
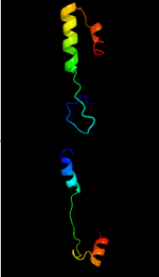
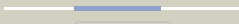




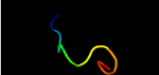




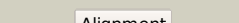
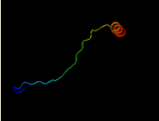

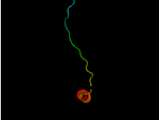

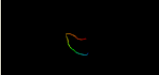



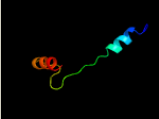


Phyre2

Email hurlibertj@winthrop.edu
 Description ASR85460.1_hypothetical_protein_SEA_CAIN_61_[Mycobacterium_phage_Cain]
 Date Mon Jun 7 16:50:03 BST 2021
 Unique Job ID a66f857893246aee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6urfB_	 Alignment		44.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent malic enzyme; PDBTitle: malic enzyme from mycobacterium tuberculosis
2	d1u6ra2	 Alignment		20.7	23	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
3	d1d4ca2	 Alignment		15.3	50	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
4	c3ktyA_	 Alignment		15.3	25	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase; PDBTitle: crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
5	c2ha8A_	 Alignment		14.8	50	PDB header: rna binding protein Chain: A: PDB Molecule: tar (hiv-1) rna loop binding protein; PDBTitle: methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
6	d1oxk1	 Alignment		14.4	20	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
7	d1p30a1	 Alignment		14.4	33	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group II dsDNA viruses VP Family: Adenovirus hexon
8	d1p2za1	 Alignment		14.2	33	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group II dsDNA viruses VP Family: Adenovirus hexon
9	c3ic6A_	 Alignment		13.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methylase family protein; PDBTitle: crystal structure of putative methylase family protein from neisseria2 gonorrhoeae
10	c6ahwB_	 Alignment		13.7	50	PDB header: transferase Chain: B: PDB Molecule: circular-permuted trna (cytidine(34)-2'-o)- PDBTitle: crystal structure of circular-permuted yibk methyltransferase from2 haemophilus influenzae
11	d1crka2	 Alignment		13.7	23	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain

12	c6xfjA_	Alignment		13.0	67	PDB header: protein transport Chain: A: PDB Molecule: type 3 secretion system pilotin; PDBTitle: crystal structure of the type iii secretion pilotin inh
13	c4pzka_	Alignment		12.7	50	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: crystal structure of putative rna methyltransferase from bacillus2 anthracis.
14	c6qkvA_	Alignment		12.2	50	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: structure of yibk from p. aeruginosa
15	c5kzka_	Alignment		12.1	50	PDB header: rna binding protein Chain: A: PDB Molecule: probable rna methyltransferase, trmh family; PDBTitle: crystal structure of rna methyltransferase from sinorhizobium2 meliloti
16	c4x3mB_	Alignment		11.4	75	PDB header: transferase Chain: B: PDB Molecule: rna 2'-o ribose methyltransferase; PDBTitle: crystal structure of ttha0275 from thermus thermophilus (hb8) in2 complex with adenosine in space group p212121
17	c4cndB_	Alignment		10.6	25	PDB header: transferase Chain: B: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of e.coli trmj
18	c3gyqB_	Alignment		10.2	42	PDB header: transferase Chain: B: PDB Molecule: rrna (adenosine-2'-o)-methyltransferase; PDBTitle: structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
19	d1v2xa_	Alignment		10.1	42	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
20	c2bvik_	Alignment		9.9	33	PDB header: virus Chain: K: PDB Molecule: hexon protein; PDBTitle: the quasi-atomic model of human adenovirus type 52 capsid (part 2)
21	d2ja9a1	Alignment	not modelled	9.9	50	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
22	c3onpA_	Alignment	not modelled	9.6	25	PDB header: transferase Chain: A: PDB Molecule: trna/rrna methyltransferase (spou); PDBTitle: crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
23	d1m15a2	Alignment	not modelled	9.4	24	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
24	c3zifD_	Alignment	not modelled	9.1	33	PDB header: virus Chain: D: PDB Molecule: hexon protein; PDBTitle: cryo-em structures of two intermediates provide insight into2 adenovirus assembly and disassembly
25	c1x7pB_	Alignment	not modelled	9.0	58	PDB header: transferase Chain: B: PDB Molecule: rrna methyltransferase; PDBTitle: crystal structure of the spou methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
26	c3e5yB_	Alignment	not modelled	9.0	58	PDB header: transferase Chain: B: PDB Molecule: trmh family rna methyltransferase; PDBTitle: crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
27	c2xdhA_	Alignment	not modelled	8.9	41	PDB header: cell adhesion Chain: A: PDB Molecule: cohesin; PDBTitle: non-cellulosomal cohesin from the hyperthermophilic2 archaeon archaeoglobus fulgidus
28	c1ipaA_	Alignment	not modelled	8.8	67	PDB header: transferase Chain: A: PDB Molecule: rna 2'-o-ribose methyltransferase; PDBTitle: crystal structure of rna 2'-o ribose methyltransferase

29	c5gm8A_	Alignment	not modelled	8.6	33	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine-2'-o)-methyltransferase trmj; PDBTitle: methylation at position 32 of trna catalyzed by trmj alters oxidative2 stress response in pseudomonas aeruginosa
30	c1plpA_	Alignment	not modelled	8.1	88	PDB header: membrane protein Chain: A: PDB Molecule: phospholamban; PDBTitle: solution structure of the cytoplasmic domain of2 phospholamban
31	c2i6dA_	Alignment	not modelled	8.0	50	PDB header: transferase Chain: A: PDB Molecule: rna methyltransferase, trmh family; PDBTitle: the structure of a putative rna methyltransferase of the trmh family2 from porphyromonas gingivalis.
32	c2inyA_	Alignment	not modelled	7.9	33	PDB header: viral protein Chain: A: PDB Molecule: hexon protein; PDBTitle: nanoporous crystals of chicken embryo lethal orphan (celo) adenovirus2 major coat protein, hexon
33	d1ipaa1	Alignment	not modelled	7.7	67	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
34	c4cngB_	Alignment	not modelled	7.5	17	PDB header: transferase Chain: B: PDB Molecule: spou rrna methylase; PDBTitle: crystal structure of sulfolobus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
35	c2ja9A_	Alignment	not modelled	7.5	50	PDB header: rna-binding protein Chain: A: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the n-terminal deletion of yeast exosome2 component rrp40
36	d1gz0a1	Alignment	not modelled	7.5	31	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
37	c1zjrA_	Alignment	not modelled	7.3	50	PDB header: transferase Chain: A: PDB Molecule: trna (guanosine-2'-o)-methyltransferase; PDBTitle: crystal structure of a. aeolicus trmh/spou trna modifying enzyme
38	d1mxia_	Alignment	not modelled	7.3	50	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
39	c2je6I_	Alignment	not modelled	7.1	42	PDB header: hydrolase Chain: I: PDB Molecule: exosome complex rna-binding protein 1; PDBTitle: structure of a 9-subunit archaeal exosome
40	c1gz0G_	Alignment	not modelled	7.0	31	PDB header: transferase Chain: G: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase rimb
41	c2nn6H_	Alignment	not modelled	6.9	39	PDB header: hydrolase/transferase Chain: H: PDB Molecule: exosome complex exonuclease rrp4; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
42	d1kk8a1	Alignment	not modelled	6.9	33	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
43	c5flgA_	Alignment	not modelled	6.4	29	PDB header: ligase Chain: A: PDB Molecule: 6-carboxyhexanoate--coa ligase; PDBTitle: crystal structure of the 6-carboxyhexanoate-coa ligase (biow)from2 bacillus subtilis in complex with amppnp
44	c1gz0H_	Alignment	not modelled	6.3	33	PDB header: transferase Chain: H: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase rimb
45	d2nn6g1	Alignment	not modelled	6.2	50	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
46	c3qkbB_	Alignment	not modelled	6.2	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
47	c2mfzA_	Alignment	not modelled	5.9	50	PDB header: structural protein Chain: A: PDB Molecule: minor ampullate spidroin; PDBTitle: nmr structure of c-terminal domain from a. ventricosus minor ampullate2 spidroin (misp)
48	c5co4A_	Alignment	not modelled	5.8	50	PDB header: transferase Chain: A: PDB Molecule: putative trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: structural insights into the 2-oh methylation of c/u34 on trna
49	c5ikjB_	Alignment	not modelled	5.8	70	PDB header: transcription Chain: B: PDB Molecule: cryptic loci regulator protein 1; PDBTitle: structure of clr2 bound to the clr1 c-terminus
50	c3izxE_	Alignment	not modelled	5.7	39	PDB header: virus Chain: E: PDB Molecule: viral structural protein 5; PDBTitle: 3.1 angstrom cryoem structure of cytoplasmic polyhedrosis virus
51	c3iz3D_	Alignment	not modelled	5.7	41	PDB header: virus Chain: D: PDB Molecule: viral structural protein 5; PDBTitle: cryoem structure of cytoplasmic polyhedrosis virus
52	c6d6rH_	Alignment	not modelled	5.3	39	PDB header: hydrolase Chain: H: PDB Molecule: exosome complex component rrp4; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
53	c4ifdG_	Alignment	not modelled	5.2	50	PDB header: hydrolase/rna Chain: G: PDB Molecule: exosome complex component rrp40; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna