
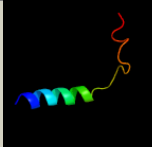

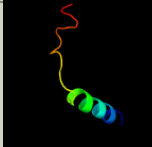

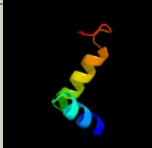


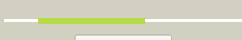
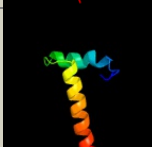

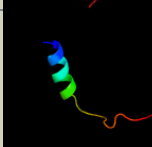
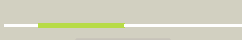
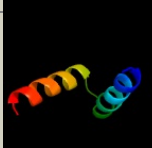

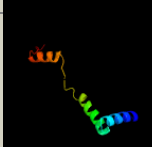
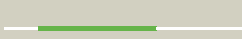
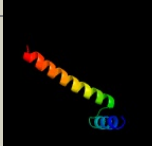



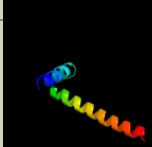


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0623 (-) _716413_716667
Date	Fri Jul 26 01:50:18 BST 2019
Unique Job ID	0a58b80bf1e45223

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xgqD_	 Alignment		94.3	100	PDB header: toxin/antitoxin Chain: D: PDB Molecule: antitoxin vapb30; PDBTitle: crystal structure of addiction module from mycobacterial species
2	c4xgqB_	 Alignment		94.1	100	PDB header: toxin/antitoxin Chain: B: PDB Molecule: antitoxin vapb30; PDBTitle: crystal structure of addiction module from mycobacterial species
3	c6a7vU_	 Alignment		84.6	35	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
4	c4xgrH_	 Alignment		79.4	100	PDB header: toxin/antitoxin Chain: H: PDB Molecule: antitoxin vapb30; PDBTitle: crystal structure of addiction module from mycobacterial species
5	c6iyaD_	 Alignment		67.3	23	PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso
6	c4xgrF_	 Alignment		67.0	100	PDB header: toxin/antitoxin Chain: F: PDB Molecule: antitoxin vapb30; PDBTitle: crystal structure of addiction module from mycobacterial species
7	c2k5jB_	 Alignment		63.3	12	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
8	c6gtsC_	 Alignment		63.2	15	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
9	c6ajnF_	 Alignment		56.4	17	PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atatr bound with accoa
10	c2kelB_	 Alignment		51.9	40	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
11	d1y9ba1	 Alignment		42.3	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like

12	c4q2uM_	Alignment		42.2	18	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
13	c2q2kB_	Alignment		26.0	25	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
14	c2q2kA_	Alignment		24.9	24	PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
15	c2rbfB_	Alignment		22.6	13	PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
16	d2hzaa1	Alignment		18.2	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
17	d2bsqe1	Alignment		16.0	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
18	c2xc7A_	Alignment		15.9	14	PDB header: rna binding protein Chain: A: PDB Molecule: phosphorylated adapter rna export protein; PDBTitle: solution structure of phax-rbd in complex with ssrna
19	d1myla_	Alignment		15.6	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
20	c2k9iB_	Alignment		15.5	23	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus
21	c2h1oH_	Alignment	not modelled	14.9	16	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
22	d1mnta_	Alignment	not modelled	14.2	13	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
23	d2gg2a1	Alignment	not modelled	13.3	30	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
24	d1u9pa1	Alignment	not modelled	12.1	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
25	c5h64b_	Alignment	not modelled	11.0	23	PDB header: transferase Chain: B: PDB Molecule: regulatory-associated protein of mtor; PDBTitle: cryo-em structure of mtorc1
26	d2bj7a1	Alignment	not modelled	10.8	17	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
27	d1q9ja2	Alignment	not modelled	10.7	16	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
28	d1myka_	Alignment	not modelled	10.6	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
29	c3m92B_	Alignment	not modelled	10.5	63	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ycin; PDBTitle: the structure of ycin, an uncharacterized protein from

						shigella2 flexneri.
30	d1bdta_	Alignment	not modelled	10.4	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
31	c1wkBA_	Alignment	not modelled	10.4	25	PDB header: ligase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation
32	c4zp3M_	Alignment	not modelled	10.3	19	PDB header: signaling protein Chain: M: PDB Molecule: a-kinase anchor protein 7 isoforms alpha and beta; PDBTitle: akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
33	c4zp3N_	Alignment	not modelled	9.7	21	PDB header: signaling protein Chain: N: PDB Molecule: a-kinase anchor protein 7 isoforms alpha and beta; PDBTitle: akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
34	d1baza_	Alignment	not modelled	9.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
35	d1mylb_	Alignment	not modelled	9.7	22	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
36	c4ariA_	Alignment	not modelled	9.2	63	PDB header: ligase/rna Chain: A: PDB Molecule: leucine--trna ligase; PDBTitle: ternary complex of e. coli leucyl-trna synthetase, trna(leu) and the2 benzoxaborole an2679 in the editing conformation
37	c2xpiE_	Alignment	not modelled	9.2	35	PDB header: cell cycle Chain: E: PDB Molecule: anaphase-promoting complex subunit hcn1 hcn1/cdc26,20s PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
38	c4zp3R_	Alignment	not modelled	9.1	21	PDB header: signaling protein Chain: R: PDB Molecule: a-kinase anchor protein 7 isoforms alpha and beta; PDBTitle: akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
39	c4zp3Q_	Alignment	not modelled	9.1	21	PDB header: signaling protein Chain: Q: PDB Molecule: a-kinase anchor protein 7 isoforms alpha and beta; PDBTitle: akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
40	c4zp3O_	Alignment	not modelled	8.8	21	PDB header: signaling protein Chain: O: PDB Molecule: a-kinase anchor protein 7 isoforms alpha and beta; PDBTitle: akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
41	c5bs7F_	Alignment	not modelled	8.8	67	PDB header: transcription regulator Chain: F: PDB Molecule: protein spt2 homolog; PDBTitle: structure of histone h3/h4 in complex with spt2
42	c4qvrA_	Alignment	not modelled	8.7	33	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized hypothetical protein ftt_1539c; PDBTitle: 2.3 angstrom crystal structure of hypothetical protein ftt1539c from2 francisella tularensis.
43	c5bsaF_	Alignment	not modelled	8.6	67	PDB header: transcription regulator Chain: F: PDB Molecule: protein spt2 homolog; PDBTitle: structure of histone h3/h4 in complex with spt2
44	c2xpiB_	Alignment	not modelled	8.5	35	PDB header: cell cycle Chain: B: PDB Molecule: anaphase-promoting complex subunit hcn1 hcn1/cdc26,20s PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
45	c5h7pB_	Alignment	not modelled	8.4	30	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: nmr structure of the vta1ntd-did2(176-204) complex
46	c2hs5A_	Alignment	not modelled	8.3	15	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator gntr; PDBTitle: structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
47	d1p94a_	Alignment	not modelled	8.2	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
48	c4fo7B_	Alignment	not modelled	8.1	22	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: pseudomonas aeruginosa metap, in mn form
49	d1cuka1	Alignment	not modelled	8.1	33	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
50	c3um2B_	Alignment	not modelled	8.0	56	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: charged multivesicular body protein 5; PDBTitle: crystal structure of the brox bro1 domain in complex with the c-2 terminal tail of chmp5
51	c3um1E_	Alignment	not modelled	8.0	56	PDB header: membrane protein/transport protein Chain: E: PDB Molecule: charged multivesicular body protein 5; PDBTitle: crystal structure of the brox bro1 domain in complex with the c-2 terminal tail of chmp5
52	c3um2E_	Alignment	not modelled	8.0	56	PDB header: membrane protein/transport protein Chain: E: PDB Molecule: charged multivesicular body protein 5; PDBTitle: crystal structure of the brox bro1 domain in complex with the c-2 terminal tail of chmp5
53	c3um0B_	Alignment	not modelled	8.0	56	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: charged multivesicular body protein 5; PDBTitle: crystal structure of the brox bro1 domain in complex with the c-2 terminal tail of chmp5
						PDB header: transcription

54	c3sztB	Alignment	not modelled	7.9	19	Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
55	d2a4da1	Alignment	not modelled	7.8	28	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
56	c2bj3D	Alignment	not modelled	7.8	16	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr- <i>apo</i>
57	c2k29A	Alignment	not modelled	7.6	24	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
58	c1h0mD	Alignment	not modelled	7.6	16	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
59	c5ydcA	Alignment	not modelled	7.4	37	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator rv1828; PDBTitle: crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis
60	c4zp3P	Alignment	not modelled	7.4	19	PDB header: signaling protein Chain: P: PDB Molecule: a-kinase anchor protein 7 isoforms alpha and beta; PDBTitle: akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
61	c4egcA	Alignment	not modelled	7.3	50	PDB header: transcription/hydrolase Chain: A: PDB Molecule: maltose-binding periplasmic protein, homeobox protein six1 PDBTitle: crystal structure of mbp-fused human six1 bound to human eya2 eya2 domain
62	c1wz2B	Alignment	not modelled	7.2	20	PDB header: ligase/rna Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
63	d2hzab1	Alignment	not modelled	7.2	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
64	d1riqa1	Alignment	not modelled	7.1	14	Fold: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Superfamily: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Family: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
65	d1b28a	Alignment	not modelled	7.1	22	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
66	d1o0xa	Alignment	not modelled	7.1	19	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
67	c4lfuA	Alignment	not modelled	7.1	16	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
68	c2ml7A	Alignment	not modelled	7.0	50	PDB header: unknown function Chain: A: PDB Molecule: specific abundant protein 3; PDBTitle: ginsentides: characterization, structure and application of a new2 class of highly stable cystine knot peptides in ginseng
69	c2mdvB	Alignment	not modelled	6.9	32	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
70	c3hxxA	Alignment	not modelled	6.7	24	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
71	c1qu2A	Alignment	not modelled	6.6	50	PDB header: ligase/rna Chain: A: PDB Molecule: isoleucyl-trna synthetase; PDBTitle: insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin
72	c3gkuB	Alignment	not modelled	6.6	53	PDB header: rna binding protein Chain: B: PDB Molecule: probable rna-binding protein; PDBTitle: crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
73	c5ah5B	Alignment	not modelled	6.6	63	PDB header: ligase/rna Chain: B: PDB Molecule: leucine--trna ligase; PDBTitle: crystal structure of the ternary complex of agrobacterium2 radiobacter k84 agnb2 leurs-trna-leuams
74	c3o0B	Alignment	not modelled	6.5	43	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
75	c5ca8A	Alignment	not modelled	6.5	50	PDB header: hydrolase Chain: A: PDB Molecule: protein sey1; PDBTitle: structures of the yeast dynamin-like gtpase sey1p in complex with gdp
76	d1bazb	Alignment	not modelled	6.5	22	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
77	d1efva2	Alignment	not modelled	6.4	28	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
78	c2ca9B	Alignment	not modelled	6.3	17	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
						PDB header: transcription

79	c4p9fA_	Alignment	not modelled	6.2	35	Chain: A; PDB Molecule: hth-type transcriptional regulator mcbr; PDBTitle: e. coli mcbr/yncc
80	c3qp5C_	Alignment	not modelled	6.2	16	PDB header: transcription Chain: C; PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
81	c6q8aA_	Alignment	not modelled	5.9	50	PDB header: ligase Chain: A; PDB Molecule: leucine--trna ligase; PDBTitle: neisseria gonorrhoeae leucyl-trna synthetase in complex with 5'-o-(n-2 (l-leucyl)-sulfamoyl)cytidine
82	c1yx3A_	Alignment	not modelled	5.8	24	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein dsrc; PDBTitle: nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
83	c4v1af_	Alignment	not modelled	5.7	16	PDB header: ribosome Chain: F; PDB Molecule: ; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
84	c5vgtA_	Alignment	not modelled	5.5	70	PDB header: viral protein Chain: A; PDB Molecule: gene 7 protein; PDBTitle: x-ray structure of bacteriophage sf6 tail adaptor protein gp7
85	c3tavA_	Alignment	not modelled	5.5	13	PDB header: hydrolase Chain: A; PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
86	d1efpa2	Alignment	not modelled	5.5	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
87	d1mula_	Alignment	not modelled	5.5	24	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
88	c2kvcA_	Alignment	not modelled	5.4	16	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
89	c1zvva_	Alignment	not modelled	5.3	14	PDB header: transcription/dna Chain: A; PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
90	c2bytD_	Alignment	not modelled	5.2	63	PDB header: synthetase Chain: D; PDB Molecule: leucyl-trna synthetase; PDBTitle: thermus thermophilus leucyl-trna synthetase complexed with2 a trnaleu transcript in the post-editing conformation
91	c3iwfA_	Alignment	not modelled	5.2	11	PDB header: transcription regulator Chain: A; PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
92	c3utmC_	Alignment	not modelled	5.1	29	PDB header: transferase/signaling protein Chain: C; PDB Molecule: axin-1; PDBTitle: crystal structure of a mouse tankyrase-axin complex
93	c2l8nA_	Alignment	not modelled	5.1	7	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
94	d1ef1c_	Alignment	not modelled	5.0	17	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Moesin tail domain Family: Moesin tail domain
95	c5bsaE_	Alignment	not modelled	5.0	50	PDB header: transcription regulator Chain: E; PDB Molecule: protein spt2 homolog; PDBTitle: structure of histone h3/h4 in complex with spt2
96	c2akfB_	Alignment	not modelled	5.0	54	PDB header: protein binding Chain: B; PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
97	c2akfA_	Alignment	not modelled	5.0	54	PDB header: protein binding Chain: A; PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1