











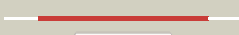

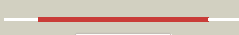







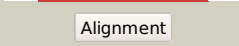
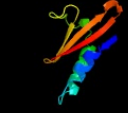



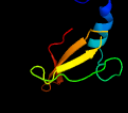


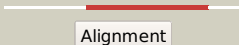
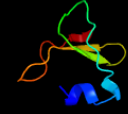
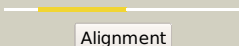

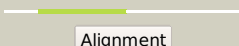

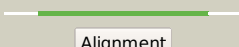

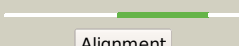
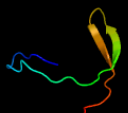
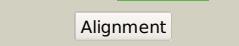
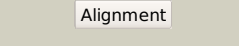
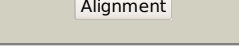
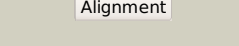

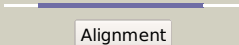
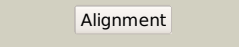


# Phyre2

|               |                              |
|---------------|------------------------------|
| Email         | mdejesus@rockefeller.edu     |
| Description   | RVBD2866_(-)_3177832_3178095 |
| Date          | Wed Aug 7 12:50:53 BST 2019  |
| Unique Job ID | Of1540e3691abe7c             |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">c3g5oC_</a> | <br>Alignment   |    | 99.9       | 100    | <b>PDB header:</b> toxin/antitoxin<br><b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein rv2866;<br><b>PDBTitle:</b> the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis |
| 2  | <a href="#">c2kheA_</a> | <br>Alignment   |    | 99.9       | 35     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> toxin-like protein;<br><b>PDBTitle:</b> solution structure of the bacterial toxin rele from thermus2 thermophilus hb8   |
| 3  | <a href="#">d1wmia1</a> | <br>Alignment   |    | 99.9       | 25     | <b>Fold:</b> RelE-like<br><b>Superfamily:</b> RelE-like<br><b>Family:</b> RelE-like   |
| 4  | <a href="#">c3kixy_</a> | <br>Alignment   |   | 99.9       | 22     | <b>PDB header:</b> ribosome<br><b>Chain:</b> Y: <b>PDB Molecule:</b><br><b>PDBTitle:</b> structure of rele nuclease bound to the 70s ribosome (postcleavage2 state; part 3 of 4)  |
| 5  | <a href="#">c3bpgD_</a> | <br>Alignment |  | 99.9       | 23     | <b>PDB header:</b> toxin<br><b>Chain:</b> D: <b>PDB Molecule:</b> toxin rele3;<br><b>PDBTitle:</b> crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii  |
| 6  | <a href="#">c2otrA_</a> | <br>Alignment |  | 99.6       | 19     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hp0892;<br><b>PDBTitle:</b> solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori    |
| 7  | <a href="#">c3oeiH_</a> | <br>Alignment |  | 99.3       | 29     | <b>PDB header:</b> toxin, protein binding<br><b>Chain:</b> H: <b>PDB Molecule:</b> relk (toxin rv3358);<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)                                  |
| 8  | <a href="#">d2a6sa1</a> | <br>Alignment |  | 99.2       | 24     | <b>Fold:</b> RelE-like<br><b>Superfamily:</b> RelE-like<br><b>Family:</b> YoeB/Txe-like   |
| 9  | <a href="#">d1z8ma1</a> | <br>Alignment |  | 99.1       | 19     | <b>Fold:</b> RelE-like<br><b>Superfamily:</b> RelE-like<br><b>Family:</b> RelE-like   |
| 10 | <a href="#">c4q2uH_</a> | <br>Alignment |  | 98.9       | 16     | <b>PDB header:</b> toxin/toxin repressor<br><b>Chain:</b> H: <b>PDB Molecule:</b> mrna interferase yafq;<br><b>PDBTitle:</b> crystal structure of the e. coli dinj-yafq toxin-antitoxin complex   |
| 11 | <a href="#">c5cegB_</a> | <br>Alignment |  | 98.7       | 20     | <b>PDB header:</b> toxin<br><b>Chain:</b> B: <b>PDB Molecule:</b> plasmid stabilization system;<br><b>PDBTitle:</b> x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum   |

|    |                         |   |   |      |    |  |
|----|-------------------------|---|---|------|----|--|
| 12 | <a href="#">c5cw7H_</a> |  Alignment   |    | 97.9 | 23 | <b>PDB header:</b> toxin<br><b>Chain:</b> H: <b>PDB Molecule:</b> plasmid stabilization protein pare;<br><b>PDBTitle:</b> crystal structure of the paaa2-pare2 antitoxin-toxin complex   |
| 13 | <a href="#">c3kxeB_</a> |  Alignment   |    | 97.9 | 23 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> toxin protein pare-1;<br><b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex  |
| 14 | <a href="#">c4mctD_</a> |  Alignment   |    | 97.5 | 18 | <b>PDB header:</b> toxin<br><b>Chain:</b> D: <b>PDB Molecule:</b> killer protein;<br><b>PDBTitle:</b> p. vulgaris higba structure, crystal form 1  |
| 15 | <a href="#">c5ja9D_</a> |  Alignment   |    | 97.0 | 17 | <b>PDB header:</b> toxin<br><b>Chain:</b> D: <b>PDB Molecule:</b> toxin higb-2;<br><b>PDBTitle:</b> crystal structure of the higb2 toxin in complex with nb6   |
| 16 | <a href="#">c6f8sD_</a> |  Alignment   |    | 92.8 | 21 | <b>PDB header:</b> toxin<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative killer protein;<br><b>PDBTitle:</b> toxin-antitoxin complex grata   |
| 17 | <a href="#">c2kruA_</a> |  Alignment   |   | 77.6 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b;<br><b>PDBTitle:</b> solution nmr structure of the pcpr_red domain of light-independent2 protochlorophyllide reductase subunit b from chlorobium tepidum.3 northeast structural genomics consortium target ctr69a                     |
| 18 | <a href="#">c2I09A_</a> |  Alignment |  | 69.9 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asr4154 protein;<br><b>PDBTitle:</b> solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143   |
| 19 | <a href="#">c5ifgC_</a> |  Alignment |  | 57.6 | 17 | <b>PDB header:</b> hydrolase/antitoxin<br><b>Chain:</b> C: <b>PDB Molecule:</b> mrna interferase higb;<br><b>PDBTitle:</b> crystal structure of higa-higb complex from e. coli   |
| 20 | <a href="#">c4b2gB_</a> |  Alignment |  | 51.8 | 17 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> gh3-1 auxin conjugating enzyme;<br><b>PDBTitle:</b> crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis   |
| 21 | <a href="#">c6avhA_</a> |  Alignment | not modelled  | 51.7 | 14 | <b>PDB header:</b> ligase, plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gh3.15 acyl acid amido synthetase;<br><b>PDBTitle:</b> gh3.15 acyl acid amido synthetase   |
| 22 | <a href="#">c4ewvB_</a> |  Alignment | not modelled  | 47.3 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 4-substituted benzoates-glutamate ligase gh3.12;<br><b>PDBTitle:</b> crystal structure of gh3.12 in complex with ampcpp   |
| 23 | <a href="#">c4eplA_</a> |  Alignment | not modelled  | 46.2 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> jasmonic acid-amido synthetase jar1;<br><b>PDBTitle:</b> crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile  |
| 24 | <a href="#">c5kodA_</a> |  Alignment | not modelled  | 40.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-acetic acid-amido synthetase gh3.5;<br><b>PDBTitle:</b> crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana   |
| 25 | <a href="#">c2ynmD_</a> |  Alignment | not modelled  | 15.8 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b;<br><b>PDBTitle:</b> structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a |
| 26 | <a href="#">c2lc0A_</a> |  Alignment | not modelled  | 15.0 | 9  | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein tb39.8;<br><b>PDBTitle:</b> rv0020c_ nter structure   |
| 27 | <a href="#">c2apnA_</a> |  Alignment | not modelled  | 11.8 | 22 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein hi1723;<br><b>PDBTitle:</b> hi1723 solution structure  |
|    |                         |   |   |      |    | <b>PDB header:</b> hydrolase   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 28 | <a href="#">c4le6B_</a> | Alignment | not modelled | 11.8 | 13 | <b>Chain:</b> B: <b>PDB Molecule:</b> organophosphorus hydrolase;<br><b>PDBTitle:</b> crystal structure of the phosphotriesterase ophc2 from pseudomonas2 pseudoalcaligenes   |
| 29 | <a href="#">c4xukB_</a> | Alignment | not modelled | 11.0 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative hydrolase;<br><b>PDBTitle:</b> crystal structure of hydrolase aboph in beta lactamase superfamily  |
| 30 | <a href="#">d1ugja_</a> | Alignment | not modelled | 8.2  | 12 | <b>Fold:</b> PRC-barrel domain<br><b>Superfamily:</b> PRC-barrel domain<br><b>Family:</b> RIKEN cDNA 2310057j16 protein (KIAA1543)  |
| 31 | <a href="#">c2lf0A_</a> | Alignment | not modelled | 7.2  | 22 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yibI;<br><b>PDBTitle:</b> solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scattering, nesg4 target sfr339/ocsp target sf3636 |
| 32 | <a href="#">d1p9ea_</a> | Alignment | not modelled | 7.2  | 17 | <b>Fold:</b> Metallo-hydrolase/oxidoreductase<br><b>Superfamily:</b> Metallo-hydrolase/oxidoreductase<br><b>Family:</b> Methyl parathion hydrolase  |
| 33 | <a href="#">c1p9eA_</a> | Alignment | not modelled | 7.2  | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyl parathion hydrolase;<br><b>PDBTitle:</b> crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3   |
| 34 | <a href="#">c1x60A_</a> | Alignment | not modelled | 6.7  | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sporulation-specific n-acetylmuramoyl-l-alanine<br><b>PDBTitle:</b> solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc  |
| 35 | <a href="#">c5m5cC_</a> | Alignment | not modelled | 6.6  | 17 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> calmodulin-regulated spectrin-associated protein 1;<br><b>PDBTitle:</b> mechanism of microtubule minus-end recognition and protection by2 camsap proteins   |
| 36 | <a href="#">c2h5gA_</a> | Alignment | not modelled | 5.8  | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> delta 1-pyrroline-5-carboxylate synthetase;<br><b>PDBTitle:</b> crystal structure of human pyrroline-5-carboxylate synthetase  |
| 37 | <a href="#">c6fkfd_</a> | Alignment | not modelled | 5.5  | 21 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit beta, chloroplastic;<br><b>PDBTitle:</b> chloroplast f1fo conformation 1  |