








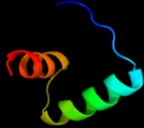

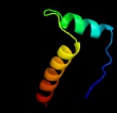






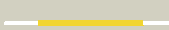

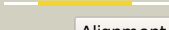

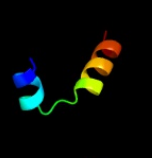
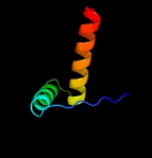


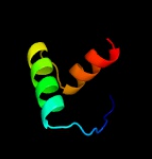

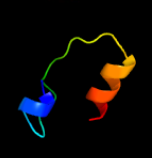
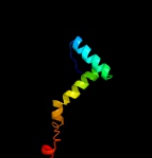



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0298 (-)_363252_363479
Date	Tue Jul 23 14:50:36 BST 2019
Unique Job ID	e9b404e848b43d56

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6g1nB_	 Alignment		95.0	28	PDB header: antitoxin Chain: B; PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
2	c4p7dA_	 Alignment		94.9	28	PDB header: toxin Chain: A; PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure
3	c1q5vB_	 Alignment		94.5	32	PDB header: transcription Chain: B; PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
4	c2ca9B_	 Alignment		94.3	25	PDB header: transcription Chain: B; PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
5	c2bj3D_	 Alignment		94.3	29	PDB header: transcription Chain: D; PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
6	d2hzaa1	 Alignment		94.2	28	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
7	d2hza1	 Alignment		93.0	32	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
8	d2bj7a1	 Alignment		92.8	28	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
9	c4me7E_	 Alignment		92.7	24	PDB header: hydrolase/hydrolase inhibitor Chain: E; PDB Molecule: antitoxin endoaï; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
10	c3h87D_	 Alignment		71.8	35	PDB header: toxin/antitoxin Chain: D; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
11	c2mdvB_	 Alignment		70.0	34	PDB header: de novo protein Chain: B; PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38

12	c5yrzC_	Alignment		51.9	30	PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
13	c6ajnf_	Alignment		44.9	13	PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atatr bound with accoa
14	c2k5jB_	Alignment		39.1	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
15	c1ea4K_	Alignment		32.6	38	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
16	d2cpga_	Alignment		32.6	38	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
17	c2k29A_	Alignment		26.1	25	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
18	c2qrvA_	Alignment		24.9	14	PDB header: transferase/transferase regulator Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: structure of dnmt3a-dnmt3l c-terminal domain complex
19	c6gtsC_	Alignment		21.1	12	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
20	d2c7pa1	Alignment		18.9	41	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: C5 cytosine-specific DNA methylase, DCM
21	c4u7pA_	Alignment	not modelled	18.7	14	PDB header: transferase/transferase regulator Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: crystal structure of dnmt3a-dnmt3l complex
22	d1g55a_	Alignment	not modelled	18.1	38	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: C5 cytosine-specific DNA methylase, DCM
23	d2ebfx3	Alignment	not modelled	15.8	36	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: PMT C-terminal domain like
24	c2hepa_	Alignment	not modelled	15.5	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0291 protein yznc; PDBTitle: solution nmr structure of the upf0291 protein yznc from2 bacillus subtilis. northeast structural genomics target3 sr384.
25	d2hepa1	Alignment	not modelled	15.5	43	Fold: Long alpha-hairpin Superfamily: Yznc-like Family: Yznc-like
26	c6qeqD_	Alignment	not modelled	14.5	9	PDB header: dna binding protein Chain: D: PDB Molecule: pcf;f; PDBTitle: pcff from enterococcus faecalis pcf10
27	c2bn5A_	Alignment	not modelled	14.3	41	PDB header: nuclear protein Chain: A: PDB Molecule: psi; PDBTitle: p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
28	d1dcta_	Alignment	not modelled	13.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: C5 cytosine-specific DNA methylase, DCM
						Fold: EF-Ts domain-like

29	d1wina_	Alignment	not modelled	13.8	28	Superfamily: Band 7/SPFH domain Family: Band 7/SPFH domain
30	c5l85A_	Alignment	not modelled	13.5	32	PDB header: signaling protein Chain: A: PDB Molecule: zinc finger hit domain-containing protein 3; PDBTitle: solution structure of the complex between human znhit3 and nufip12 proteins
31	c4onqA_	Alignment	not modelled	13.3	17	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: dna methyltransferase; PDBTitle: crystal structure of ntrdm e283s/r309s/f310s/y590s/d591s mutant
32	c3me5A_	Alignment	not modelled	13.2	24	PDB header: transferase Chain: A: PDB Molecule: cytosine-specific methyltransferase; PDBTitle: crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 2457t
33	c3bhpA_	Alignment	not modelled	12.9	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0291 protein ynzc; PDBTitle: crystal structure of upf0291 protein ynzc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
34	c2jvdA_	Alignment	not modelled	12.8	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0291 protein ynzc; PDBTitle: solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynzc from bacillus subtilis. northeast3 structural genomics target sr384-1-46
35	c2bn6A_	Alignment	not modelled	11.3	41	PDB header: nuclear protein Chain: A: PDB Molecule: psi; PDBTitle: p-element somatic inhibitor protein
36	d2o97b1	Alignment	not modelled	11.3	33	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
37	c4q2uM_	Alignment	not modelled	11.1	15	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
38	c4dkjA_	Alignment	not modelled	10.0	17	PDB header: transferase/dna Chain: A: PDB Molecule: cytosine-specific methyltransferase; PDBTitle: cpg specific methyltransferase in complex with target dna
39	c5v1eA_	Alignment	not modelled	9.8	100	PDB header: antimicrobial protein Chain: A: PDB Molecule: guavanin 2; PDBTitle: suboptimization of a glycine rich peptide allows the combinatorial2 space exploration for designing novel antimicrobial peptides
40	c2adB_	Alignment	not modelled	8.9	32	PDB header: dna binding protein Chain: B: PDB Molecule: ccda; PDBTitle: solution structure of the bacterial antitoxin ccda:2 implications for dna and toxin binding
41	c4a54B_	Alignment	not modelled	8.8	83	PDB header: rna binding protein/hydrolase Chain: B: PDB Molecule: mrna decapping complex subunit 2; PDBTitle: structural basis of the dcp1:dcp2 mrna decapping complex activation2 by edc3 and scd6
42	d1lrqa_	Alignment	not modelled	8.3	32	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Omega transcriptional repressor
43	c4h0nA_	Alignment	not modelled	8.1	31	PDB header: transferase Chain: A: PDB Molecule: dnmt2; PDBTitle: crystal structure of spodoptera frugiperda dnmt2 e260a/e261a/k263a2 mutant
44	c3g7uA_	Alignment	not modelled	8.1	21	PDB header: transferase Chain: A: PDB Molecule: cytosine-specific methyltransferase; PDBTitle: crystal structure of putative dna modification methyltransferase2 encoded within prophage cp-933r (e.coli)
45	c1irqB_	Alignment	not modelled	8.1	32	PDB header: gene regulation Chain: B: PDB Molecule: omega transcriptional repressor; PDBTitle: crystal structure of omega transcriptional repressor at2 1.5a resolution
46	c3b4qA_	Alignment	not modelled	8.0	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a conserved protein domain (unknown2 function) from corynebacterium diphtheriae
47	c4fxeB_	Alignment	not modelled	7.9	24	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
48	d1fvpa_	Alignment	not modelled	7.6	27	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
49	c3pt9A_	Alignment	not modelled	7.0	17	PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 1; PDBTitle: crystal structure of mouse dnmt1(731-1602) in the free state
50	c3qv2A_	Alignment	not modelled	6.7	28	PDB header: transferase Chain: A: PDB Molecule: 5-cytosine dna methyltransferase; PDBTitle: structure analysis of entamoeba histolytica methyltransferase ehmeth
51	d3orca_	Alignment	not modelled	6.6	31	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
52	d1b8za_	Alignment	not modelled	6.4	19	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
53	c5e6mA_	Alignment	not modelled	6.0	14	PDB header: ligase/rna Chain: A: PDB Molecule: glycine--trna ligase; PDBTitle: crystal structure of human wild type glyrs bound with trnagly
54	d1y9ba1	Alignment	not modelled	5.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix

					Family: VCA0319-like
55	d2hevf1	Alignment	not modelled	5.5	23 Fold: TNF-like Superfamily: TNF-like Family: TNF-like
56	d2c1ca1	Alignment	not modelled	5.5	15 Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases
57	c2do5A	Alignment	not modelled	5.4	52 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: splicing factor 3b subunit 2; PDBTitle: solution structure of the sap domain of human splicing2 factor 3b subunit 2