
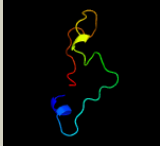



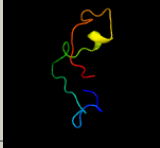

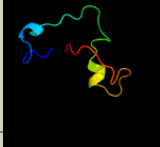

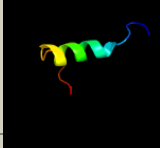
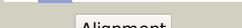
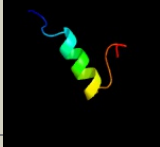
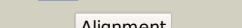
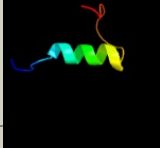
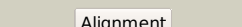
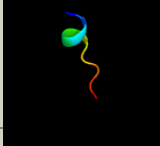
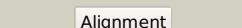
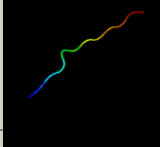
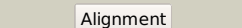
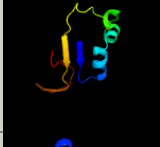




Phyre2

Email hurlibertj@winthrop.edu
 Description ASR85416.1_tail_terminator_[Mycobacterium_phage_Cain]
 Date Mon Jun 7 16:50:02 BST 2021
 Unique Job ID c321ccfb25c09133

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pnoa_	 Alignment		36.5	27	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
2	c2bruC_	 Alignment		30.7	35	PDB header: oxidoreductase Chain: C: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
3	d1d4oa_	 Alignment		27.9	24	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
4	c1pt9B_	 Alignment		27.4	24	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase, mitochondrial; PDBTitle: crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
5	d1tmqb_	 Alignment		25.4	24	Fold: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin Superfamily: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin Family: Proteinase/alpha-amylase inhibitors
6	d1beaa_	 Alignment		23.5	29	Fold: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin Superfamily: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin Family: Proteinase/alpha-amylase inhibitors
7	c4cwwD_	 Alignment		23.0	23	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: limit dextrinase inhibitor; PDBTitle: structure of the barley limit dextrinase-limit dextrinase2 inhibitor complex
8	c2lzqA_	 Alignment		22.5	70	PDB header: viral protein Chain: A: PDB Molecule: ns2 peptide; PDBTitle: structure of ns2(32-57) gbvb protein
9	c3kwrA_	 Alignment		20.5	67	PDB header: rna binding protein Chain: A: PDB Molecule: putative rna-binding protein; PDBTitle: crystal structure of putative rna-binding protein (np_785364.1) from2 lactobacillus plantarum at 1.45 a resolution
10	d2dbsa1	 Alignment		16.8	45	Fold: TTHC002-like Superfamily: TTHC002-like Family: TTHC002-like
11	c7a24z_	 Alignment		16.4	15	PDB header: membrane protein Chain: Z: PDB Molecule: b16.6; PDBTitle: assembly intermediate of the plant mitochondrial complex i

12	c6yaqA	Alignment		14.5	10	PDB header: flavoprotein Chain: A: PDB Molecule: cytokinin dehydrogenase 8; PDBTitle: crystal structure of zmck08 in complex with inhibitor 1-(3-chloro-5-2 trifluoromethoxy-phenyl)-3-[2-(2-hydroxy-ethyl)-phenyl]-urea
13	c4agyA	Alignment		10.8	8	PDB header: virus Chain: A: PDB Molecule: vp1 protein; PDBTitle: coxsackievirus a7 (cav7) empty capsid reconstruction at 6.092 angstrom resolution.
14	c6yjiA	Alignment		9.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-binding pcmh-type domain-containing protein; PDBTitle: structure of fgceldh7c
15	c3h1yA	Alignment		9.6	19	PDB header: isomerase Chain: A: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose 6-phosphate isomerase from salmonella2 typhimurium bound to substrate (f6p)and metal atom (zn)
16	c3lxxB	Alignment		9.0	32	PDB header: chaperone Chain: B: PDB Molecule: nascent polypeptide-associated complex subunit alpha; PDBTitle: human nac dimerization domain
17	d1lka	Alignment		8.9	10	Fold: Head-binding domain of phage P22 tailspike protein Superfamily: Head-binding domain of phage P22 tailspike protein Family: Head-binding domain of phage P22 tailspike protein
18	d1br2a1	Alignment		8.8	47	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
19	c3mxtA	Alignment		8.6	28	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
20	c2q7rA	Alignment		8.4	63	PDB header: hydrolase Chain: A: PDB Molecule: mucosa-associated lymphoid tissue lymphoma translocation PDBTitle: x-ray structure of the death domain of the human mucosa associated2 lymphoid tissue lymphoma translocation protein 1
21	d2o5ha1	Alignment	not modelled	8.0	44	Fold: NMB0513-like Superfamily: NMB0513-like Family: NMB0513-like
22	c1n2dC	Alignment	not modelled	8.0	27	PDB header: cell cycle Chain: C: PDB Molecule: iq2 and iq3 motifs from myo2p, a class v myosin; PDBTitle: ternary complex of mlc1p bound to iq2 and iq3 of myo2p, a class v2 myosin
23	c5gpdB	Alignment	not modelled	7.6	31	PDB header: dna binding protein Chain: B: PDB Molecule: sterol regulatory element-binding protein 1; PDBTitle: crystal structure of the binding domain of srebp from fission yeast
24	c2vfvA	Alignment	not modelled	7.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
25	c3bw7A	Alignment	not modelled	7.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
26	c3witA	Alignment	not modelled	6.8	50	PDB header: structural protein Chain: A: PDB Molecule: putative vgr protein; PDBTitle: crystal structure of the c-terminal region of vgrg1 from e. coli o1572 edl933
27	c6u7hB	Alignment	not modelled	6.7	16	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: cryo-em structure of the hcov-229e spike glycoprotein
28	c6b15A	Alignment	not modelled	6.3	63	PDB header: sugar binding protein Chain: A: PDB Molecule: amy13k; PDBTitle: crystal structure of cbmbc (family cbm26) from eubacterium rectale2 amy13k

29	c6dlmA_	Alignment	not modelled	6.1	70	PDB header: de novo protein Chain: A: PDB Molecule: dhd127_a; PDBTitle: dhd127
30	c6i08B_	Alignment	not modelled	6.0	40	PDB header: metal binding protein Chain: B: PDB Molecule: cytidine deaminase 1; PDBTitle: crystal structure of arabidopsis cytidine deaminase
31	c2ev2B_	Alignment	not modelled	5.9	24	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cylcase rv1264, at ph 8.5
32	d1ihoa_	Alignment	not modelled	5.9	41	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
33	d1hssa_	Alignment	not modelled	5.9	33	Fold: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin Superfamily: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin Family: Proteinase/alpha-amylase inhibitors
34	c5d2hA_	Alignment	not modelled	5.9	17	PDB header: lyase Chain: A: PDB Molecule: 4-oxalocrotonate decarboxylase nahk; PDBTitle: 4-oxalocrotonate decarboxylase from pseudomonas putida g7 - complexed2 with magnesium and alpha-ketoglutarate
35	c7cc9C_	Alignment	not modelled	5.8	19	PDB header: dna binding protein/dna Chain: C: PDB Molecule: hnhc domain-containing protein; PDBTitle: sulfur binding domain of sprmcra complexed with phosphorothioated dna
36	c3cwfA_	Alignment	not modelled	5.8	64	PDB header: transferase Chain: A: PDB Molecule: alkaline phosphatase synthesis sensor protein phor; PDBTitle: crystal structure of pas domain of two-component sensor histidine2 kinase
37	d1i27a_	Alignment	not modelled	5.8	63	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of the rap74 subunit of TFIIIF
38	c2vkyB_	Alignment	not modelled	5.8	10	PDB header: viral protein Chain: B: PDB Molecule: tail protein, piigcn4; PDBTitle: headbinding domain of phage p22 tailspike c-terminally fused to2 isoleucine zipper piigcn4 (chimera i)
39	c3ag5A_	Alignment	not modelled	5.3	21	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantothenate synthetase from staphylococcus2 aureus
40	c6qtiB_	Alignment	not modelled	5.2	24	PDB header: membrane protein Chain: B: PDB Molecule: nicotinamide nucleotide transhydrogenase; PDBTitle: structure of ovine transhydrogenase in the presence of nadp+ in a2 "double face-down" conformation