
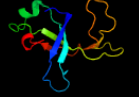

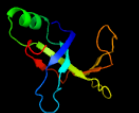




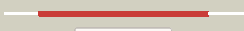








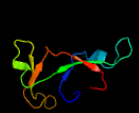

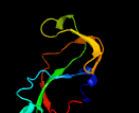

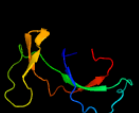
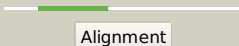
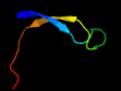

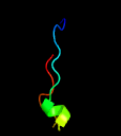
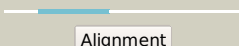
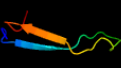
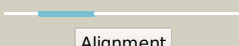

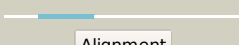

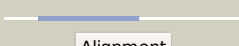
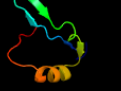
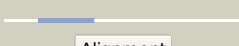
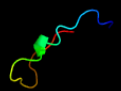
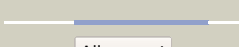
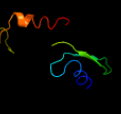

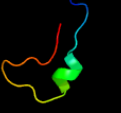
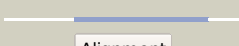

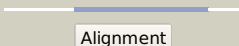
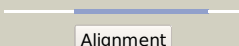
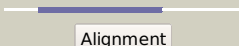




# Phyre2

|               |                                 |
|---------------|---------------------------------|
| Email         | mdejesus@rockefeller.edu        |
| Description   | RVBD0456A (-)<br>_547079_547360 |
| Date          | Tue Jul 23 14:50:53 BST<br>2019 |
| Unique Job ID | ab7cfd2e2ec9e584                |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">d1m1fa_</a> |  Alignment   |    | 100.0      | 33     | <b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component<br><b>Family:</b> Kid/PemK   |
| 2  | <a href="#">c5hjzA_</a> |  Alignment   |    | 100.0      | 60     | <b>PDB header:</b> hydrolase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> endoribonuclease mazf9;<br><b>PDBTitle:</b> structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna                      |
| 3  | <a href="#">c4mzpC_</a> |  Alignment   |    | 100.0      | 25     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> mazf mrna interferase;<br><b>PDBTitle:</b> mazf from s. aureus crystal form iii, c2221, 2.7 a  |
| 4  | <a href="#">d1ne8a_</a> |  Alignment   |    | 99.9       | 24     | <b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component<br><b>Family:</b> Kid/PemK   |
| 5  | <a href="#">d1ub4a_</a> |  Alignment |  | 99.9       | 30     | <b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component<br><b>Family:</b> Kid/PemK   |
| 6  | <a href="#">c5hk3B_</a> |  Alignment |  | 99.9       | 29     | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> endoribonuclease mazf6;<br><b>PDBTitle:</b> crystal structure of m. tuberculosis mazf-mt3 t52d-f62d mutant in2 complex with dna      |
| 7  | <a href="#">c5xe3B_</a> |  Alignment |  | 99.9       | 32     | <b>PDB header:</b> hydrolase/antitoxin<br><b>Chain:</b> B: <b>PDB Molecule:</b> endoribonuclease mazf4;<br><b>PDBTitle:</b> endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species |
| 8  | <a href="#">c5wygC_</a> |  Alignment |  | 99.9       | 33     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> probable endoribonuclease mazf7;<br><b>PDBTitle:</b> the crystal structure of the apo form of mtb mazf                                   |
| 9  | <a href="#">c5ccaA_</a> |  Alignment |  | 99.8       | 17     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endoribonuclease mazf3;<br><b>PDBTitle:</b> crystal structure of mtb toxin   |
| 10 | <a href="#">c3jrzA_</a> |  Alignment |  | 89.2       | 16     | <b>PDB header:</b> toxin<br><b>Chain:</b> A: <b>PDB Molecule:</b> ccdb;<br><b>PDBTitle:</b> ccdvfi-formii-ph5.6  |
| 11 | <a href="#">d3vuba_</a> |  Alignment |  | 66.1       | 14     | <b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component<br><b>Family:</b> CcdB   |

|    |                         |   |   |      |    |  |
|----|-------------------------|---|---|------|----|--|
| 12 | <a href="#">c5ikjA_</a> |  Alignment   |    | 59.8 | 38 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> cryptic loci regulator 2;<br><b>PDBTitle:</b> structure of clr2 bound to the clr1 c-terminus   |
| 13 | <a href="#">c3mxuA_</a> |  Alignment   |    | 41.5 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein;<br><b>PDBTitle:</b> crystal structure of glycine cleavage system protein h from bartonella2 henselae   |
| 14 | <a href="#">c6n1bA_</a> |  Alignment   |    | 39.3 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate-binding protein;<br><b>PDBTitle:</b> crystal structure of an n-acetylgalactosamine deacetylase from f.2 plautii in complex with blood group b trisaccharide                                 |
| 15 | <a href="#">c2edgA_</a> |  Alignment   |    | 35.1 | 17 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein;<br><b>PDBTitle:</b> solution structure of the gcv_h domain from mouse glycine  |
| 16 | <a href="#">d1onla_</a> |  Alignment   |    | 30.3 | 25 | <b>Fold:</b> Barrel-sandwich hybrid<br><b>Superfamily:</b> Single hybrid motif<br><b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains  |
| 17 | <a href="#">d1okja2</a> |  Alignment   |    | 29.8 | 11 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Actin-like ATPase domain<br><b>Family:</b> YeaZ-like   |
| 18 | <a href="#">c3a8jF_</a> |  Alignment |  | 26.8 | 25 | <b>PDB header:</b> transferase/transport protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> glycine cleavage system h protein;<br><b>PDBTitle:</b> crystal structure of et-ehred complex   |
| 19 | <a href="#">c2vhl_</a>  |  Alignment |  | 26.4 | 14 | <b>PDB header:</b> ribosome<br><b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l11;<br><b>PDBTitle:</b> structure of pdf binding helix in complex with the ribosome2 (part 1 of 4)   |
| 20 | <a href="#">d1hpca_</a> |  Alignment |  | 22.8 | 29 | <b>Fold:</b> Barrel-sandwich hybrid<br><b>Superfamily:</b> Single hybrid motif<br><b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains  |
| 21 | <a href="#">c3cjqB_</a> |  Alignment | not modelled  | 22.6 | 14 | <b>PDB header:</b> transferase/ribosomal protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l11;<br><b>PDBTitle:</b> ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11 in space group p212121             |
| 22 | <a href="#">c3iftA_</a> |  Alignment | not modelled  | 22.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein;<br><b>PDBTitle:</b> crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.        |
| 23 | <a href="#">c2ftcG_</a> |  Alignment | not modelled  | 21.5 | 11 | <b>PDB header:</b> ribosome<br><b>Chain:</b> G: <b>PDB Molecule:</b> 39s ribosomal protein l11, mitochondrial;<br><b>PDBTitle:</b> structural model for the large subunit of the mammalian mitochondrial2 ribosome   |
| 24 | <a href="#">c3j21H_</a> |  Alignment | not modelled  | 21.3 | 19 | <b>PDB header:</b> ribosome<br><b>Chain:</b> H: <b>PDB Molecule:</b> 50s ribosomal protein l11p;<br><b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) |
| 25 | <a href="#">d1ex0a1</a> |  Alignment | not modelled  | 17.9 | 21 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Transglutaminase N-terminal domain   |
| 26 | <a href="#">c1vw4V_</a> |  Alignment | not modelled  | 16.4 | 15 | <b>PDB header:</b> ribosome<br><b>Chain:</b> V: <b>PDB Molecule:</b> 54s ribosomal protein l36, mitochondrial;<br><b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit  |
| 27 | <a href="#">c1l1kA_</a> |  Alignment | not modelled  | 15.9 | 14 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> barstar;<br><b>PDBTitle:</b> nmr identification and characterization of the flexible2 regions in the 160 kd molten globule-like aggregate of3 barstar at low ph                                    |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 28 | <a href="#">d2daqa1</a> | Alignment | not modelled | 13.4 | 21 | <b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> Tudor/PWWP/MBT<br><b>Family:</b> PWWP domain   |
| 29 | <a href="#">c2fqpD</a>  | Alignment | not modelled | 11.9 | 14 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein bp2299;<br><b>PDBTitle:</b> crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution   |
| 30 | <a href="#">c1cffB</a>  | Alignment | not modelled | 10.5 | 30 | <b>PDB header:</b> calmodulin<br><b>Chain:</b> B: <b>PDB Molecule:</b> calcium pump;<br><b>PDBTitle:</b> nmr solution structure of a complex of calmodulin with a binding2 peptide of the ca2+-pump  |
| 31 | <a href="#">c1jqmA</a>  | Alignment | not modelled | 9.8  | 23 | <b>PDB header:</b> ribosome<br><b>Chain:</b> A: <b>PDB Molecule:</b> 50s ribosomal protein l11;<br><b>PDBTitle:</b> fitting of l11 protein and elongation factor g (ef-g) in2 the cryo-em map of e. coli 70s ribosome bound with ef-g,3 gdp and fusidic acid   |
| 32 | <a href="#">c1vowJ</a>  | Alignment | not modelled | 8.7  | 13 | <b>PDB header:</b> ribosome<br><b>Chain:</b> J: <b>PDB Molecule:</b> 50s ribosomal protein l11;<br><b>PDBTitle:</b> crystal structure of five 70s ribosomes from escherichia coli in2 complex with protein y. this file contains the 50s subunit of one 70s3 ribosome. the entire crystal structure contains five 70s ribosomes4 and is described in remark 400.     |
| 33 | <a href="#">c4mnoA</a>  | Alignment | not modelled | 8.5  | 18 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 1a;<br><b>PDBTitle:</b> crystal structure of aif1a from pyrococcus abyssi  |
| 34 | <a href="#">c3d55A</a>  | Alignment | not modelled | 8.5  | 31 | <b>PDB header:</b> toxin inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rv3357/mt3465;<br><b>PDBTitle:</b> crystal structure of m. tuberculosis yefm antitoxin   |
| 35 | <a href="#">c5o60J</a>  | Alignment | not modelled | 8.1  | 20 | <b>PDB header:</b> ribosome<br><b>Chain:</b> J: <b>PDB Molecule:</b> 50s ribosomal protein l11;<br><b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis   |
| 36 | <a href="#">c4p7xA</a>  | Alignment | not modelled | 7.9  | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-proline cis-4-hydroxylase;<br><b>PDBTitle:</b> l-pipecolic acid-bound l-proline cis-4-hydroxylase   |
| 37 | <a href="#">c5a35A</a>  | Alignment | not modelled | 7.8  | 9  | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein;<br><b>PDBTitle:</b> crystal structure of glycine cleavage protein h-like (gcvh-l)2 from streptococcus pyogenes  |
| 38 | <a href="#">c2jysA</a>  | Alignment | not modelled | 7.6  | 0  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protease/reverse transcriptase;<br><b>PDBTitle:</b> solution structure of simian foamy virus (mac) protease  |
| 39 | <a href="#">d2gycg2</a> | Alignment | not modelled | 7.5  | 15 | <b>Fold:</b> Ribosomal L11/L12e N-terminal domain<br><b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain<br><b>Family:</b> Ribosomal L11/L12e N-terminal domain   |
| 40 | <a href="#">c2wseE</a>  | Alignment | not modelled | 7.4  | 17 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> E: <b>PDB Molecule:</b> photosystem i reaction center subunit iv a, chloroplastic;<br><b>PDBTitle:</b> improved model of plant photosystem i  |
| 41 | <a href="#">c3bboK</a>  | Alignment | not modelled | 7.2  | 24 | <b>PDB header:</b> ribosome<br><b>Chain:</b> K: <b>PDB Molecule:</b> ribosomal protein l11;<br><b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome   |
| 42 | <a href="#">c4rmoA</a>  | Alignment | not modelled | 7.1  | 24 | <b>PDB header:</b> toxin/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> cptn toxin;<br><b>PDBTitle:</b> crystal structure of the cptn type iii toxin-antitoxin system from2 eubacterium rectale  |
| 43 | <a href="#">c3oeiB</a>  | Alignment | not modelled | 7.1  | 31 | <b>PDB header:</b> toxin, protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> relj (antitoxin rv3357);<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)   |
| 44 | <a href="#">d1zaka2</a> | Alignment | not modelled | 6.2  | 21 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain<br><b>Family:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain  |
| 45 | <a href="#">c3cezA</a>  | Alignment | not modelled | 6.1  | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase;<br><b>PDBTitle:</b> crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei   |
| 46 | <a href="#">c2ka7A</a>  | Alignment | not modelled | 6.0  | 25 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein;<br><b>PDBTitle:</b> nmr solution structure of tm0212 at 40 c  |
| 47 | <a href="#">c1s1iK</a>  | Alignment | not modelled | 5.7  | 11 | <b>PDB header:</b> ribosome<br><b>Chain:</b> K: <b>PDB Molecule:</b> 60s ribosomal protein l12;<br><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, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h. |
| 48 | <a href="#">c2dgyA</a>  | Alignment | not modelled | 5.6  | 40 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> mgc11102 protein;<br><b>PDBTitle:</b> solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein   |
| 49 | <a href="#">c5cuza</a>  | Alignment | not modelled | 5.4  | 29 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonic aciduria and homocystinuria type d protein,<br><b>PDBTitle:</b> crystal structure of semet-substituted n-terminal truncated human b12-2 chaperone cblD (108-296)   |