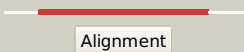
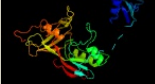
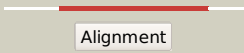
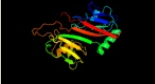

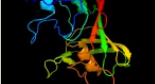
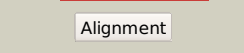



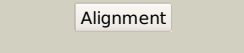

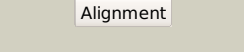



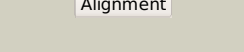

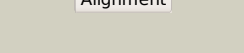

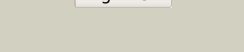



# Phyre2

|               |                               |
|---------------|-------------------------------|
| Email         | mdejesus@rockefeller.edu      |
| Description   | RVBD3300c_(-)_3685980_3686897 |
| Date          | Thu Aug 8 16:20:51 BST 2019   |
| Unique Job ID | 8278820ae0a8e0af              |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c2istA_</a> | <br>Alignment   |    | 100.0      | 23     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase d;<br><b>PDBTitle:</b> crystal structure of rlud from e. coli   |
| 2  | <a href="#">c1qyuA_</a> | <br>Alignment   |    | 100.0      | 23     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase d;<br><b>PDBTitle:</b> structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud   |
| 3  | <a href="#">d1v9fa_</a> | <br>Alignment   |    | 100.0      | 24     | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase RsuA/RLuD   |
| 4  | <a href="#">c1v9fa_</a> | <br>Alignment   |    | 100.0      | 24     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase d;<br><b>PDBTitle:</b> crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli                            |
| 5  | <a href="#">c2i82D_</a> | <br>Alignment |  | 100.0      | 29     | <b>PDB header:</b> lyase/rna<br><b>Chain:</b> D; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase a;<br><b>PDBTitle:</b> crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure |
| 6  | <a href="#">d1v9ka_</a> | <br>Alignment |  | 100.0      | 26     | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase RsuA/RLuD   |
| 7  | <a href="#">c5vbbA_</a> | <br>Alignment |  | 100.0      | 24     | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> rna pseudouridylate synthase domain-containing protein 1;<br><b>PDBTitle:</b> human rna pseudouridylate synthase domain containing 1   |
| 8  | <a href="#">c5ubaA_</a> | <br>Alignment |  | 100.0      | 25     | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> rna pseudouridylate synthase domain-containing protein 4;<br><b>PDBTitle:</b> human rna pseudouridylate synthase domain containing 4   |
| 9  | <a href="#">c1kskA_</a> | <br>Alignment |  | 100.0      | 20     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal small subunit pseudouridine synthase a;<br><b>PDBTitle:</b> structure of rsua  |
| 10 | <a href="#">c1vioA_</a> | <br>Alignment |  | 100.0      | 19     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal small subunit pseudouridine synthase a;<br><b>PDBTitle:</b> crystal structure of pseudouridylate synthase  |
| 11 | <a href="#">c3dh3C_</a> | <br>Alignment |  | 100.0      | 17     | <b>PDB header:</b> isomerase/rna<br><b>Chain:</b> C; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase f;<br><b>PDBTitle:</b> crystal structure of rluf in complex with a 22 nucleotide rna2 substrate                                       |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | <a href="#">c4lgtA_</a> | Alignment |              | 100.0 | 21 | <b>PDB header:</b> isomerase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase b;<br><b>PDBTitle:</b> crystal structure of the catalytic domain of rlub in complex with a2 21-nucleotide rna substrate |
| 13 | <a href="#">c2omIA_</a> | Alignment |              | 100.0 | 16 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase e;<br><b>PDBTitle:</b> crystal structure of e. coli pseudouridine synthase rlue   |
| 14 | <a href="#">c2olwB_</a> | Alignment |              | 100.0 | 15 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase e;<br><b>PDBTitle:</b> crystal structure of e. coli pseudouridine synthase rlue   |
| 15 | <a href="#">d1vioa1</a> | Alignment |              | 100.0 | 23 | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase RsuA/RLuD   |
| 16 | <a href="#">d1kska4</a> | Alignment |              | 100.0 | 22 | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase RsuA/RLuD   |
| 17 | <a href="#">c2gmIA_</a> | Alignment |              | 100.0 | 15 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase f;<br><b>PDBTitle:</b> crystal structure of catalytic domain of e.coli rluf   |
| 18 | <a href="#">c2k6pA_</a> | Alignment |              | 99.2  | 16 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hp_1423;<br><b>PDBTitle:</b> solution structure of hypothetical protein, hp1423   |
| 19 | <a href="#">c5z81A_</a> | Alignment |              | 98.2  | 13 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 15;<br><b>PDBTitle:</b> trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution   |
| 20 | <a href="#">d1dm9a_</a> | Alignment |              | 98.2  | 12 | <b>Fold:</b> Alpha-L RNA-binding motif<br><b>Superfamily:</b> Alpha-L RNA-binding motif<br><b>Family:</b> Heat shock protein 15 kD   |
| 21 | <a href="#">c1dm9A_</a> | Alignment | not modelled | 98.2  | 12 | <b>PDB header:</b> structural genomics<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 15.5 kd protein in mrca-pcka intergenic<br><b>PDBTitle:</b> heat shock protein 15 kd  |
| 22 | <a href="#">c3bbnD_</a> | Alignment | not modelled | 98.1  | 7  | <b>PDB header:</b> ribosome<br><b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s4;<br><b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.                     |
| 23 | <a href="#">d1k8wa5</a> | Alignment | not modelled | 98.0  | 23 | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase II TruB   |
| 24 | <a href="#">d2ey4a2</a> | Alignment | not modelled | 97.9  | 21 | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase II TruB   |
| 25 | <a href="#">c2ey4A_</a> | Alignment | not modelled | 97.9  | 22 | <b>PDB header:</b> isomerase/biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable trna pseudouridine synthase b;<br><b>PDBTitle:</b> crystal structure of a cbf5-nop10-gar1 complex  |
| 26 | <a href="#">d1r3ea2</a> | Alignment | not modelled | 97.8  | 21 | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase II TruB   |
| 27 | <a href="#">d2apoa2</a> | Alignment | not modelled | 97.8  | 26 | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase II TruB   |
| 28 | <a href="#">d1sgva2</a> | Alignment | not modelled | 97.7  | 29 | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase II TruB   |
| 29 | <a href="#">c3uaIA_</a> | Alignment | not modelled | 97.7  | 16 | <b>PDB header:</b> isomerase/chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 4;<br><b>PDBTitle:</b> structure of the shq1-cbf5-nop10-qar1 complex from  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | saccharomyces2 cerevisiae  |
| 30 | <a href="#">c2apoA</a>  | Alignment | not modelled | 97.6 | 24 | <b>PDB header:</b> isomerase/rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable trna pseudouridine synthase b;<br><b>PDBTitle:</b> crystal structure of the methanococcus jannaschii cbf52 nop10 complex  |
| 31 | <a href="#">c1k8wA</a>  | Alignment | not modelled | 97.4 | 20 | <b>PDB header:</b> lyase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna pseudouridine synthase b;<br><b>PDBTitle:</b> crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna  |
| 32 | <a href="#">c1sgvA</a>  | Alignment | not modelled | 97.4 | 29 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna pseudouridine synthase b;<br><b>PDBTitle:</b> structure of trna psi55 pseudouridine synthase (trub)   |
| 33 | <a href="#">d1c06a</a>  | Alignment | not modelled | 97.2 | 12 | <b>Fold:</b> Alpha-L RNA-binding motif<br><b>Superfamily:</b> Alpha-L RNA-binding motif<br><b>Family:</b> Ribosomal protein S4   |
| 34 | <a href="#">d1vioa2</a> | Alignment | not modelled | 97.2 | 11 | <b>Fold:</b> Alpha-L RNA-binding motif<br><b>Superfamily:</b> Alpha-L RNA-binding motif<br><b>Family:</b> Pseudouridine synthase RsuA N-terminal domain  |
| 35 | <a href="#">c5o5jD</a>  | Alignment | not modelled | 97.0 | 25 | <b>PDB header:</b> ribosome<br><b>Chain:</b> D: <b>PDB Molecule:</b> 30s ribosomal protein s4;<br><b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis  |
| 36 | <a href="#">d2uubd1</a> | Alignment | not modelled | 96.7 | 11 | <b>Fold:</b> Alpha-L RNA-binding motif<br><b>Superfamily:</b> Alpha-L RNA-binding motif<br><b>Family:</b> Ribosomal protein S4   |
| 37 | <a href="#">d2gy9d1</a> | Alignment | not modelled | 96.4 | 19 | <b>Fold:</b> Alpha-L RNA-binding motif<br><b>Superfamily:</b> Alpha-L RNA-binding motif<br><b>Family:</b> Ribosomal protein S4   |
| 38 | <a href="#">c1ze2B</a>  | Alignment | not modelled | 96.4 | 26 | <b>PDB header:</b> lyase/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> trna pseudouridine synthase b;<br><b>PDBTitle:</b> conformational change of pseudouridine 55 synthase upon its2 association with rna substrate   |
| 39 | <a href="#">d1p9ka</a>  | Alignment | not modelled | 95.6 | 20 | <b>Fold:</b> Alpha-L RNA-binding motif<br><b>Superfamily:</b> Alpha-L RNA-binding motif<br><b>Family:</b> Ybcj-like  |
| 40 | <a href="#">c2cqjA</a>  | Alignment | not modelled | 94.0 | 12 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar ribonucleoprotein protein<br><b>PDBTitle:</b> solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog                           |
| 41 | <a href="#">c6nd4Z</a>  | Alignment | not modelled | 89.7 | 9  | <b>PDB header:</b> ribosome<br><b>Chain:</b> Z: <b>PDB Molecule:</b> imp3;<br><b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit   |
| 42 | <a href="#">d1fm0d</a>  | Alignment | not modelled | 87.7 | 15 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> Moad/ThiS<br><b>Family:</b> Moad   |
| 43 | <a href="#">c6jzbD</a>  | Alignment | not modelled | 87.4 | 27 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> moad/this family protein;<br><b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens  |
| 44 | <a href="#">c3po0A</a>  | Alignment | not modelled | 87.3 | 15 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> small archaeal modifier protein 1;<br><b>PDBTitle:</b> crystal structure of samp1 from haloferax volcanii  |
| 45 | <a href="#">c3j20E</a>  | Alignment | not modelled | 87.3 | 20 | <b>PDB header:</b> ribosome<br><b>Chain:</b> E: <b>PDB Molecule:</b> 30s ribosomal protein s4e;<br><b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit) |
| 46 | <a href="#">c5xyij</a>  | Alignment | not modelled | 86.9 | 4  | <b>PDB header:</b> ribosome<br><b>Chain:</b> J: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome  |
| 47 | <a href="#">c2qieB</a>  | Alignment | not modelled | 86.6 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin synthase small subunit;<br><b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex with precursor2 z  |
| 48 | <a href="#">c3iz6D</a>  | Alignment | not modelled | 86.1 | 17 | <b>PDB header:</b> ribosome<br><b>Chain:</b> D: <b>PDB Molecule:</b> 40s ribosomal protein s4 (s4e);<br><b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome                        |
| 49 | <a href="#">c3hp7A</a>  | Alignment | not modelled | 86.0 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hemolysin, putative;<br><b>PDBTitle:</b> putative hemolysin from streptococcus thermophilus.   |
| 50 | <a href="#">c5fwhA</a>  | Alignment | not modelled | 85.8 | 16 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> essc;<br><b>PDBTitle:</b> n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus  |
| 51 | <a href="#">c3j20D</a>  | Alignment | not modelled | 85.6 | 10 | <b>PDB header:</b> ribosome<br><b>Chain:</b> D: <b>PDB Molecule:</b> 30s ribosomal protein s4p;<br><b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit) |
| 52 | <a href="#">c5wxmA</a>  | Alignment | not modelled | 84.8 | 16 | <b>PDB header:</b> ribosomal protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar ribonucleoprotein protein imp3;<br><b>PDBTitle:</b> crystal structure of the imp3 and mpp10 complex   |
| 53 | <a href="#">c3zey1</a>  | Alignment | not modelled | 84.5 | 17 | <b>PDB header:</b> ribosome<br><b>Chain:</b> 1: <b>PDB Molecule:</b> 40s ribosomal protein s4, putative;<br><b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome  |
| 54 | <a href="#">c3izbD</a>  | Alignment | not modelled | 84.5 | 18 | <b>PDB header:</b> ribosome<br><b>Chain:</b> D: <b>PDB Molecule:</b> 40s ribosomal protein rps4 (s4e);<br><b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome               |
|    |                         |           |              |      |    | <b>Fold:</b> beta-Grasp (ubiquitin-like)   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 55 | <a href="#">d1vjka_</a> | Alignment | not modelled | 84.1 | 19 | <b>Superfamily:</b> MoaD/ThiS<br><b>Family:</b> MoaD  |
| 56 | <a href="#">c5jpbq_</a> | Alignment | not modelled | 83.5 | 13 | <b>PDB header:</b> ribosome<br><b>Chain:</b> B: <b>PDB Molecule:</b> wd40 domain proteins;<br><b>PDBTitle:</b> cryo-em structure of the 90s pre-ribosome  |
| 57 | <a href="#">c5xxuE_</a> | Alignment | not modelled | 83.4 | 14 | <b>PDB header:</b> ribosome<br><b>Chain:</b> E: <b>PDB Molecule:</b> ribosomal protein es4;<br><b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome   |
| 58 | <a href="#">c1s1hD_</a> | Alignment | not modelled | 83.3 | 7  | <b>PDB header:</b> ribosome<br><b>Chain:</b> D: <b>PDB Molecule:</b> 40s ribosomal protein s9-a;<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, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i. |
| 59 | <a href="#">c6jc0A_</a> | Alignment | not modelled | 83.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative molybdenum cofactor biosynthesis protein d2<br><b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens  |
| 60 | <a href="#">c5xyiE_</a> | Alignment | not modelled | 82.9 | 13 | <b>PDB header:</b> ribosome<br><b>Chain:</b> E: <b>PDB Molecule:</b> 40s ribosomal protein s4;<br><b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome  |
| 61 | <a href="#">d1xo3a_</a> | Alignment | not modelled | 81.5 | 14 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> MoaD/ThiS<br><b>Family:</b> C9orf74 homolog   |
| 62 | <a href="#">c2xzmD_</a> | Alignment | not modelled | 80.8 | 2  | <b>PDB header:</b> ribosome<br><b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s4 containing protein;<br><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   |
| 63 | <a href="#">c3dwmA_</a> | Alignment | not modelled | 80.2 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 9.5 kda culture filtrate antigen cfp10a;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cyso, an antigen   |
| 64 | <a href="#">c2kmmA_</a> | Alignment | not modelled | 79.9 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> guanosine-3',5'-bis(diphosphate) 3'-<br><b>PDBTitle:</b> solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)  |
| 65 | <a href="#">d1h3fa2</a> | Alignment | not modelled | 78.8 | 15 | <b>Fold:</b> Alpha-L RNA-binding motif<br><b>Superfamily:</b> Alpha-L RNA-binding motif<br><b>Family:</b> Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain  |
| 66 | <a href="#">d2piea1</a> | Alignment | not modelled | 78.0 | 16 | <b>Fold:</b> SMAD/FHA domain<br><b>Superfamily:</b> SMAD/FHA domain<br><b>Family:</b> FHA domain  |
| 67 | <a href="#">d1wgka_</a> | Alignment | not modelled | 77.5 | 12 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> MoaD/ThiS<br><b>Family:</b> C9orf74 homolog   |
| 68 | <a href="#">c4eqxA_</a> | Alignment | not modelled | 77.5 | 20 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif1a;<br><b>PDBTitle:</b> crystal structure of kif1a cc1-fha tandem   |
| 69 | <a href="#">c3u5cE_</a> | Alignment | not modelled | 77.4 | 18 | <b>PDB header:</b> ribosome<br><b>Chain:</b> E: <b>PDB Molecule:</b> 40s ribosomal protein s4-a;<br><b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a   |
| 70 | <a href="#">c2g1eA_</a> | Alignment | not modelled | 77.3 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0895;<br><b>PDBTitle:</b> solution structure of ta0895   |
| 71 | <a href="#">d1jh3a_</a> | Alignment | not modelled | 77.2 | 10 | <b>Fold:</b> Alpha-L RNA-binding motif<br><b>Superfamily:</b> Alpha-L RNA-binding motif<br><b>Family:</b> Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain  |
| 72 | <a href="#">c5mpoA_</a> | Alignment | not modelled | 76.8 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin synthase sulfur carrier subunit;<br><b>PDBTitle:</b> crystal structure of human molybdopterin synthase complex  |
| 73 | <a href="#">d2g1la1</a> | Alignment | not modelled | 76.7 | 23 | <b>Fold:</b> SMAD/FHA domain<br><b>Superfamily:</b> SMAD/FHA domain<br><b>Family:</b> FHA domain  |
| 74 | <a href="#">c3kbgA_</a> | Alignment | not modelled | 76.1 | 21 | <b>PDB header:</b> ribosomal protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s4e;<br><b>PDBTitle:</b> crystal structure of the 30s ribosomal protein s4e from thermoplasma2 acidophilum. northeast structural genomics consortium target tar28.  |
| 75 | <a href="#">c2xzmW_</a> | Alignment | not modelled | 76.1 | 21 | <b>PDB header:</b> ribosome<br><b>Chain:</b> W: <b>PDB Molecule:</b> 40s ribosomal protein s4;<br><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  |
| 76 | <a href="#">c3hvvB_</a> | Alignment | not modelled | 75.2 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a  |
| 77 | <a href="#">c5djoB_</a> | Alignment | not modelled | 74.2 | 24 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> kinesin-like protein;<br><b>PDBTitle:</b> crystal structure of the cc1-fha tandem of kinesin-3 kif13a   |
| 78 | <a href="#">c4ejqB_</a> | Alignment | not modelled | 74.2 | 19 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> kinesin-like protein kif1a;<br><b>PDBTitle:</b> crystal structure of kif1a c-cc1-fha  |
| 79 | <a href="#">c4n6aB_</a> | Alignment | not modelled | 70.7 | 13 | <b>PDB header:</b> lyase/biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> this/moad family protein;  |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
| 79  | <a href="#">c1v8cA</a>  | Alignment | not modelled | 70.7 | 13 | <b>PDBTitle:</b> crystal structure of amycolatopsis orientalis bexx/cyso complex<br><b>PDB header:</b> protein binding   |
| 80  | <a href="#">c1v8cA</a>  | Alignment | not modelled | 70.7 | 32 | <b>Chain:</b> A; <b>PDB Molecule:</b> moad related protein;<br><b>PDBTitle:</b> crystal structure of moad related protein from thermus2 thermophilus hb8   |
| 81  | <a href="#">c3zey6</a>  | Alignment | not modelled | 67.5 | 5  | <b>PDB header:</b> ribosome<br><b>Chain:</b> 6; <b>PDB Molecule:</b> 40s ribosomal protein s9, putative;<br><b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome  |
| 82  | <a href="#">c2eh0A</a>  | Alignment | not modelled | 65.9 | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> kinesin-like protein kif1b;<br><b>PDBTitle:</b> solution structure of the fha domain from human kinesin-2 like protein kif1b   |
| 83  | <a href="#">c3fm8A</a>  | Alignment | not modelled | 65.6 | 20 | <b>PDB header:</b> transport protein/hydrolase activator<br><b>Chain:</b> A; <b>PDB Molecule:</b> kinesin-like protein kif13b;<br><b>PDBTitle:</b> crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)    |
| 84  | <a href="#">c2m19A</a>  | Alignment | not modelled | 64.8 | 28 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A; <b>PDB Molecule:</b> molybdopterin converting factor subunit 1;<br><b>PDBTitle:</b> solution structure of the haloferax volcanii hvo 2177 protein   |
| 85  | <a href="#">c2qjlA</a>  | Alignment | not modelled | 63.0 | 8  | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin-related modifier 1;<br><b>PDBTitle:</b> crystal structure of urm1  |
| 86  | <a href="#">c3rpfC</a>  | Alignment | not modelled | 62.4 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> C; <b>PDB Molecule:</b> molybdopterin converting factor, subunit 1 (moad);<br><b>PDBTitle:</b> protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695 |
| 87  | <a href="#">c1r21A</a>  | Alignment | not modelled | 61.5 | 20 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A; <b>PDB Molecule:</b> antigen ki-67;<br><b>PDBTitle:</b> solution structure of human ki67 fha domain  |
| 88  | <a href="#">d2affa1</a> | Alignment | not modelled | 58.9 | 20 | <b>Fold:</b> SMAD/FHA domain<br><b>Superfamily:</b> SMAD/FHA domain<br><b>Family:</b> FHA domain   |
| 89  | <a href="#">d1wxqa2</a> | Alignment | not modelled | 57.7 | 14 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> TGS-like<br><b>Family:</b> G domain-linked domain  |
| 90  | <a href="#">d1v8ca1</a> | Alignment | not modelled | 57.6 | 32 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> MoaD/ThiS<br><b>Family:</b> MoaD   |
| 91  | <a href="#">c2l52A</a>  | Alignment | not modelled | 57.2 | 17 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A; <b>PDB Molecule:</b> methanosarcina acetivorans samp1 homolog;<br><b>PDBTitle:</b> solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans               |
| 92  | <a href="#">c4a0eB</a>  | Alignment | not modelled | 54.5 | 32 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> type iii secretion protein;<br><b>PDBTitle:</b> crystal structure of the cytoplasmic n-terminal domain of yersinia2 pestis yscd  |
| 93  | <a href="#">d1wlna1</a> | Alignment | not modelled | 54.4 | 20 | <b>Fold:</b> SMAD/FHA domain<br><b>Superfamily:</b> SMAD/FHA domain<br><b>Family:</b> FHA domain   |
| 94  | <a href="#">c2ekiA</a>  | Alignment | not modelled | 53.5 | 17 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> developmentally-regulated gtp-binding protein 1;<br><b>PDBTitle:</b> solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1           |
| 95  | <a href="#">c4oudA</a>  | Alignment | not modelled | 53.4 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine   |
| 96  | <a href="#">c2hj1A</a>  | Alignment | not modelled | 49.8 | 23 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae                    |
| 97  | <a href="#">d2hj1a1</a> | Alignment | not modelled | 49.8 | 23 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> MoaD/ThiS<br><b>Family:</b> HI0395-like  |
| 98  | <a href="#">c3elsA</a>  | Alignment | not modelled | 48.3 | 20 | <b>PDB header:</b> splicing<br><b>Chain:</b> A; <b>PDB Molecule:</b> pre-mrna leakage protein 1;<br><b>PDBTitle:</b> crystal structure of yeast pml1p, residues 51-204   |
| 99  | <a href="#">c2janD</a>  | Alignment | not modelled | 48.2 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> D; <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state   |
| 100 | <a href="#">d1nyra2</a> | Alignment | not modelled | 48.2 | 11 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> TGS-like<br><b>Family:</b> TGS domain  |
| 101 | <a href="#">d1kska3</a> | Alignment | not modelled | 48.2 | 22 | <b>Fold:</b> Alpha-L RNA-binding motif<br><b>Superfamily:</b> Alpha-L RNA-binding motif<br><b>Family:</b> Pseudouridine synthase RsuA N-terminal domain  |
| 102 | <a href="#">c2k9xA</a>  | Alignment | not modelled | 47.9 | 18 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution structure of urm1 from trypanosoma brucei   |
| 103 | <a href="#">d2ff4a3</a> | Alignment | not modelled | 46.3 | 16 | <b>Fold:</b> SMAD/FHA domain<br><b>Superfamily:</b> SMAD/FHA domain<br><b>Family:</b> FHA domain   |
| 104 | <a href="#">d1rwsa</a>  | Alignment | not modelled | 39.4 | 20 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> MoaD/ThiS<br><b>Family:</b> ThiS   |
|     |                         |           |              |      |    | <b>Fold:</b> beta-Grasp (ubiquitin-like)   |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
| 105 | <a href="#">d1tkea1</a> | Alignment | not modelled | 38.4 | 14 | <b>Superfamily:</b> TGS-like<br><b>Family:</b> TGS domain  |
| 106 | <a href="#">c3gqsB_</a> | Alignment | not modelled | 35.2 | 24 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> adenylate cyclase-like protein;<br><b>PDBTitle:</b> crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis   |
| 107 | <a href="#">c2jkdB_</a> | Alignment | not modelled | 35.1 | 20 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna leakage protein 1;<br><b>PDBTitle:</b> structure of the yeast pm11 splicing factor and its2 integration into the res complex  |
| 108 | <a href="#">d1we3o_</a> | Alignment | not modelled | 32.7 | 19 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> GroES  |
| 109 | <a href="#">c1vj5C_</a> | Alignment | not modelled | 31.5 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 5' polynucleotide kinase-3' phosphatase fha domain;<br><b>PDBTitle:</b> molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme  |
| 110 | <a href="#">c2jqIA_</a> | Alignment | not modelled | 31.4 | 12 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna damage response protein kinase dun1;<br><b>PDBTitle:</b> nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1  |
| 111 | <a href="#">c3splC_</a> | Alignment | not modelled | 29.3 | 38 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> C: <b>PDB Molecule:</b> aprataxin-like protein;<br><b>PDBTitle:</b> crystal structure of aprataxin ortholog hnt3 in complex with dna and2 amp  |
| 112 | <a href="#">c4jonA_</a> | Alignment | not modelled | 28.4 | 8  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> centrosomal protein of 170 kda;<br><b>PDBTitle:</b> crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom) |
| 113 | <a href="#">c1h3eA_</a> | Alignment | not modelled | 27.3 | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> tyrosyl-trna synthetase from thermus thermophilus complexed with wild-2 type trnatyr(gua) and with atp and tyrosinol   |
| 114 | <a href="#">c6ccdA_</a> | Alignment | not modelled | 26.6 | 14 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding/permease protein rv1747;<br><b>PDBTitle:</b> the crystal structure of mycobacterium tuberculosis rv1747 fha-1  |
| 115 | <a href="#">c2kkIA_</a> | Alignment | not modelled | 26.5 | 25 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mb1858;<br><b>PDBTitle:</b> solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).                   |
| 116 | <a href="#">c2zodB_</a> | Alignment | not modelled | 26.4 | 30 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase;<br><b>PDBTitle:</b> crystal structure of selenophosphate synthetase from aquifex aeolicus  |
| 117 | <a href="#">d1lgpa_</a> | Alignment | not modelled | 25.5 | 17 | <b>Fold:</b> SMAD/FHA domain<br><b>Superfamily:</b> SMAD/FHA domain<br><b>Family:</b> FHA domain   |
| 118 | <a href="#">c3nx6A_</a> | Alignment | not modelled | 25.4 | 17 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> 10kda chaperonin;<br><b>PDBTitle:</b> crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331  |
| 119 | <a href="#">c6cahA_</a> | Alignment | not modelled | 25.3 | 33 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding/permease protein rv1747;<br><b>PDBTitle:</b> nmr-based structure of the fha-2 domain from mycobacterium2 tuberculosis abc transporter rv1747   |
| 120 | <a href="#">c3kt9A_</a> | Alignment | not modelled | 25.1 | 32 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin;<br><b>PDBTitle:</b> aprataxin fha domain  |