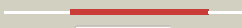










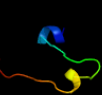

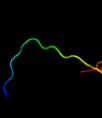

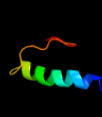

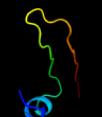

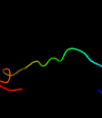


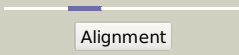
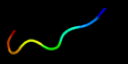
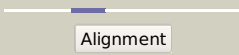



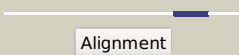

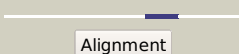

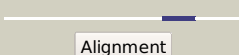


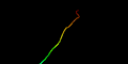
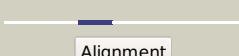

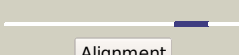
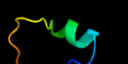
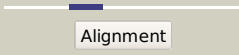
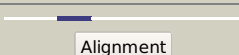
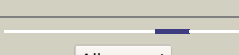
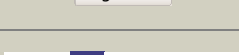
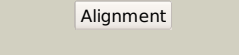

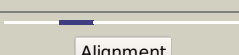
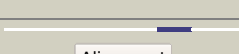


Phyre2

Email	hurlbertj@winthrop.edu
Description	ASR85474.1_RusA-like_resolvase_[Mycobacterium_phage_Cain]
Date	Mon Jun 7 16:50:03 BST 2021
Unique Job ID	598d3ef984dcf719

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1q8ra_	 Alignment		99.6	32	Fold: Bacillus chorismate mutase-like Superfamily: Holliday junction resolvase RusA Family: Holliday junction resolvase RusA
2	c6idyC_	 Alignment		33.3	26	PDB header: lipid binding protein Chain: C: PDB Molecule: lipase aflb; PDBTitle: crystal structure of aspergillus fumigatus lipase b
3	c5zc1A_	 Alignment		26.4	21	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: cystatin-1; PDBTitle: x-ray diffraction analysis of the csstefin-1
4	c7crcB_	 Alignment		23.0	15	PDB header: plant protein Chain: B: PDB Molecule: nad+ hydrolase (nadase); PDBTitle: cryo-em structure of plant nlr rpp1 tetramer in complex with atr1
5	c3vh5D_	 Alignment		20.0	63	PDB header: dna binding protein Chain: D: PDB Molecule: cenp-x; PDBTitle: crystal structure of the chicken cenp-t histone fold/cenp-w/cenp-2 s/cenp-x heterotetrameric complex, crystal form i
6	c3w06A_	 Alignment		12.7	19	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, alpha/beta fold family protein; PDBTitle: crystal structure of arabidopsis thaliana dwarf14 like (atd14l)
7	c4wnxA_	 Alignment		12.4	24	PDB header: laminin binding protein Chain: A: PDB Molecule: netrin-4; PDBTitle: netrin 4 lacking the c-terminal domain
8	d1hywa_	 Alignment		12.0	30	Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW
9	c6u08H_	 Alignment		11.5	37	PDB header: toxin Chain: H: PDB Molecule: ddd; PDBTitle: double-stranded dna-specific cytidine deaminase type vi secretion2 system effector and cognate immunity complex from burkholderia3 cenocepacia
10	c4ploA_	 Alignment		11.3	48	PDB header: protein binding Chain: A: PDB Molecule: netrin-1; PDBTitle: crystal structure of chicken netrin-1 (ln-le3) in complex with mouse2 dcc (fn4-5)
11	c4aqsA_	 Alignment		11.1	24	PDB header: cell adhesion Chain: A: PDB Molecule: laminin subunit beta-1; PDBTitle: laminin beta1 ln-le1-4 structure

12	c4knbF_			10.3	38	PDB header: transcription/replication Chain: F: PDB Molecule: uncharacterized protein pob3n; PDBTitle: structure of the spt16d pob3n heterodimer
13	d1e5qa2			10.0	30	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
14	c6losH_			8.9	35	PDB header: signaling protein Chain: H: PDB Molecule: collagen model peptide, type i, alpha 1; PDBTitle: crystal structure of mouse pedf in complex with heterotrimeric2 collagen model peptide.
15	c3b6nA_			8.8	24	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase pv003920 from plasmodium vivax
16	c5gn0H_			8.5	42	PDB header: transcription Chain: H: PDB Molecule: ww domain-containing transcription regulator protein 1; PDBTitle: structure of taz-tead complex
17	c6m9kD_			8.4	25	PDB header: hydrolase Chain: D: PDB Molecule: recombination protein bet; PDBTitle: crystal structure of lambda exonuclease in complex with the red beta2 c-terminal domain
18	c6losG_			7.7	38	PDB header: signaling protein Chain: G: PDB Molecule: collagen model peptide, type i, alpha 1; PDBTitle: crystal structure of mouse pedf in complex with heterotrimeric2 collagen model peptide.
19	c2ezeA_			7.5	40	PDB header: dna binding protein/dna Chain: A: PDB Molecule: high mobility group protein hmg-i/hmg-y; PDBTitle: solution structure of a complex of the second dna binding2 domain of human hmg-i(y) bound to dna dodecamer containing3 the prdi1 site of the interferon-beta promoter, nmr, 354 structures
20	d1dgsa2			7.4	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
21	c4knbE_		not modelled	6.6	26	PDB header: transcription/replication Chain: E: PDB Molecule: uncharacterized protein spt16d; PDBTitle: structure of the spt16d pob3n heterodimer
22	c2xuaH_		not modelled	6.3	21	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the eno-lactonase from burkholderia2 xenovorans lb400
23	c2k4fA_		not modelled	6.2	32	PDB header: immune system, signaling protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 epsilon chain; PDBTitle: mouse cd3epsilon cytoplasmic tail
24	c7c9r9_		not modelled	6.0	45	PDB header: photosynthesis Chain: 9: PDB Molecule: alpha subunit 2 of light-harvesting 1 complex; PDBTitle: structure of photosynthetic lh1-rc super-complex of thiorhodovibrio2 strain 970
25	c4r33A_		not modelled	6.0	26	PDB header: lyase Chain: A: PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
26	d1fx7a3		not modelled	6.0	40	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like
27	d1cf7b_		not modelled	5.8	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp
28	c6k31B_		not modelled	5.6	43	PDB header: lyase Chain: B: PDB Molecule: aipepck; PDBTitle: crystal structure of pyrophosphate-dependent phosphoenolpyruvate2 carboxykinase (ppi-pepck)

29	c4aqtA_	Alignment	not modelled	5.4	29	PDB header: cell adhesion Chain: A: PDB Molecule: laminin subunit gamma-1; PDBTitle: laminin gamma1 In-le1-2 structure
30	c6x61H_	Alignment	not modelled	5.3	40	PDB header: transcription/transferase Chain: H: PDB Molecule: adaptive-response sensory-kinase sasa; PDBTitle: crystal structure of the n-terminal thioredoxin domain of sasa in2 complex with the n-terminal ci domain of kaic from thermosynchococcus3 elongatus
31	d1zo0a1	Alignment	not modelled	5.2	44	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Ornithine decarboxylase antizyme-like
32	c2y38A_	Alignment	not modelled	5.1	29	PDB header: structural protein Chain: A: PDB Molecule: laminin subunit alpha-5; PDBTitle: laminin alpha5 chain n-terminal fragment
33	d1pkpa1	Alignment	not modelled	5.1	38	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
34	c2rsyB_	Alignment	not modelled	5.1	28	PDB header: transferase/signaling protein Chain: B: PDB Molecule: phosphoprotein associated with glycosphingolipid-enriched PDBTitle: solution structure of the sh2 domain of csk in complex with a2 phosphopeptide from cbp