


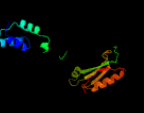






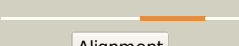
















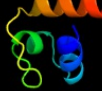
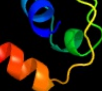




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2666 (-) _2983081_2983884
Date	Wed Aug 7 12:50:31 BST 2019
Unique Job ID	c8a957de89a23272

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k78a1	 Alignment		91.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
2	c4fcyA_	 Alignment		89.9	19	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
3	d1pdnc_	 Alignment		89.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
4	d6paxa1	 Alignment		89.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
5	c6paxA_	 Alignment		87.1	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
6	d1bcoa2	 Alignment		80.6	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
7	c1u78A_	 Alignment		77.8	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
8	d1e3oc2	 Alignment		77.3	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
9	c2m8eA_	 Alignment		74.2	17	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
10	c1rp3G_	 Alignment		73.2	20	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
11	c2r0qF_	 Alignment		71.4	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

12	d1au7a2	Alignment		69.7	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
13	d1jhga_	Alignment		69.6	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
14	c2k27A_	Alignment		69.5	13	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
15	c3l1pA_	Alignment		64.7	22	PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex
16	c3frwF_	Alignment		63.8	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		62.0	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	c3korD_	Alignment		60.0	21	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
19	c3izbO_	Alignment		58.6	7	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
20	c2gm4B_	Alignment		58.5	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
21	c1au7B_	Alignment	not modelled	57.4	11	PDB header: transcription/dna Chain: B: PDB Molecule: protein pit-1; PDBTitle: pit-1 mutant/dna complex
22	d1trra_	Alignment	not modelled	55.5	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
23	d1l3la1	Alignment	not modelled	55.1	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)
24	c1iufA_	Alignment	not modelled	51.8	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
25	c2jpcA_	Alignment	not modelled	51.8	13	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
26	d1fsea_	Alignment	not modelled	51.6	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)
27	c2rnjA_	Alignment	not modelled	48.0	8	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: nmr structure of the s. aureus vrar dna binding domain
28	d1c6va_	Alignment	not modelled	47.9	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
29	c2zevG_	Alignment	not modelled	47.8	12	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s13, putative;

29	c2eygD	Alignment	not modelled	47.8	14	PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
30	d1xsva	Alignment	not modelled	46.0	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
31	d1hyva	Alignment	not modelled	45.6	23	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
32	c6jqsA	Alignment	not modelled	45.1	13	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
33	c1hf0A	Alignment	not modelled	44.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: CgI2762-like
34	d2jn6a1	Alignment	not modelled	43.9	9	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
35	c1e1cA	Alignment	not modelled	43.3	14	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)
36	d1yioa1	Alignment	not modelled	43.2	10	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
37	c3mzyA	Alignment	not modelled	41.9	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)
38	d1p4wa	Alignment	not modelled	41.8	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)
39	d1a04a1	Alignment	not modelled	41.4	13	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
40	c2xzmO	Alignment	not modelled	40.6	2	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
41	c3d1nK	Alignment	not modelled	39.7	15	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
42	c3u5cN	Alignment	not modelled	39.2	4	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
43	c5nwtM	Alignment	not modelled	38.8	11	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
44	c2krfB	Alignment	not modelled	38.8	10	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
45	c1bcoA	Alignment	not modelled	38.4	23	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
46	c1c0mA	Alignment	not modelled	38.2	17	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
47	c3sztB	Alignment	not modelled	37.3	8	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
48	d1lasua	Alignment	not modelled	36.6	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
49	c3cloC	Alignment	not modelled	36.5	14	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
50	c1x3uA	Alignment	not modelled	35.4	9	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
51	c2mqkA	Alignment	not modelled	35.1	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)
52	c3j20Q	Alignment	not modelled	35.1	13	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0408; PDBTitle: crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
53	c2ogfD	Alignment	not modelled	34.7	13	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein;
54	c2lvsA	Alignment	not modelled	34.2	18	

						PDBTitle: nmr solution structure of a crispr repeat binding protein
55	c3hosA	Alignment	not modelled	33.2	9	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
56	c3c3wB	Alignment	not modelled	32.1	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
57	d1iufa1	Alignment	not modelled	31.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
58	d2p5ka1	Alignment	not modelled	31.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
59	c6jnyA	Alignment	not modelled	30.8	15	PDB header: transcription Chain: A: PDB Molecule: antiterminator q protein; PDBTitle: crystal structure of bacteriophage 21 q protein
60	c3nf9A	Alignment	not modelled	30.2	26	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
61	c4kisA	Alignment	not modelled	28.5	10	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex
62	c5u1cD	Alignment	not modelled	27.2	16	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
63	c5xyiN	Alignment	not modelled	26.8	9	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
64	c3klnC	Alignment	not modelled	26.7	13	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
65	c4go1A	Alignment	not modelled	25.9	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsr; PDBTitle: crystal structure of full length transcription repressor lsr from e.2 coli.
66	d1cxqa	Alignment	not modelled	25.8	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
67	c2xsdC	Alignment	not modelled	24.3	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
68	d1f9na1	Alignment	not modelled	23.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
69	c5f64C	Alignment	not modelled	22.8	18	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
70	c5ejkG	Alignment	not modelled	22.3	13	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
71	d1b4aa1	Alignment	not modelled	21.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
72	c3qyxD	Alignment	not modelled	20.5	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
73	c3vf1A	Alignment	not modelled	19.6	10	PDB header: oxidoreductase Chain: A: PDB Molecule: 11r-lipoxygenase; PDBTitle: structure of a calcium-dependent 11r-lipoxygenase suggests a mechanism2 for ca-regulation
74	c3c65A	Alignment	not modelled	19.6	18	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearothermophilus uvr5 5' endonuclease2 domain
75	d1aoya	Alignment	not modelled	19.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
76	d1yb3a1	Alignment	not modelled	19.0	12	Fold: YktB/PF0168-like Superfamily: YktB/PF0168-like Family: PF0168-like
77	c5o8yG	Alignment	not modelled	18.5	17	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
78	d1s7oa	Alignment	not modelled	18.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
79	c4lfuA	Alignment	not modelled	16.8	13	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
80	d2bw3a2	Alignment	not modelled	16.7	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like

						Family: Hermes transposase-like
81	c5jpmF_	Alignment	not modelled	16.2	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
82	d1stza1	Alignment	not modelled	15.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
83	d1c0ma2	Alignment	not modelled	15.2	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
84	c4nreA_	Alignment	not modelled	15.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: arachidonate 15-lipoxygenase b; PDBTitle: the structure of human 15-lipoxygenase-2 with a substrate mimic
85	c2q0oA_	Alignment	not modelled	14.9	13	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
86	c2w48D_	Alignment	not modelled	14.9	16	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
87	c3hefB_	Alignment	not modelled	14.8	12	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
88	d1smyf2	Alignment	not modelled	14.6	4	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
89	c4if4A_	Alignment	not modelled	14.5	6	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and beryllofluoride-activated vvar2 from staphylococcus aureus
90	c1h0mD_	Alignment	not modelled	14.4	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
91	c2derA_	Alignment	not modelled	14.0	23	PDB header: transferase/rna Chain: A: PDB Molecule: trna-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
92	c6ideA_	Alignment	not modelled	14.0	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
93	c2rn7A_	Alignment	not modelled	13.6	4	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
94	d2fca1	Alignment	not modelled	13.5	15	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
95	c5uxxC_	Alignment	not modelled	13.5	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
96	c5hevC_	Alignment	not modelled	13.3	10	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryllofluoride-activated liar from2 enterococcus faecium
97	c1k6yB_	Alignment	not modelled	13.2	21	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
98	c1b4aA_	Alignment	not modelled	13.0	14	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
99	c2jd3B_	Alignment	not modelled	12.9	14	PDB header: dna binding protein Chain: B: PDB Molecule: stbb protein; PDBTitle: parr from plasmid pb171