
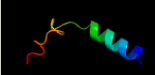

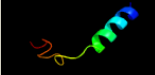

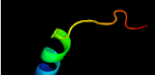

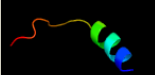
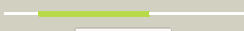
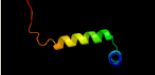

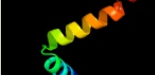







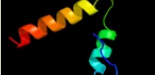






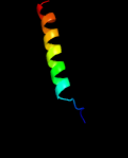

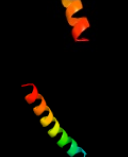
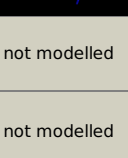
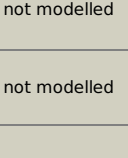


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2760c_(-)_3071277_3071546
Date	Wed Aug 7 12:50:42 BST 2019
Unique Job ID	36c2c2df195073eb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xgqD_	 Alignment		91.0	14	PDB header: toxin/antitoxin Chain: D: PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
2	c4xgqB_	 Alignment		90.8	14	PDB header: toxin/antitoxin Chain: B: PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
3	c4xgrH_	 Alignment		74.8	19	PDB header: toxin/antitoxin Chain: H: PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
4	c4xgrF_	 Alignment		74.7	19	PDB header: toxin/antitoxin Chain: F: PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
5	c2k5jB_	 Alignment		65.3	11	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	c6gtsC_	 Alignment		57.2	15	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
7	c6ajnF_	 Alignment		54.3	15	PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atar bound with accoa
8	d1y9ba1	 Alignment		42.9	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
9	c2kelB_	 Alignment		37.6	33	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
10	c2q2kA_	 Alignment		24.0	23	PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
11	c2q2kB_	 Alignment		21.1	24	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein

12	c6a7vU	Alignment		17.3	34	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
13	c3eabK	Alignment		16.2	35	PDB header: cell cycle Chain: K: PDB Molecule: chmp1b; PDBTitle: crystal structure of spastin mit in complex with escrt iii
14	c3mx6A	Alignment		13.6	7	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
15	d2gg2a1	Alignment		12.7	12	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
16	d1u9pa1	Alignment		12.2	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
17	c4fo7B	Alignment		12.0	11	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: pseudomonas aeruginosa metap, in mn form
18	d1myka	Alignment		10.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
19	d1bdta	Alignment		10.5	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
20	c3tavA	Alignment		10.0	6	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
21	d1baza	Alignment	not modelled	9.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
22	c3f0nB	Alignment	not modelled	9.5	19	PDB header: lyase Chain: B: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: mus musculus mevalonate pyrophosphate decarboxylase
23	c5ca8A	Alignment	not modelled	9.4	38	PDB header: hydrolase Chain: A: PDB Molecule: protein sey1; PDBTitle: structures of the yeast dynamin-like gtpase sey1p in complex with gdp
24	d1myla	Alignment	not modelled	9.3	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
25	c2k9iB	Alignment	not modelled	9.3	14	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus
26	d1p94a	Alignment	not modelled	9.1	27	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
27	c3um2E	Alignment	not modelled	9.0	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
28	c3um1E	Alignment	not modelled	9.0	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
						PDB header: membrane protein/transport protein

29	c3um2B_	Alignment	not modelled	9.0	56	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
30	c3um0B_	Alignment	not modelled	9.0	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
31	d1o0xa_	Alignment	not modelled	8.9	8	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
32	d1q9ja2	Alignment	not modelled	8.2	20	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
33	d2hzaa1	Alignment	not modelled	8.1	14	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
34	d2a4da1	Alignment	not modelled	7.9	28	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
35	c3hxxA_	Alignment	not modelled	7.8	18	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
36	d1cuka1	Alignment	not modelled	7.7	21	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
37	c4egcA_	Alignment	not modelled	7.6	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
38	c5h64b_	Alignment	not modelled	7.3	16	PDB header: transferase Chain: B: PDB Molecule: regulatory-associated protein of mtor; PDBTitle: cryo-em structure of mtorc1
39	c2g6pA_	Alignment	not modelled	7.2	11	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	c1wkbA_	Alignment	not modelled	6.9	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
41	d1efva2	Alignment	not modelled	6.9	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
42	c5vgtA_	Alignment	not modelled	6.8	64	PDB header: viral protein Chain: A: PDB Molecule: gene 7 protein; PDBTitle: x-ray structure of bacteriophage sf6 tail adaptor protein gp7
43	c1zvva_	Alignment	not modelled	6.5	16	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
44	c3m92B_	Alignment	not modelled	6.4	67	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ycin; PDBTitle: the structure of ycin, an uncharacterized protein from shigella2 flexneri.
45	d1mylb_	Alignment	not modelled	6.1	22	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
46	c2gz5A_	Alignment	not modelled	5.9	11	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 1; PDBTitle: human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
47	c6n10A_	Alignment	not modelled	5.9	19	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase mvd1, peroxisomal; PDBTitle: crystal structure of arabidopsis thaliana mevalonate 5-diphosphate2 decarboxylase 1 complexed with (r)-mvapp
48	c4ifdK_	Alignment	not modelled	5.7	37	PDB header: hydrolase/rna Chain: K: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
49	c4ariA_	Alignment	not modelled	5.7	50	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
50	d1bazb_	Alignment	not modelled	5.7	22	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
51	d1efpa2	Alignment	not modelled	5.6	33	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
52	c3o0lB_	Alignment	not modelled	5.3	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