Chain: C: PDB Molecule: cell cycle regulatory protein gcra; PDBTitle: caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
43	c5syszA_	Alignment	not modelled	25.5	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
44	d2ofya1	Alignment	not modelled	25.5	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
45	c3h5tA_	Alignment	not modelled	25.3	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
46	d1qpza1	Alignment	not modelled	25.1	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
47	c5fgmA_	Alignment	not modelled	25.0	19	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
48	c4cxfA_	Alignment	not modelled	24.8	14	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
49	c5chhA_	Alignment	not modelled	24.3	20	PDB header: transcription Chain: A: PDB Molecule: arac family transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
50	c1bdhA_	Alignment	not modelled	24.3	13	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
51	d1mkma1	Alignment	not modelled	23.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lclR, N-terminal domain
52	c2elhA_	Alignment	not modelled	23.6	13	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
53	c3mkIB_	Alignment	not modelled	23.4	17	PDB header: transcription regulator Chain: B: PDB Molecule: hth-type transcriptional regulator gadx; PDBTitle: crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
54	c1rp3G_	Alignment	not modelled	23.2	8	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
55	c6in7B_	Alignment	not modelled	22.0	16	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algi in complex with muca(cyto)
56	c6j05B_	Alignment	not modelled	22.0	23	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsrf; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
57	c1efaA_	Alignment	not modelled	21.8	17	PDB header: transcription/dna Chain: A: PDB Molecule: lac repressor; PDBTitle: crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
58	c6c03A_	Alignment	not modelled	21.8	19	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
59	c1sgmA_	Alignment	not modelled	20.1	14	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator yxaf; PDBTitle: crystal structure of hypothetical protein yxaf
60	c3korD_	Alignment	not modelled	19.0	18	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
61	c5ipmF_	Alignment	not modelled	18.9	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
62	c2y75F_	Alignment	not modelled	18.4	23	PDB header: transcription Chain: F: PDB Molecule: hth-type transcriptional regulator cymr; PDBTitle: the structure of cymr (yrzc) the global cysteine regulator of b.2 subtilis
63	d1z0xa1	Alignment	not modelled	18.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
64	c5dukA_	Alignment	not modelled	18.0	17	PDB header: transcription Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
65	d2bjca1	Alignment	not modelled	17.4	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
66	d2hsqa1	Alignment	not modelled	17.3	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
67	d2hkua1	Alignment	not modelled	16.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
68	c3b7hA_	Alignment	not modelled	16.4	20	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
69	c1zvva_	Alignment	not modelled	16.3	13	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
70	c3neuA_	Alignment	not modelled	16.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
71	c5zx3F_	Alignment	not modelled	16.0	19	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
72	c2l8nA_	Alignment	not modelled	15.6	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
73	c2hxiA_	Alignment	not modelled	15.4	33	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a putative2 transcriptional regulator from streptomyces coelicolor a3(2)
74	d1efaa1	Alignment	not modelled	14.9	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
75	c3g7rB_	Alignment	not modelled	14.5	10	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of sco4454, a tet-family transcriptional regulator2 from streptomyces coelicolor
76	d2fx0a1	Alignment	not modelled	14.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
77	d1r1ua_	Alignment	not modelled	13.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
78	d3bwga1	Alignment	not modelled	13.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
79	d1adra_	Alignment	not modelled	13.6	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
80	c5d50I_	Alignment	not modelled	13.5	17	PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage

81	d1tc3c_	Alignment	not modelled	13.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
82	c2g7gA_	Alignment	not modelled	13.4	18	PDB header: transcription Chain: A: PDB Molecule: rha04620, putative transcriptional regulator; PDBTitle: the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1
83	c3cuoB_	Alignment	not modelled	13.1	26	PDB header: transcription regulator Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator ygav; PDBTitle: crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
84	c2i0kA_	Alignment	not modelled	13.1	31	PDB header: transcription Chain: A: PDB Molecule: stage iii sporulation protein d; PDBTitle: nmr solution structure of a transcription factor spoiiiid in complex2 with dna
85	c1bl0A_	Alignment	not modelled	12.9	17	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
86	c2wuiA_	Alignment	not modelled	12.7	29	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
87	c1or7A_	Alignment	not modelled	12.7	16	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
88	c3j3wO_	Alignment	not modelled	12.7	31	PDB header: ribosome Chain: Q: PDB Molecule: 50s ribosomal protein l20; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
89	d2iu5a1	Alignment	not modelled	12.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
90	d1gyza_	Alignment	not modelled	12.6	19	Fold: PABP domain-like Superfamily: Ribosomal protein L20 Family: Ribosomal protein L20
91	c4za6A_	Alignment	not modelled	12.6	16	PDB header: signaling protein Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: structure of the r. erythropolis transcriptional repressor qsdr from2 tetr family
92	c2lvsA_	Alignment	not modelled	12.6	26	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
93	c2kkoB_	Alignment	not modelled	12.4	23	PDB header: dna binding protein Chain: B: PDB Molecule: possible transcriptional regulatory protein PDBTitle: 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.
94	c6mj1A_	Alignment	not modelled	12.3	24	PDB header: dna binding protein Chain: A: PDB Molecule: probable hth-type transcriptional regulator ytpb; PDBTitle: crystal structure of refz (regulator of ftsz) from bacillus subtilis
95	c5uxxC_	Alignment	not modelled	12.2	18	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
96	d2d6ya1	Alignment	not modelled	12.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
97	d2a6ca1	Alignment	not modelled	12.1	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
98	c3frwF_	Alignment	not modelled	12.0	18	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
99	d2j01u1	Alignment	not modelled	12.0	19	Fold: PABP domain-like Superfamily: Ribosomal protein L20 Family: Ribosomal protein L20