


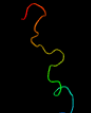




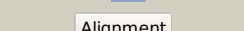
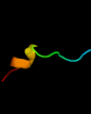
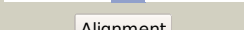

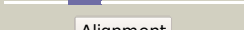
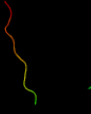


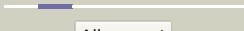

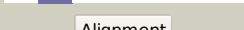
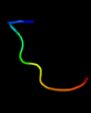


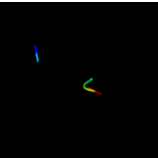



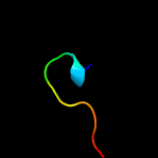
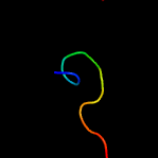
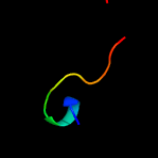

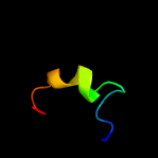


# Phyre2

|               |                                  |
|---------------|----------------------------------|
| Email         | mdejesus@rockefeller.edu         |
| Description   | RVBD3847 (-)<br>_4321716_4322249 |
| Date          | Sat Aug 10 22:05:02 BST<br>2019  |
| Unique Job ID | 9ffabde378e94df2                 |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">d2diga1</a> |  Alignment   |    | 46.9       | 50     | <b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> Tudor/PWWP/MBT<br><b>Family:</b> Tudor domain   |
| 2  | <a href="#">c2digA_</a> |  Alignment   |    | 35.9       | 46     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> lamin-b receptor;<br><b>PDBTitle:</b> solusion structure of the tudor domain of human lamin-b2 receptor   |
| 3  | <a href="#">c6bvvb_</a> |  Alignment   |    | 32.6       | 56     | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein w;<br><b>PDBTitle:</b> nipah virus w protein c-terminus in complex with importin alpha 3  |
| 4  | <a href="#">c2qe9B_</a> |  Alignment   |    | 26.6       | 19     | <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                   |
| 5  | <a href="#">c6bwbB_</a> |  Alignment |  | 25.9       | 56     | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein w;<br><b>PDBTitle:</b> hendra virus w protein c-terminus in complex with importin alpha 32 crystal form 3   |
| 6  | <a href="#">c6bwaB_</a> |  Alignment |  | 24.9       | 56     | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein w;<br><b>PDBTitle:</b> hendra virus w protein c-terminus in complex with importin alpha 32 crystal form 2   |
| 7  | <a href="#">c6hc2L_</a> |  Alignment |  | 19.7       | 38     | <b>PDB header:</b> cell cycle<br><b>Chain:</b> L: <b>PDB Molecule:</b> nuclear mitotic apparatus protein 1;<br><b>PDBTitle:</b> crystal structure of numa/lgn hetero-hexamers   |
| 8  | <a href="#">c3oqvA_</a> |  Alignment |  | 17.8       | 44     | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> albc;<br><b>PDBTitle:</b> albc, a cyclodi peptide synthase from streptomyces noursei  |
| 9  | <a href="#">c4m8rA_</a> |  Alignment |  | 16.1       | 31     | <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 duf4784 family protein (baccac_01631) from2 bacteroides caccae atcc 43185 at 2.50 a resolution |
| 10 | <a href="#">d2jldq1</a> |  Alignment |  | 15.1       | 50     | <b>Fold:</b> PB2 C-terminal domain-like<br><b>Superfamily:</b> PB2 C-terminal domain-like<br><b>Family:</b> PB2 C-terminal domain-like  |
| 11 | <a href="#">c2omIA_</a> |  Alignment |  | 12.9       | 23     | <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  |

|    |                         |           |   |      |    |  |
|----|-------------------------|-----------|---|------|----|--|
| 12 | <a href="#">c5okzj_</a> | Alignment |     | 11.3 | 86 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> J; <b>PDB Molecule:</b> m-phase phosphoprotein 6 homolog;<br><b>PDBTitle:</b> crystal structure of the mpp6 exosome complex  |
| 13 | <a href="#">c3oqhB_</a> | Alignment |    | 11.0 | 67 | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> putative uncharacterized protein yvmc;<br><b>PDBTitle:</b> crystal structure of b. licheniformis cdps yvmc-blic   |
| 14 | <a href="#">d2fb5a1</a> | Alignment |    | 10.9 | 32 | <b>Fold:</b> Yoij-like<br><b>Superfamily:</b> Yoij-like<br><b>Family:</b> Yoij-like  |
| 15 | <a href="#">c5zt0H_</a> | Alignment |    | 10.2 | 58 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> H; <b>PDB Molecule:</b> protein phosphatase 1 regulatory subunit 3b;<br><b>PDBTitle:</b> crystal structure of protein phosphatase 1 complexed with pp1 binding2 domain of gl   |
| 16 | <a href="#">c5zt0J_</a> | Alignment |    | 10.2 | 58 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> J; <b>PDB Molecule:</b> protein phosphatase 1 regulatory subunit 3b;<br><b>PDBTitle:</b> crystal structure of protein phosphatase 1 complexed with pp1 binding2 domain of gl   |
| 17 | <a href="#">c5zt0G_</a> | Alignment |   | 10.2 | 58 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> G; <b>PDB Molecule:</b> protein phosphatase 1 regulatory subunit 3b;<br><b>PDBTitle:</b> crystal structure of protein phosphatase 1 complexed with pp1 binding2 domain of gl   |
| 18 | <a href="#">c5zt0I_</a> | Alignment |  | 10.2 | 58 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> I; <b>PDB Molecule:</b> protein phosphatase 1 regulatory subunit 3b;<br><b>PDBTitle:</b> crystal structure of protein phosphatase 1 complexed with pp1 binding2 domain of gl   |
| 19 | <a href="#">c6ez3C_</a> | Alignment |  | 10.2 | 56 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> C; <b>PDB Molecule:</b> cyclo(l-leucyl-l-leucyl) synthase;<br><b>PDBTitle:</b> structure of cdps from staphylococcus haemolyticus  |
| 20 | <a href="#">c3ktbD_</a> | Alignment |  | 10.1 | 21 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D; <b>PDB Molecule:</b> arsenical resistance operon trans-acting repressor;<br><b>PDBTitle:</b> crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482 |
| 21 | <a href="#">d1vj1a1</a> | Alignment | not modelled  | 9.6  | 32 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain  |
| 22 | <a href="#">c2x9qA_</a> | Alignment | not modelled  | 9.0  | 50 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> cyclodipeptide synthetase;<br><b>PDBTitle:</b> structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.    |
| 23 | <a href="#">d1jmx1</a>  | Alignment | not modelled  | 9.0  | 31 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2  |
| 24 | <a href="#">c3wzhA_</a> | Alignment | not modelled  | 9.0  | 80 | <b>PDB header:</b> transcription<br><b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein af_1864;<br><b>PDBTitle:</b> crystal structure of afcsx3   |
| 25 | <a href="#">d1ynya1</a> | Alignment | not modelled  | 8.7  | 14 | <b>Fold:</b> Composite domain of metallo-dependent hydrolases<br><b>Superfamily:</b> Composite domain of metallo-dependent hydrolases<br><b>Family:</b> Hydantoinase (dihydropyrimidinase)   |
| 26 | <a href="#">d1pbya1</a> | Alignment | not modelled  | 8.5  | 28 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2  |
| 27 | <a href="#">c1m0gA_</a> | Alignment | not modelled  | 8.5  | 78 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> metallothionein mt_nc;<br><b>PDBTitle:</b> solution structure of the alpha domain of mt_nc   |
| 28 | <a href="#">d1m0ga_</a> | Alignment | not modelled  | 8.5  | 78 | <b>Fold:</b> Metallothionein<br><b>Superfamily:</b> Metallothionein<br><b>Family:</b> Metallothionein  |

|    |                         |           |              |     |    |   |
|----|-------------------------|-----------|--------------|-----|----|---|
| 29 | <a href="#">d2i4sa1</a> | Alignment | not modelled | 7.3 | 14 | <b>Fold:</b> PDZ domain-like<br><b>Superfamily:</b> PDZ domain-like<br><b>Family:</b> EpsC C-terminal domain-like   |
| 30 | <a href="#">c3e74D</a>  | Alignment | not modelled | 6.9 | 37 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D; <b>PDB Molecule:</b> allantoinase;<br><b>PDBTitle:</b> crystal structure of e. coli allantoinase with iron ions at the metal2 center   |
| 31 | <a href="#">c4e82B</a>  | Alignment | not modelled | 6.9 | 58 | <b>PDB header:</b> antimicrobial protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> defensin-5;<br><b>PDBTitle:</b> crystal structure of monomeric variant of human alpha-defensin 5, hd52 (glu21eme mutant)  |
| 32 | <a href="#">c4e82A</a>  | Alignment | not modelled | 6.9 | 58 | <b>PDB header:</b> antimicrobial protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> defensin-5;<br><b>PDBTitle:</b> crystal structure of monomeric variant of human alpha-defensin 5, hd52 (glu21eme mutant)  |
| 33 | <a href="#">c1ecjB</a>  | Alignment | not modelled | 6.9 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> B; <b>PDB Molecule:</b> glutamine phosphoribosylpyrophosphate<br><b>PDBTitle:</b> escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer |
| 34 | <a href="#">c1z65A</a>  | Alignment | not modelled | 6.8 | 88 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> prion-like protein doppel;<br><b>PDBTitle:</b> mouse doppel 1-30 peptide   |
| 35 | <a href="#">d2at2a2</a> | Alignment | not modelled | 6.5 | 19 | <b>Fold:</b> ATC-like<br><b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase<br><b>Family:</b> Aspartate/ornithine carbamoyltransferase  |
| 36 | <a href="#">d1qw1a1</a> | Alignment | not modelled | 6.4 | 30 | <b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> C-terminal domain of transcriptional repressors<br><b>Family:</b> FeoA-like   |
| 37 | <a href="#">c4m5dA</a>  | Alignment | not modelled | 6.1 | 57 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> u3 small nucleolar rna-associated protein 22;<br><b>PDBTitle:</b> crystal structure of the utp22 and rrp7 complex from saccharomyces2 cerevisiae                    |
| 38 | <a href="#">c4rv7C</a>  | Alignment | not modelled | 6.1 | 42 | <b>PDB header:</b> transferase<br><b>Chain:</b> C; <b>PDB Molecule:</b> diadenylate cyclase;<br><b>PDBTitle:</b> characterization of an essential diadenylate cyclase   |
| 39 | <a href="#">d3bzka1</a> | Alignment | not modelled | 5.8 | 33 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> RuvA domain 2-like<br><b>Family:</b> Tex HhH-containing domain-like   |
| 40 | <a href="#">c2hmcA</a>  | Alignment | not modelled | 5.7 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens      |
| 41 | <a href="#">c3cw4A</a>  | Alignment | not modelled | 5.5 | 50 | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> polymerase basic protein 2;<br><b>PDBTitle:</b> large c-terminal domain of influenza a virus rna-dependent polymerase2 pb2  |