
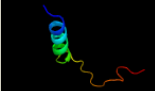
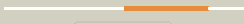
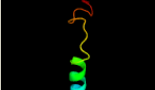




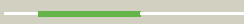
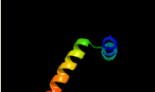

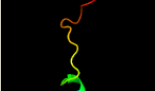



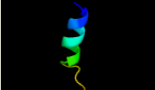






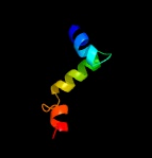


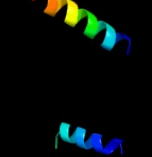
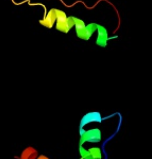


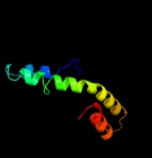
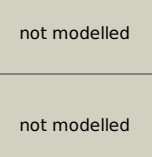


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0608 (-) _703247_703492
Date	Fri Jul 26 01:50:16 BST 2019
Unique Job ID	8fa684571d1dbfc0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xgqD_	 Alignment		87.0	27	PDB header: toxin/antitoxin Chain: D; PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
2	c4xgqB_	 Alignment		86.6	27	PDB header: toxin/antitoxin Chain: B; PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
3	c6ajnF_	 Alignment		60.1	15	PDB header: toxin Chain: F; PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atatr bound with accoa
4	c6gtsC_	 Alignment		58.6	15	PDB header: transcription Chain: C; PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
5	c2k5jB_	 Alignment		53.6	13	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
6	c4xgrH_	 Alignment		46.9	25	PDB header: toxin/antitoxin Chain: H; PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
7	d1y9ba1	 Alignment		44.2	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
8	c4xgrF_	 Alignment		36.5	27	PDB header: toxin/antitoxin Chain: F; PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
9	c2h1oH_	 Alignment		34.4	20	PDB header: gene regulation/dna complex Chain: H; PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
10	d2bsqe1	 Alignment		32.6	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
11	c1zvva_	 Alignment		31.8	21	PDB header: transcription/dna Chain: A; PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex

12	c6a7vU	Alignment		29.0	15	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
13	c2q2kA	Alignment		26.5	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
14	c2kelB	Alignment		25.8	27	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
15	c3eabK	Alignment		24.9	50	PDB header: cell cycle Chain: K: PDB Molecule: chmp1b; PDBTitle: crystal structure of spastin mit in complex with escrt iii
16	c5h64b	Alignment		19.7	15	PDB header: transferase Chain: B: PDB Molecule: regulatory-associated protein of mtor; PDBTitle: cryo-em structure of mtorc1
17	c2q2kB	Alignment		19.1	14	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
18	d2a4da1	Alignment		18.7	11	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
19	d1o0xa	Alignment		15.3	22	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
20	c3hxxA	Alignment		15.1	20	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
21	c3tavA	Alignment	not modelled	14.7	13	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
22	c1wkbA	Alignment	not modelled	14.4	22	PDB header: ligase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of the leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation
23	c4v1af	Alignment	not modelled	13.7	8	PDB header: ribosome Chain: F: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
24	c3um2B	Alignment	not modelled	13.1	67	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
25	c3um2E	Alignment	not modelled	13.1	67	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
26	c3um1E	Alignment	not modelled	13.1	67	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
27	c3um0B	Alignment	not modelled	13.0	67	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
28	c4egcA	Alignment	not modelled	12.5	21	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
29	c3iacA	Alignment	not modelled	10.8	14	PDB header: isomerase Chain: A: PDB Molecule: glucuronate isomerase; PDBTitle: 2.2 angstrom crystal structure of glucuronate isomerase from <i>Salmonella typhimurium</i> .
30	d1p94a	Alignment	not modelled	10.5	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
31	d2gg2a1	Alignment	not modelled	10.1	16	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
32	c3dfuB	Alignment	not modelled	10.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein from 6-phosphogluconate PDBTitle: crystal structure of a putative rosmann-like dehydrogenase (cgl2689)2 from <i>Corynebacterium glutamicum</i> at 2.07 Å resolution
33	c5vgtA	Alignment	not modelled	9.7	60	PDB header: viral protein Chain: A: PDB Molecule: gene 7 protein; PDBTitle: x-ray structure of bacteriophage sf6 tail adaptor protein gp7
34	c6ci7A	Alignment	not modelled	9.6	28	PDB header: biosynthetic protein Chain: A: PDB Molecule: ycao; PDBTitle: the structure of ycao from <i>Methanopyrus kandleri</i> bound with amppcp and 2 Mg ²⁺
35	d1cuka1	Alignment	not modelled	8.9	24	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
36	c2kvcA	Alignment	not modelled	8.9	8	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
37	c4ariA	Alignment	not modelled	8.5	50	PDB header: ligase/rna Chain: A: PDB Molecule: leucine--trna ligase; PDBTitle: ternary complex of <i>E. coli</i> leucyl-trna synthetase, trna(leu) and the benzoxaborole an2679 in the editing conformation
38	c3m92B	Alignment	not modelled	8.4	63	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ycin; PDBTitle: the structure of ycin, an uncharacterized protein from <i>Shigella flexneri</i> .
39	c2g6pA	Alignment	not modelled	8.4	7	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 1; PDBTitle: crystal structure of truncated (delta 1-89) human methionine2 aminopeptidase type 1 in complex with pyridyl pyrimidine derivative
40	c3tb5C	Alignment	not modelled	8.2	7	PDB header: hydrolase Chain: C: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of the <i>Enterococcus faecalis</i> methionine2 aminopeptidase apo form
41	c3gkuB	Alignment	not modelled	8.1	33	PDB header: rna binding protein Chain: B: PDB Molecule: probable rna-binding protein; PDBTitle: crystal structure of a probable rna-binding protein from <i>Clostridium symbiosum</i> ATCC 14940
42	c4qvrA	Alignment	not modelled	8.1	22	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized hypothetical protein ftt_1539c; PDBTitle: 2.3 Å crystal structure of hypothetical protein ftt1539c from <i>Francisella tularensis</i> .
43	c2gz5A	Alignment	not modelled	7.6	7	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 1; PDBTitle: human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 Å
44	d2bj7a1	Alignment	not modelled	7.1	15	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
45	c4fo7B	Alignment	not modelled	7.0	19	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: <i>Pseudomonas aeruginosa</i> metap, in Mn form
46	d1efva2	Alignment	not modelled	7.0	11	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
47	c5ydcA	Alignment	not modelled	6.8	13	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 from <i>Mycobacterium tuberculosis</i>
48	d1efpa2	Alignment	not modelled	6.5	11	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
49	d1j74a	Alignment	not modelled	6.5	12	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
50	c5z5mB	Alignment	not modelled	6.4	17	PDB header: lyase Chain: B: PDB Molecule: predicted protein; PDBTitle: crystal structure of (s)-allantoin synthase
51	c3t0yB	Alignment	not modelled	6.4	17	PDB header: transcription regulator/protein binding Chain: B: PDB Molecule: nepr; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
52	c2akfC	Alignment	not modelled	6.4	46	PDB header: protein binding Chain: C: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1

53	c2akfB_	Alignment	not modelled	6.4	46	PDB header: protein binding Chain: B: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
54	c2akfA_	Alignment	not modelled	6.4	46	PDB header: protein binding Chain: A: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
55	c5ah5B_	Alignment	not modelled	6.3	50	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
56	c2kiIA_	Alignment	not modelled	6.2	11	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
57	c5jhiA_	Alignment	not modelled	6.2	13	PDB header: de novo protein Chain: A: PDB Molecule: w35; PDBTitle: solution structure of the de novo mini protein gehe_06
58	c1ileA_	Alignment	not modelled	6.2	44	PDB header: aminoacyl-trna synthetase Chain: A: PDB Molecule: isoleucyl-trna synthetase; PDBTitle: isoleucyl-trna synthetase
59	c3mx6A_	Alignment	not modelled	6.1	14	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
60	c5x3tA_	Alignment	not modelled	6.0	25	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapb26; PDBTitle: vapbc from mycobacterium tuberculosis
61	c1wz2B_	Alignment	not modelled	6.0	25	PDB header: ligase/rna Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
62	d2hzaa1	Alignment	not modelled	5.9	10	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
63	d1u9pa1	Alignment	not modelled	5.8	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
64	c5h7pB_	Alignment	not modelled	5.8	15	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: nmr structure of the vta1ntd-did2(176-204) complex
65	d1st6a5	Alignment	not modelled	5.8	10	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
66	c3o0lB_	Alignment	not modelled	5.7	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
67	c2l8nA_	Alignment	not modelled	5.7	29	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
68	c5jr6B_	Alignment	not modelled	5.5	9	PDB header: hydrolase Chain: B: PDB Molecule: peptidase, putative; PDBTitle: the xray crystal structure of p. falciparum aminopeptidase p in2 complex with apstatin
69	c3t0yD_	Alignment	not modelled	5.5	17	PDB header: transcription regulator/protein binding Chain: D: PDB Molecule: nepr; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
70	c1qu2A_	Alignment	not modelled	5.5	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
71	c2xc7A_	Alignment	not modelled	5.4	18	PDB header: rna binding protein Chain: A: PDB Molecule: phosphorylated adapter rna export protein; PDBTitle: solution structure of phax-rbd in complex with ssrna
72	d1chma2	Alignment	not modelled	5.4	26	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
73	c2xpiE_	Alignment	not modelled	5.3	45	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
74	c6q8aA_	Alignment	not modelled	5.2	38	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
75	c2bytD_	Alignment	not modelled	5.2	50	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
76	d1myka_	Alignment	not modelled	5.1	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
77	c5v2gC_	Alignment	not modelled	5.1	20	PDB header: de novo protein Chain: C: PDB Molecule: 20-mer peptide; PDBTitle: de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
78	c5v2gB_	Alignment	not modelled	5.1	20	PDB header: de novo protein Chain: B: PDB Molecule: 20-mer peptide; PDBTitle: de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
79	c5v2gA_	Alignment	not modelled	5.1	20	PDB header: de novo protein Chain: A: PDB Molecule: 20-mer peptide;

79	c3vz9A	Alignment	not modelled	5.1	20	PDBTitle: de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
80	c2bj3D	Alignment	not modelled	5.0	14	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nkr-apo