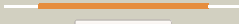
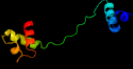
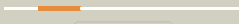
















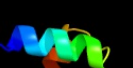


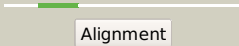


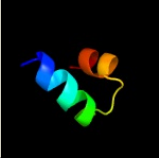


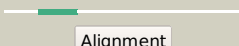

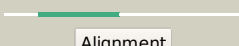

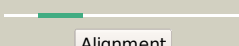

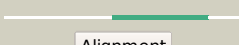







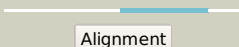
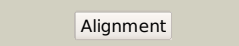
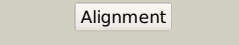


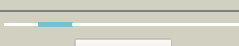


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2805 (-)_3112877_3113281
Date	Wed Aug 7 12:50:46 BST 2019
Unique Job ID	259d0780624087a1

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u78A_	 Alignment		89.0	14	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
2	d1v92a_	 Alignment		88.7	33	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TAP-C domain-like
3	d2hza1	 Alignment		66.1	32	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
4	c6dk4A_	 Alignment		65.4	9	PDB header: metal transport Chain: A; PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni peroxide stress regulator
5	d2hzaa1	 Alignment		64.5	32	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
6	c3hosA_	 Alignment		64.4	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
7	c2bj3D_	 Alignment		63.3	32	PDB header: transcription Chain: D; PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
8	d2bj7a1	 Alignment		62.9	32	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
9	c1q5vB_	 Alignment		62.1	32	PDB header: transcription Chain: B; PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
10	d1oaia_	 Alignment		60.2	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TAP-C domain-like
11	d1mkma1	 Alignment		52.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain

12	c3bq3A_	 Alignment		52.0	16	PDB header: cell cycle, ligase Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: crystal structure of s. cerevisiae dcn1
13	c2jp7A_	 Alignment		50.3	8	PDB header: translation Chain: A: PDB Molecule: mrna export factor mex67; PDBTitle: nmr structure of the mex67 uba domain
14	d1lvaa4	 Alignment		49.7	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
15	c6exzA_	 Alignment		48.9	8	PDB header: transport protein Chain: A: PDB Molecule: mrna export factor mex67; PDBTitle: crystal structure of mex67 c-term
16	c2zhhA_	 Alignment		48.8	11	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
17	d1ifya_	 Alignment		47.2	19	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
18	c5tjja_	 Alignment		47.0	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of iclr transcriptional regulator from2 alicyclobacillus acidocaldarius
19	d1go5a_	 Alignment		47.0	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TAP-C domain-like
20	c5k7IA_	 Alignment		46.2	25	PDB header: metal transport/calcium binding protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: single particle cryo-em structure of the voltage-gated k+ channel eag12 bound to the channel inhibitor calmodulin
21	c2ca9B_	 Alignment	not modelled	43.6	19	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
22	c2l4fA_	 Alignment	not modelled	39.6	13	PDB header: protein binding Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: nmr structure of the uba domain of s. cerevisiae dcn1 bound to2 ubiquitin
23	c2k9mA_	 Alignment	not modelled	39.2	13	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
24	c2dzIA_	 Alignment	not modelled	39.0	22	PDB header: structural genomics unknown function Chain: A: PDB Molecule: protein fam100b; PDBTitle: solution structure of the uba domain in human protein2 fam100b
25	c5ui5I_	 Alignment	not modelled	38.4	13	PDB header: transcription/dna Chain: I: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: crystal structure of aquifex aeolicus sigman bound to promoter dna
26	c4wp2D_	 Alignment	not modelled	38.0	17	PDB header: transport protein Chain: D: PDB Molecule: putative mrna export protein; PDBTitle: chaetomium mex67 uba domain
27	c1wsuA_	 Alignment	not modelled	37.5	21	PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: c-terminal domain of elongation factor selb complexed with2 secis rna
28	c2pjpA_	 Alignment	not modelled	37.2	32	PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna Fold: Left-handed superhelix

29	d2hh6a1	Alignment	not modelled	34.9	15	Superfamily: BH3980-like Family: BH3980-like
30	c2xroE	Alignment	not modelled	34.2	10	PDB header: dna-binding protein/dna Chain: E: PDB Molecule: hth-type transcriptional regulator ttg; PDBTitle: crystal structure of ttgV in complex with its dna operator
31	c6opfA	Alignment	not modelled	33.4	13	PDB header: rna binding protein Chain: A: PDB Molecule: nuclear rna export factor 2, panoramix fusion; PDBTitle: crystal structure of dmxf2 uba domain fused with panoramix helix
32	c5fg0B	Alignment	not modelled	32.2	12	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase listerin; PDBTitle: structure of the conserved yeast listerin (ltn1) n-terminal domain,2 monoclinic form
33	c5byhM	Alignment	not modelled	31.9	13	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
34	c2plyB	Alignment	not modelled	31.3	21	PDB header: translation/rna Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: structure of the mrna binding fragment of elongation factor2 selB in complex with secis rna.
35	c5whmB	Alignment	not modelled	31.2	15	PDB header: transcription Chain: B: PDB Molecule: iclR family transcriptional regulator; PDBTitle: crystal structure of iclR family transcriptional regulator from2 brucella abortus
36	c6fkgC	Alignment	not modelled	30.9	18	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
37	d1i5za1	Alignment	not modelled	29.8	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
38	d2o3la1	Alignment	not modelled	29.5	13	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
39	c5y6iB	Alignment	not modelled	29.0	16	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of pseudomonas aeruginosa hmgr
40	c1lvaA	Alignment	not modelled	28.8	21	PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of a c-terminal fragment of moorella2 thermoacetica elongation factor selB
41	c1z4hA	Alignment	not modelled	28.7	17	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator torI belongs to a new family of2 atypical excisionase
42	c2dalA	Alignment	not modelled	28.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein kiaa0794; PDBTitle: solution structure of the novel identified uba-like domain2 in the n-terminal of human fas associated factor 1 protein
43	d2oz6a1	Alignment	not modelled	27.9	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
44	c5nwtM	Alignment	not modelled	27.6	13	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
45	c3eyyA	Alignment	not modelled	27.6	12	PDB header: transport Chain: A: PDB Molecule: putative iron uptake regulatory protein; PDBTitle: structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
46	c5jqpG	Alignment	not modelled	26.9	11	PDB header: ribosome Chain: G: PDB Molecule: utp10; PDBTitle: cryo-em structure of the 90s pre-ribosome
47	c6gh5M	Alignment	not modelled	25.6	13	PDB header: transcription Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
48	d1oqya1	Alignment	not modelled	24.6	18	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
49	d2bgca1	Alignment	not modelled	23.0	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
50	d1kcfA1	Alignment	not modelled	22.7	29	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
51	c2mroB	Alignment	not modelled	22.7	16	PDB header: transport protein/signaling protein Chain: B: PDB Molecule: dna damage-inducible protein 1; PDBTitle: structure of the complex of ubiquitin and the uba domain from dna-2 damage-inducible 1 protein (ddi1)
52	d1k78a1	Alignment	not modelled	22.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
53	c2cwoD	Alignment	not modelled	21.9	29	PDB header: rna binding protein Chain: D: PDB Molecule: rna silencing suppressor; PDBTitle: crystal structure of rna silencing suppressor p21 from beet yellows2 virus
54	c4xfeA	Alignment	not modelled	21.8	12	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter subunit dctp; PDBTitle: crystal structure of a trap periplasmic solute binding

						protein from2 pseudomonas putida f1 (pput_1203), target efi-500184, with bound d-3 glucuronate
55	d2gaua1	Alignment	not modelled	21.7	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
56	d1veka	Alignment	not modelled	21.4	15	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
57	d2coha1	Alignment	not modelled	21.4	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
58	d2g3qa1	Alignment	not modelled	21.3	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
59	c3mwmA	Alignment	not modelled	21.0	12	PDB header: transcription Chain: A: PDB Molecule: putative metal uptake regulation protein; PDBTitle: graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
60	c2mx7A	Alignment	not modelled	20.9	34	PDB header: protein binding Chain: A: PDB Molecule: synergina gamma; PDBTitle: solution structure of the internal eh domain of gamma-synergina
61	c4razB	Alignment	not modelled	20.6	14	PDB header: metal binding protein Chain: B: PDB Molecule: dna-binding transcriptional dual regulator of siderophore PDBTitle: crystal structure of magnetospirillum gryphiswaldense msr-1 holo-fur
62	c4mtdA	Alignment	not modelled	19.5	15	PDB header: dna binding protein/dna Chain: A: PDB Molecule: zinc uptake regulation protein; PDBTitle: zinc uptake regulator complexed with zinc and dna
63	d6paxa1	Alignment	not modelled	19.3	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
64	c2vz4A	Alignment	not modelled	19.2	17	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
65	d1r8da	Alignment	not modelled	17.1	20	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
66	d1adra	Alignment	not modelled	17.1	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
67	c5cukA	Alignment	not modelled	16.9	19	PDB header: cell invasion Chain: A: PDB Molecule: ruler protein; PDBTitle: crystal structure of the pscp ss domain
68	d1z05a1	Alignment	not modelled	16.7	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
69	c1stzB	Alignment	not modelled	16.7	20	PDB header: transcription Chain: B: PDB Molecule: heat-inducible transcription repressor hrca homolog; PDBTitle: crystal structure of a hypothetical protein at 2.2 a resolution
70	c2o0yB	Alignment	not modelled	16.1	11	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
71	d1sd4a	Alignment	not modelled	15.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
72	d1szpa1	Alignment	not modelled	15.4	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
73	c6paxA	Alignment	not modelled	15.0	12	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
74	d1q06a	Alignment	not modelled	14.7	15	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
75	d1mzba	Alignment	not modelled	14.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FUR-like
76	c1bdhA	Alignment	not modelled	14.4	13	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
77	d1szpb1	Alignment	not modelled	14.4	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
78	c4r24B	Alignment	not modelled	14.1	19	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
79	c3gp4B	Alignment	not modelled	14.0	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
80	d3e46a1	Alignment	not modelled	13.9	19	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain

81	c2ev5B_	Alignment	not modelled	13.9	11	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
82	c2fu4B_	Alignment	not modelled	13.9	12	PDB header: dna binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
83	d1j9ia_	Alignment	not modelled	13.5	13	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
84	c2crnA_	Alignment	not modelled	13.5	37	PDB header: immune system Chain: A: PDB Molecule: ubash3a protein; PDBTitle: solution structure of the uba domain of human ubash3a2 protein
85	d2obpa1	Alignment	not modelled	13.4	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ReutB4095-like
86	d1z6ra1	Alignment	not modelled	13.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
87	d1z7ua1	Alignment	not modelled	13.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
88	c5fd6A_	Alignment	not modelled	13.2	12	PDB header: transcription Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: zinc-bound manganese uptake regulator
89	c3t76A_	Alignment	not modelled	13.1	8	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
90	d2ofya1	Alignment	not modelled	13.0	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
91	d1luxda_	Alignment	not modelled	12.9	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
92	c4pe3A_	Alignment	not modelled	12.5	11	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_3620, target efi-510199), apo open3 structure
93	c2xcjB_	Alignment	not modelled	12.3	16	PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
94	d1h7ca_	Alignment	not modelled	12.1	16	Fold: Spectrin repeat-like Superfamily: Tubulin chaperone cofactor A Family: Tubulin chaperone cofactor A
95	c2w57A_	Alignment	not modelled	12.0	12	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
96	c5ecjA_	Alignment	not modelled	11.8	17	PDB header: gene regulation/transcription Chain: A: PDB Molecule: pr domain zinc finger protein 14,protein cbfa2t2; PDBTitle: crystal structure of monobody mb(s4) bound to prdm14 in complex with2 mtgr1
97	c4i7ha_	Alignment	not modelled	11.7	6	PDB header: transcription Chain: A: PDB Molecule: peroxide stress sensing regulator; PDBTitle: structural basis for peroxide sensing and gene regulation by perr from2 streptococcus pyogenes
98	c4go1A_	Alignment	not modelled	11.6	9	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
99	c5fmrR_	Alignment	not modelled	11.6	17	PDB header: transcription Chain: R: PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex