


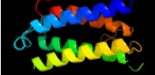
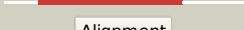

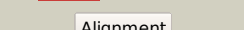

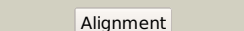





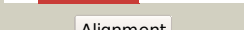



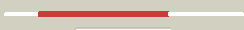





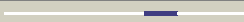


# Phyre2

|               |                               |
|---------------|-------------------------------|
| Email         | mdejesus@rockefeller.edu      |
| Description   | RVBD3773c_(-)_4218419_4219003 |
| Date          | Fri Aug 9 18:20:48 BST 2019   |
| Unique Job ID | 11f74a8b31d309a7              |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c2nsfA_</a> | <br>Alignment   |    | 100.0      | 15     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein cgl3021;<br><b>PDBTitle:</b> crystal structure of the mycothiol-dependent maleylpyruvate isomerase  |
| 2  | <a href="#">d2nsfa1</a> | <br>Alignment   |    | 100.0      | 16     | <b>Fold:</b> DinB/YfiT-like putative metalloenzymes<br><b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes<br><b>Family:</b> Maleylpyruvate isomerase-like  |
| 3  | <a href="#">c6iz2A_</a> | <br>Alignment   |    | 98.4       | 10     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> dinb/yfit family protein;<br><b>PDBTitle:</b> crystal structure of dinb/yfit protein dr0053 from d. radiodurans r1  |
| 4  | <a href="#">c5cogB_</a> | <br>Alignment   |    | 98.2       | 11     | <b>PDB header:</b> unknown function<br><b>Chain:</b> B; <b>PDB Molecule:</b> irc4;<br><b>PDBTitle:</b> crystal structure of yeast irc4   |
| 5  | <a href="#">c2rd9C_</a> | <br>Alignment |  | 98.1       | 13     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C; <b>PDB Molecule:</b> bh0186 protein;<br><b>PDBTitle:</b> crystal structure of a putative yfi-like metal-dependent hydrolase2 (bh0186) from bacillus halodurans c-125 at 2.30 a resolution |
| 6  | <a href="#">d1rxqa_</a> | <br>Alignment |  | 98.1       | 14     | <b>Fold:</b> DinB/YfiT-like putative metalloenzymes<br><b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes<br><b>Family:</b> YfiT-like putative metal-dependent hydrolases  |
| 7  | <a href="#">d2ou6a1</a> | <br>Alignment |  | 98.1       | 15     | <b>Fold:</b> DinB/YfiT-like putative metalloenzymes<br><b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes<br><b>Family:</b> DinB-like  |
| 8  | <a href="#">c5civA_</a> | <br>Alignment |  | 98.1       | 18     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> sibling bacteriocin;<br><b>PDBTitle:</b> sibling lethal factor precursor - dfsb   |
| 9  | <a href="#">c3dkaA_</a> | <br>Alignment |  | 97.9       | 9      | <b>PDB header:</b> unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> dinb-like protein;<br><b>PDBTitle:</b> crystal structure of a dinb-like protein (yjoa, bsu12410) from2 bacillus subtilis at 2.30 a resolution                 |
| 10 | <a href="#">c3cexB_</a> | <br>Alignment |  | 97.8       | 14     | <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 conserved protein of locus ef_3021 from2 enterococcus faecalis     |
| 11 | <a href="#">c3di5A_</a> | <br>Alignment |  | 97.7       | 11     | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> dinb-like protein;<br><b>PDBTitle:</b> crystal structure of a dinb-like protein (bce_4655) from bacillus2 cereus atcc 10987 at 2.01 a resolution         |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | <a href="#">c4n6cB_</a> | Alignment |              | 97.7 | 9  | <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 b1rzq2 protein from streptococcus pneumoniae.2 northeast structural genomics consortium (nesg) target spr36. |
| 13 | <a href="#">c2yqyB_</a> | Alignment |              | 97.6 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical protein ttha0303;<br><b>PDBTitle:</b> crystal structure of tt2238, a four-helix bundle protein  |
| 14 | <a href="#">d2hkva1</a> | Alignment |              | 97.6 | 11 | <b>Fold:</b> DinB/YfiT-like putative metalloenzymes<br><b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes<br><b>Family:</b> DinB-like  |
| 15 | <a href="#">c3e4xB_</a> | Alignment |              | 97.4 | 11 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B; <b>PDB Molecule:</b> apc36150;<br><b>PDBTitle:</b> crystal structure of putative metal-dependent hydrolases2 apc36150   |
| 16 | <a href="#">d2p1aa1</a> | Alignment |              | 97.2 | 12 | <b>Fold:</b> DinB/YfiT-like putative metalloenzymes<br><b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes<br><b>Family:</b> DinB-like  |
| 17 | <a href="#">c5cqyB_</a> | Alignment |              | 97.0 | 6  | <b>PDB header:</b> unknown function<br><b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of uncharacterized protein q8dvw2 from streptococcus2 agalactiae   |
| 18 | <a href="#">c5cofA_</a> | Alignment |              | 96.9 | 10 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89   |
| 19 | <a href="#">c2qe9B_</a> | Alignment |              | 96.8 | 10 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein yiza;<br><b>PDBTitle:</b> crystal structure of a putative metal-dependent hydrolase (yiza,2 bsu10800) from bacillus subtilis at 1.90 a resolution                                      |
| 20 | <a href="#">c6anrA_</a> | Alignment |              | 96.7 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> colibactin self-protection protein clbs;<br><b>PDBTitle:</b> crystal structure of a self resistance protein clbs from colibactin2 biosynthetic gene cluster  |
| 21 | <a href="#">c5wk0A_</a> | Alignment | not modelled | 70.5 | 8  | <b>PDB header:</b> unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> damage-inducible protein dinb;<br><b>PDBTitle:</b> crystal structure of the bacillithiol transferase bsta from2 staphylococcus aureus.  |
| 22 | <a href="#">d2fm9a1</a> | Alignment | not modelled | 14.5 | 19 | <b>Fold:</b> SipA N-terminal domain-like<br><b>Superfamily:</b> SipA N-terminal domain-like<br><b>Family:</b> SipA N-terminal domain-like  |
| 23 | <a href="#">c2jobA_</a> | Alignment | not modelled | 13.1 | 60 | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> antilipopolysaccharide factor;<br><b>PDBTitle:</b> solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site                                       |
| 24 | <a href="#">c4idiA_</a> | Alignment | not modelled | 12.7 | 6  | <b>PDB header:</b> protein binding<br><b>Chain:</b> A; <b>PDB Molecule:</b> oryza sativa rum1-related;<br><b>PDBTitle:</b> crystal structure of rum1-related protein from plasmodium yoelii,2 py06420  |
| 25 | <a href="#">c5uxtA_</a> | Alignment | not modelled | 10.4 | 67 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad;<br><b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad   |
| 26 | <a href="#">c2dkzA_</a> | Alignment | not modelled | 9.7  | 11 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein loc64762;<br><b>PDBTitle:</b> solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762  |
| 27 | <a href="#">c5uxtC_</a> | Alignment | not modelled | 9.1  | 67 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> C; <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad;<br><b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad   |
| 28 | <a href="#">c2k9xA_</a> | Alignment | not modelled | 9.1  | 20 | <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   |
| 29 | <a href="#">c5vszA_</a> | Alignment | not modelled | 6.3  | 13 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A; <b>PDB Molecule:</b> sacsin;<br><b>PDBTitle:</b> structure of the ubl domain of saccin mutant I78m  |

|    |                         |   |              |     |    |   |
|----|-------------------------|---|--------------|-----|----|---|
| 30 | <a href="#">c2damA_</a> |  Alignment  | not modelled | 6.0 | 44 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> etea protein;<br><b>PDBTitle:</b> solution structure of the novel identified uba-like domain2 in the n-terminal of human etea protein   |
| 31 | <a href="#">d1hk8a_</a> |  Alignment | not modelled | 5.7 | 25 | <b>Fold:</b> PFL-like glycy radical enzymes<br><b>Superfamily:</b> PFL-like glycy radical enzymes<br><b>Family:</b> Class III anaerobic ribonucleotide reductase NRDD subunit   |
| 32 | <a href="#">c1hk8A_</a> |  Alignment | not modelled | 5.7 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic ribonucleotide-triphosphate reductase;<br><b>PDBTitle:</b> structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dgtp |