



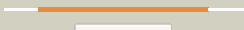



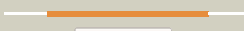















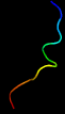


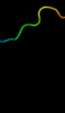


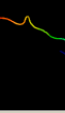


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0299 (-) _363476_363778
Date	Tue Jul 23 14:50:36 BST 2019
Unique Job ID	7de676a75bbf453b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5hk3B_</a>	 Alignment		97.2	15	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> endoribonuclease mazf6; <b>PDBTitle:</b> crystal structure of m. tuberculosis mazf-mt3 t52d-f62d mutant in2 complex with dna
2	<a href="#">c5xe3B_</a>	 Alignment		87.7	18	<b>PDB header:</b> hydrolase/antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> endoribonuclease mazf4; <b>PDBTitle:</b> endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
3	<a href="#">c5wygC_</a>	 Alignment		87.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable endoribonuclease mazf7; <b>PDBTitle:</b> the crystal structure of the apo form of mtb mazf
4	<a href="#">d1ub4a_</a>	 Alignment		83.7	18	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component <b>Family:</b> Kid/PemK
5	<a href="#">c5ccaA_</a>	 Alignment		80.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoribonuclease mazf3; <b>PDBTitle:</b> crystal structure of mtb toxin
6	<a href="#">d1ne8a_</a>	 Alignment		60.6	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component <b>Family:</b> Kid/PemK
7	<a href="#">c4mzpC_</a>	 Alignment		60.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> mazf mrna interferase; <b>PDBTitle:</b> mazf from s. aureus crystal form iii, c2221, 2.7 a
8	<a href="#">c5hizA_</a>	 Alignment		54.0	17	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> endoribonuclease mazf9; <b>PDBTitle:</b> structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
9	<a href="#">d1m1fa_</a>	 Alignment		26.4	14	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component <b>Family:</b> Kid/PemK
10	<a href="#">c5a9qZ_</a>	 Alignment		25.2	43	<b>PDB header:</b> transport protein <b>Chain:</b> Z: <b>PDB Molecule:</b> nuclear pore complex protein nup85; <b>PDBTitle:</b> human nuclear pore complex
11	<a href="#">c6g90J_</a>	 Alignment		18.2	35	<b>PDB header:</b> splicing <b>Chain:</b> J: <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein component snu71; <b>PDBTitle:</b> prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2)

12	<a href="#">c3j6vL_</a>	Alignment		17.3	67	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 28s ribosomal protein s12, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
13	<a href="#">c6fbA_</a>	Alignment		15.7	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mina-1; <b>PDBTitle:</b> nmr solution structure of mina-1(254-334)
14	<a href="#">c1zn1L_</a>	Alignment		15.7	33	<b>PDB header:</b> biosynthetic/structural protein/rna <b>Chain:</b> L: <b>PDB Molecule:</b> 30s ribosomal protein s12; <b>PDBTitle:</b> coordinates of rrf fitted into cryo-em map of the 70s post-termination2 complex
15	<a href="#">d2uubl1</a>	Alignment		15.4	42	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
16	<a href="#">d1i94L_</a>	Alignment		15.3	42	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
17	<a href="#">d2qall1</a>	Alignment		14.2	33	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
18	<a href="#">c1s1hL_</a>	Alignment		14.0	33	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 40s ribosomal protein s23; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
19	<a href="#">c5xyiX_</a>	Alignment		13.6	33	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 40s ribosomal protein s23, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
20	<a href="#">c3u5gX_</a>	Alignment		13.5	33	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 40s ribosomal protein s23-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
21	<a href="#">c3zeyS_</a>	Alignment	not modelled	13.1	25	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 40s ribosomal protein s23, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
22	<a href="#">c3j20N_</a>	Alignment	not modelled	13.0	50	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 30s ribosomal protein s12p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
23	<a href="#">c2zkqL_</a>	Alignment	not modelled	13.0	42	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> L: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
24	<a href="#">c3h7yA_</a>	Alignment	not modelled	12.1	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacilysin biosynthesis protein bacb; <b>PDBTitle:</b> crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
25	<a href="#">c2xzmL_</a>	Alignment	not modelled	11.5	25	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 40s ribosomal protein s12; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
26	<a href="#">c1meqA_</a>	Alignment	not modelled	8.1	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> exterior membrane glycoprotein (gp120); <b>PDBTitle:</b> hiv gp120 c5
27	<a href="#">d1t98a1</a>	Alignment	not modelled	7.9	83	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MukF N-terminal domain-like
						<b>PDB header:</b> lipid transport

28	<a href="#">c6roiC_</a>	Alignment	not modelled	7.5	26	<b>Chain:</b> C; <b>PDB Molecule:</b> cell division control protein 50; <b>PDBTitle:</b> cryo-em structure of the partially activated drs2p-cdc50p
29	<a href="#">d2es7a1</a>	Alignment	not modelled	7.0	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> HyaE-like
30	<a href="#">c5vbaA_</a>	Alignment	not modelled	7.0	23	<b>PDB header:</b> chaperone, hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lysozyme, esx-1 secretion-associated protein espg1 chimera; <b>PDBTitle:</b> structure of espg1 chaperone from the type vii (esx-1) secretion2 system determined with the assistance of n-terminal t4 lysozyme3 fusion
31	<a href="#">c2kpoA_</a>	Alignment	not modelled	6.0	56	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> rossmann 2x2 fold protein; <b>PDBTitle:</b> solution nmr structure of de novo designed rossmann 2x2 fold protein,2 northeast structural genomics consortium target or16
32	<a href="#">c6fcxA_</a>	Alignment	not modelled	5.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> methylenetetrahydrofolate reductase; <b>PDBTitle:</b> structure of human 5,10-methylenetetrahydrofolate reductase (mthfr)
33	<a href="#">c2lpeA_</a>	Alignment	not modelled	5.6	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> kinase suppressor of ras 1; <b>PDBTitle:</b> solution nmr structure of the ksr1 ca1-ca1a domain