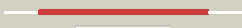

























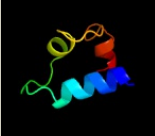






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1316c_ (ogt)_1477140_1477637
Date	Wed Jul 31 22:05:41 BST 2019
Unique Job ID	c52f2ba3805c0f3a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4bhcA_	 Alignment		100.0	99	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r371 variant
2	c1sfeA_	 Alignment		100.0	36	PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
3	c4zyeA_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
4	c1wrjA_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
5	c1t39A_	 Alignment		100.0	37	PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
6	c2g7hA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529)
7	c1mgtA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: protein (o6-methylguanine-dna methyltransferase); PDBTitle: crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
8	d1sfeal	 Alignment		100.0	52	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
9	d1qntal	 Alignment		100.0	44	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
10	c3gx4X_	 Alignment		100.0	37	PDB header: dna binding protein/dna Chain: X: PDB Molecule: alkyltransferase-like protein 1; PDBTitle: crystal structure analysis of s. pombe atl in complex with dna
11	c2kimA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: o6-methylguanine-dna methyltransferase; PDBTitle: 1.7-mm microcryoprobe solution nmr structure of an o6-methylguanine2 dna methyltransferase family protein from vibrio parahaemolyticus.3 northeast structural genomics consortium target vpr247.

12	d1mgta1	Alignment		100.0	39	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
13	d1sfea2	Alignment		99.3	17	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
14	d1qnta2	Alignment		98.1	26	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
15	d1dpua	Alignment		76.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of RPA32
16	c1dpuA	Alignment		76.1	18	PDB header: dna binding protein Chain: A: PDB Molecule: replication protein a (rpa32) c-terminal domain; PDBTitle: solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
17	d2gxba1	Alignment		74.0	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
18	c4lhfa	Alignment		71.4	26	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
19	d1qgpa	Alignment		69.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
20	c3k69A	Alignment		69.3	24	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
21	d1qbjc	Alignment	not modelled	68.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
22	d1stza1	Alignment	not modelled	60.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
23	c4czdA	Alignment	not modelled	51.0	14	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the Lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
24	c1rr7A	Alignment	not modelled	46.5	19	PDB header: transcription Chain: A: PDB Molecule: middle operon regulator; PDBTitle: crystal structure of the middle operon regulator protein of 2 bacteriophage mu
25	d1rr7a	Alignment	not modelled	46.5	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Middle operon regulator, Mor
26	c4czdD	Alignment	not modelled	45.6	18	PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the Lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
27	d2cyya1	Alignment	not modelled	41.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
28	d1jhfa1	Alignment	not modelled	41.1	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

						Family: LexA repressor, N-terminal DNA-binding domain
29	c3t8tA_	Alignment	not modelled	39.3	16	PDB header: unknown function Chain: A: PDB Molecule: staphylococcus aureus cymr (oxidized form); PDBTitle: crystal structure of staphylococcus aureus cymr oxidized form
30	c2y75F_	Alignment	not modelled	38.3	14	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
31	c2d7dA_	Alignment	not modelled	37.3	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein b; PDBTitle: structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
32	d1s6la1	Alignment	not modelled	35.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MerB N-terminal domain-like
33	c5muul_	Alignment	not modelled	33.7	32	PDB header: virus Chain: I: PDB Molecule: major outer capsid protein; PDBTitle: dsrna bacteriophage phi6 nucleocapsid
34	c5c17A_	Alignment	not modelled	32.8	13	PDB header: lyase Chain: A: PDB Molecule: merb2; PDBTitle: crystal structure of the mercury-bound form of merb2
35	d1biaa1	Alignment	not modelled	32.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
36	c4cicB_	Alignment	not modelled	31.2	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, badm/rrf2 family; PDBTitle: t. potens iscr
37	c3k2zA_	Alignment	not modelled	31.2	23	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
38	c2cfxD_	Alignment	not modelled	29.8	12	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
39	c6hsdB_	Alignment	not modelled	29.3	19	PDB header: transcription Chain: B: PDB Molecule: rrf2 family transcriptional regulator; PDBTitle: crystal structure of the oxidized form of the transcription regulator2 rsrr
40	c2dbbA_	Alignment	not modelled	27.2	15	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
41	c5n0lC_	Alignment	not modelled	26.9	28	PDB header: transcription Chain: C: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: the structure of the cofactor binding gaf domain of the nutrient2 sensor cody from clostridium difficile
42	c2e1cA_	Alignment	not modelled	25.7	18	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
43	c2l01A_	Alignment	not modelled	25.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein bvu3908 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr153
44	d1cf7b_	Alignment	not modelled	25.2	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp
45	d2cfxa1	Alignment	not modelled	25.2	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
46	d1bw6a_	Alignment	not modelled	23.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
47	c2l02B_	Alignment	not modelled	23.7	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
48	c3lwfD_	Alignment	not modelled	23.6	19	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
49	c3t72o_	Alignment	not modelled	21.9	16	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
50	d1aa7a_	Alignment	not modelled	21.3	18	Fold: Influenza virus matrix protein M1 Superfamily: Influenza virus matrix protein M1 Family: Influenza virus matrix protein M1
51	d2hs5a1	Alignment	not modelled	20.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
52	c1ilgA_	Alignment	not modelled	20.0	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
53	d1xmka1	Alignment	not modelled	19.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain

54	d2cg4a1	Alignment	not modelled	19.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
55	c4hamA	Alignment	not modelled	19.2	18	PDB header: transcription Chain: A: PDB Molecule: lmo2241 protein; PDBTitle: crystal structure of transcriptional antiterminator from listeria2 monocytogenes egd-e
56	c5c6tA	Alignment	not modelled	18.4	31	PDB header: viral protein/immune system Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of hcmv glycoprotein b in complex with 1g2 fab
57	d1i1ga1	Alignment	not modelled	18.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
58	d1ku7a	Alignment	not modelled	17.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
59	d1xd7a	Alignment	not modelled	17.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
60	c3c8lB	Alignment	not modelled	17.4	47	PDB header: unknown function Chain: B: PDB Molecule: ftsZ-like protein of unknown function; PDBTitle: crystal structure of a ftsz-like protein of unknown function2 (npun_r1471) from nostoc punctiforme pcc 73102 at 1.22 a resolution
61	c4pccC	Alignment	not modelled	16.9	16	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
62	c4hf1B	Alignment	not modelled	16.9	12	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator iscr; PDBTitle: crystal structure of iscr bound to its promoter
63	c5ys2C	Alignment	not modelled	16.7	14	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein b,envelope glycoprotein b; PDBTitle: structure of the domain iv(d_iv) of pseudorabies virus glycoprotein b(2_prv_gb)
64	c2l4aA	Alignment	not modelled	16.2	10	PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
65	c4p63A	Alignment	not modelled	16.1	18	PDB header: transferase Chain: A: PDB Molecule: probable deoxyhypusine synthase; PDBTitle: crystal structure of deoxyhypusine synthase from pyrococcus horikoshii
66	c2xzm8	Alignment	not modelled	16.0	9	PDB header: ribosome Chain: 8: PDB Molecule: rps25e,; 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
67	c6abhG	Alignment	not modelled	15.7	27	PDB header: luminescent protein Chain: G: PDB Molecule: red-bioluminescence eliciting luciferase; PDBTitle: structure of a natural red emitting luciferase from phrixothrix hirtus2 (p1 crystal form)
68	c2e7xA	Alignment	not modelled	15.6	21	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
69	d1mkma1	Alignment	not modelled	15.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lclR, N-terminal domain
70	d1dhSA	Alignment	not modelled	15.3	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Deoxyhypusine synthase, DHS
71	c2ia0A	Alignment	not modelled	15.3	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
72	c3i4pA	Alignment	not modelled	15.3	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
73	c4ch7A	Alignment	not modelled	14.2	14	PDB header: transcription Chain: A: PDB Molecule: nird-like protein; PDBTitle: crystal structure of the siroheme decarboxylase nirdl
74	d2p7vb1	Alignment	not modelled	13.9	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
75	c2lfaA	Alignment	not modelled	13.9	17	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
76	d2obpa1	Alignment	not modelled	13.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ReutB4095-like
77	c5l9wA	Alignment	not modelled	13.7	26	PDB header: ligase Chain: A: PDB Molecule: acetophenone carboxylase delta subunit; PDBTitle: crystal structure of the apc core complex
78	c3sztB	Alignment	not modelled	13.5	18	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 PDB header: toxin/antitoxin

79	c3g5oA	Alignment	not modelled	13.5	25	Chain: A; PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
80	c1z3xA	Alignment	not modelled	13.5	23	PDB header: transferase activator Chain: A; PDB Molecule: putative cytidyltransferase; PDBTitle: structure of gun4 from thermosynechococcus elongatus
81	d1s7oa	Alignment	not modelled	13.2	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
82	c2iv1J	Alignment	not modelled	13.2	29	PDB header: lyase Chain: J; PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
83	d1or7a1	Alignment	not modelled	13.1	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
84	c4fuqD	Alignment	not modelled	13.0	23	PDB header: ligase Chain: D; PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodopseudomonas palustris
85	c2p6tH	Alignment	not modelled	12.9	5	PDB header: transcription Chain: H; PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
86	c5bqtC	Alignment	not modelled	12.9	19	PDB header: dna binding protein Chain: C; PDB Molecule: putative hth-type transcriptional regulator trmb12; PDBTitle: structure of trmb12, an archaeal chromatin protein, shows a novel mode2 of dna binding.
87	c3hugA	Alignment	not modelled	12.8	23	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
88	c2gqqB	Alignment	not modelled	12.5	13	PDB header: transcription Chain: B; PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
89	c4cxfA	Alignment	not modelled	12.5	20	PDB header: transcription Chain: A; PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
90	c2cg4B	Alignment	not modelled	12.5	18	PDB header: transcription Chain: B; PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
91	d1dwka1	Alignment	not modelled	11.9	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
92	c5xohA	Alignment	not modelled	11.9	8	PDB header: transferase Chain: A; PDB Molecule: bergaptol o-methyltransferase; PDBTitle: crystal structure of bergaptol o-methyltransferase complex
93	d1rg6a	Alignment	not modelled	11.8	29	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
94	d1ttya	Alignment	not modelled	11.3	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
95	c6dftE	Alignment	not modelled	11.1	21	PDB header: transferase Chain: E; PDB Molecule: deoxyhypusine synthase; PDBTitle: trypanosoma brucei deoxyhypusine synthase
96	d1ub9a	Alignment	not modelled	11.0	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
97	c3ee6A	Alignment	not modelled	10.8	15	PDB header: hydrolase Chain: A; PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure analysis of tripeptidyl peptidase -i
98	c2fwrA	Alignment	not modelled	10.7	15	PDB header: dna binding protein Chain: A; PDB Molecule: dna repair protein rad25; PDBTitle: structure of archaeoglobus fulgidis xpb
99	c6btcA	Alignment	not modelled	10.7	21	PDB header: dna binding protein Chain: A; PDB Molecule: lp1413 - sccmec type iv-encoded dna binding protein; PDBTitle: sccmec type iv lp1413 - nucleic acids binding protein