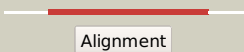

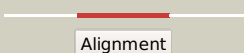

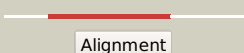

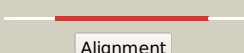



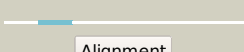
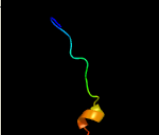

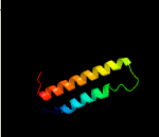
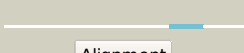
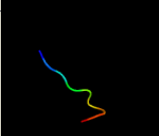

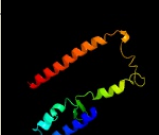

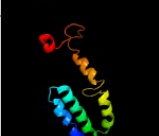

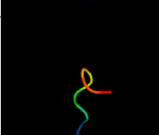


# Phyre2

|               |                               |
|---------------|-------------------------------|
| Email         | mdejesus@rockefeller.edu      |
| Description   | RVBD1459c_(-)_1644369_1646144 |
| Date          | Fri Aug 2 13:30:04 BST 2019   |
| Unique Job ID | 9d88150a2001f3ce              |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c5f15A_</a> |  Alignment   |    | 99.0       | 15     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase;<br><b>PDBTitle:</b> crystal structure of arnt from cupriavidus metallidurans bound to 2 undecaprenyl phosphate  |
| 2  | <a href="#">c6p25A_</a> |  Alignment   |    | 98.4       | 17     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dolichyl-phosphate-mannose--protein mannosyltransferase 1;<br><b>PDBTitle:</b> structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor |
| 3  | <a href="#">c6p2rB_</a> |  Alignment   |    | 98.1       | 16     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dolichyl-phosphate-mannose--protein mannosyltransferase 2;<br><b>PDBTitle:</b> structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor                        |
| 4  | <a href="#">c3wajA_</a> |  Alignment   |    | 97.8       | 14     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane oligosaccharyl transferase;<br><b>PDBTitle:</b> crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate                        |
| 5  | <a href="#">c3rceA_</a> |  Alignment |  | 96.9       | 11     | <b>PDB header:</b> transferase/peptide<br><b>Chain:</b> A: <b>PDB Molecule:</b> oligosaccharide transferase to n-glycosylate proteins;<br><b>PDBTitle:</b> bacterial oligosaccharyltransferase pglb  |
| 6  | <a href="#">c2kfvA_</a> |  Alignment |  | 36.0       | 26     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fk506-binding protein 3;<br><b>PDBTitle:</b> structure of the amino-terminal domain of human fk506-2 binding protein 3 / northeast structural genomics3 consortium target ht99a                              |
| 7  | <a href="#">c6adqP_</a> |  Alignment |  | 30.6       | 14     | <b>PDB header:</b> electron transport<br><b>Chain:</b> P: <b>PDB Molecule:</b> prokaryotic respiratory supercomplex associate factor 1<br><b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis  |
| 8  | <a href="#">d1ynjd1</a> |  Alignment |  | 30.2       | 22     | <b>Fold:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase<br><b>Superfamily:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase<br><b>Family:</b> RNA-polymerase beta-prime  |
| 9  | <a href="#">c5ir6A_</a> |  Alignment |  | 26.7       | 23     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> bd-type quinol oxidase subunit i;<br><b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans  |
| 10 | <a href="#">d2r6gf1</a> |  Alignment |  | 25.9       | 7      | <b>Fold:</b> MalF N-terminal region-like<br><b>Superfamily:</b> MalF N-terminal region-like<br><b>Family:</b> MalF N-terminal region-like  |
| 11 | <a href="#">c4g7oN_</a> |  Alignment |  | 25.5       | 25     | <b>PDB header:</b> transcription, transferase/dna<br><b>Chain:</b> N: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta';<br><b>PDBTitle:</b> crystal structure of thermus thermophilus transcription initiation2 complex containing 2 nt of rna                       |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 12 | <a href="#">c5xj0D_</a> | Alignment |              | 24.8 | 25 | <b>PDB header:</b> transferase/transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta';<br><b>PDBTitle:</b> t. thermophilus rna polymerase holoenzyme bound with gp39 and gp76   |
| 13 | <a href="#">c5x22D_</a> | Alignment |              | 18.9 | 25 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta';<br><b>PDBTitle:</b> crystal structure of thermus thermophilus transcription initiation2 complex with gpa and cmppcp  |
| 14 | <a href="#">dlzxa01</a> | Alignment |              | 18.5 | 15 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Actin-like ATPase domain<br><b>Family:</b> BadF/BadG/BcrA/BcrD-like   |
| 15 | <a href="#">d2e74b1</a> | Alignment |              | 16.7 | 16 | <b>Fold:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)<br><b>Superfamily:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)<br><b>Family:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 16 | <a href="#">dlzbsa2</a> | Alignment |              | 15.8 | 15 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Actin-like ATPase domain<br><b>Family:</b> BadF/BadG/BcrA/BcrD-like   |
| 17 | <a href="#">dlvf5b_</a> | Alignment |              | 15.2 | 16 | <b>Fold:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)<br><b>Superfamily:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)<br><b>Family:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 18 | <a href="#">dlq90d_</a> | Alignment |              | 12.8 | 10 | <b>Fold:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)<br><b>Superfamily:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)<br><b>Family:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 19 | <a href="#">dlr9fa_</a> | Alignment |              | 11.5 | 25 | <b>Fold:</b> Tombusvirus P19 core protein, VP19<br><b>Superfamily:</b> Tombusvirus P19 core protein, VP19<br><b>Family:</b> Tombusvirus P19 core protein, VP19  |
| 20 | <a href="#">c3e1kj_</a> | Alignment |              | 11.5 | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> J: <b>PDB Molecule:</b> lactose regulatory protein lac9;<br><b>PDBTitle:</b> crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p  |
| 21 | <a href="#">c3e1kl_</a> | Alignment | not modelled | 11.5 | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> L: <b>PDB Molecule:</b> lactose regulatory protein lac9;<br><b>PDBTitle:</b> crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p  |
| 22 | <a href="#">c3e1kB_</a> | Alignment | not modelled | 11.5 | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> lactose regulatory protein lac9;<br><b>PDBTitle:</b> crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p  |
| 23 | <a href="#">c3e1kD_</a> | Alignment | not modelled | 11.5 | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> lactose regulatory protein lac9;<br><b>PDBTitle:</b> crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p  |
| 24 | <a href="#">c3e1kH_</a> | Alignment | not modelled | 11.5 | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> H: <b>PDB Molecule:</b> lactose regulatory protein lac9;<br><b>PDBTitle:</b> crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p  |
| 25 | <a href="#">c3e1kP_</a> | Alignment | not modelled | 11.5 | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> P: <b>PDB Molecule:</b> lactose regulatory protein lac9;<br><b>PDBTitle:</b> crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p  |
| 26 | <a href="#">c3e1kN_</a> | Alignment | not modelled | 11.5 | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> N: <b>PDB Molecule:</b> lactose regulatory protein lac9;<br><b>PDBTitle:</b> crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p  |
| 27 | <a href="#">c3e1kF_</a> | Alignment | not modelled | 11.5 | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> F: <b>PDB Molecule:</b> lactose regulatory protein lac9;<br><b>PDBTitle:</b> crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p  |
| 28 | <a href="#">c3qqcA_</a> | Alignment | not modelled | 11.1 | 25 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit b, dna-directed rna<br><b>PDBTitle:</b> crystal structure of archaeal spt4/5 bound to the rnap clamp domain<br><b>PDB header:</b> transcription, transferase/dna/rna              |

|    |                          |           |              |     |    |  |
|----|--------------------------|-----------|--------------|-----|----|--|
| 29 | <a href="#">c3aoiN_</a>  | Alignment | not modelled | 9.4 | 25 | <b>Chain:</b> N: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta';<br><b>PDBTitle:</b> rna polymerase-gfh1 complex (crystal type 2)  |
| 30 | <a href="#">c4iuwA_</a>  | Alignment | not modelled | 8.8 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> neutral endopeptidase;<br><b>PDBTitle:</b> crystal structure of pepo from lactobacillus rhamnosis hn001 (dr20)   |
| 31 | <a href="#">c3aoil_</a>  | Alignment | not modelled | 8.7 | 25 | <b>PDB header:</b> transcription, transferase/dna/rna<br><b>Chain:</b> I: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta';<br><b>PDBTitle:</b> rna polymerase-gfh1 complex (crystal type 2)   |
| 32 | <a href="#">c2o5jN_</a>  | Alignment | not modelled | 8.1 | 25 | <b>PDB header:</b> transferase/dna-rna hybrid<br><b>Chain:</b> N: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain;<br><b>PDBTitle:</b> crystal structure of the t. thermophilus rnap polymerase elongation2 complex with the ntp substrate analog |
| 33 | <a href="#">c2owrD_</a>  | Alignment | not modelled | 8.0 | 54 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> uracil-dna glycosylase;<br><b>PDBTitle:</b> crystal structure of vaccinia virus uracil-dna glycosylase   |
| 34 | <a href="#">d1smyd_</a>  | Alignment | not modelled | 7.9 | 25 | <b>Fold:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase<br><b>Superfamily:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase<br><b>Family:</b> RNA-polymerase beta-prime  |
| 35 | <a href="#">c3fmtF_</a>  | Alignment | not modelled | 7.8 | 40 | <b>PDB header:</b> replication inhibitor/dna<br><b>Chain:</b> F: <b>PDB Molecule:</b> protein seqa;<br><b>PDBTitle:</b> crystal structure of seqa bound to dna   |
| 36 | <a href="#">d1rxra1</a>  | Alignment | not modelled | 7.3 | 50 | <b>Fold:</b> Ribbon-helix-helix<br><b>Superfamily:</b> Ribbon-helix-helix<br><b>Family:</b> SeqA N-terminal domain-like  |
| 37 | <a href="#">c1rxrD_</a>  | Alignment | not modelled | 7.3 | 50 | <b>PDB header:</b> replication inhibitor<br><b>Chain:</b> D: <b>PDB Molecule:</b> seqa protein;<br><b>PDBTitle:</b> crystal structure of a dna-binding protein   |
| 38 | <a href="#">c3dwbA_</a>  | Alignment | not modelled | 7.0 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endothelin-converting enzyme 1;<br><b>PDBTitle:</b> structure of human ece-1 complexed with phosphoramidon   |
| 39 | <a href="#">c5nn7A_</a>  | Alignment | not modelled | 6.9 | 43 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase;<br><b>PDBTitle:</b> kshv uracil-dna glycosylase, apo form  |
| 40 | <a href="#">c6eznF_</a>  | Alignment | not modelled | 6.7 | 10 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein<br><b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex   |
| 41 | <a href="#">c4y0lA_</a>  | Alignment | not modelled | 6.4 | 44 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein mmp111;<br><b>PDBTitle:</b> mycobacterial membrane protein mmp11d2  |
| 42 | <a href="#">c3w52A_</a>  | Alignment | not modelled | 6.4 | 30 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease 2;<br><b>PDBTitle:</b> zinc-dependent bifunctional nuclease   |
| 43 | <a href="#">c3sngA_</a>  | Alignment | not modelled | 6.4 | 30 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nuclease;<br><b>PDBTitle:</b> x-ray structure of fully glycosylated bifunctional nuclease tbn1 from2 solanum lycopersicum (tomato)   |
| 44 | <a href="#">d2hu7a1</a>  | Alignment | not modelled | 6.3 | 56 | <b>Fold:</b> 7-bladed beta-propeller<br><b>Superfamily:</b> Peptidase/esterase 'gauge' domain<br><b>Family:</b> Acylamino-acid-releasing enzyme, N-terminal donain   |
| 45 | <a href="#">c3gwgqB_</a> | Alignment | not modelled | 6.2 | 25 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-serine deaminase;<br><b>PDBTitle:</b> crystal structure of a putative d-serine deaminase (bx_e_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution                             |
| 46 | <a href="#">c5tw1D_</a>  | Alignment | not modelled | 6.2 | 50 | <b>PDB header:</b> transcription activator/transferase/dna<br><b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta';<br><b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA  |
| 47 | <a href="#">c2o5iD_</a>  | Alignment | not modelled | 6.1 | 25 | <b>PDB header:</b> transferase/dna-rna hybrid<br><b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain;<br><b>PDBTitle:</b> crystal structure of the t. thermophilus rna polymerase elongation2 complex                                |
| 48 | <a href="#">c5z3dA_</a>  | Alignment | not modelled | 6.1 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase 15-related protein;<br><b>PDBTitle:</b> glycosidase f290y  |
| 49 | <a href="#">c1qfqB_</a>  | Alignment | not modelled | 6.0 | 55 | <b>PDB header:</b> transcription/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> 36-mer n-terminal peptide of the n protein;<br><b>PDBTitle:</b> bacteriophage lambda n-protein-nutboxb-rna complex   |
| 50 | <a href="#">d1ak0a_</a>  | Alignment | not modelled | 5.8 | 10 | <b>Fold:</b> Phospholipase C/P1 nuclease<br><b>Superfamily:</b> Phospholipase C/P1 nuclease<br><b>Family:</b> P1 nuclease  |
| 51 | <a href="#">c4qiwA_</a>  | Alignment | not modelled | 5.7 | 25 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase;<br><b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis  |
| 52 | <a href="#">c6iu3A_</a>  | Alignment | not modelled | 5.7 | 9  | <b>PDB header:</b> metal transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> vit11;<br><b>PDBTitle:</b> crystal structure of iron transporter vit1 with zinc ions   |
| 53 | <a href="#">d1dmta_</a>  | Alignment | not modelled | 5.7 | 14 | <b>Fold:</b> Zincin-like<br><b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain<br><b>Family:</b> Neutral endopeptidase (nepriysin)   |
| 54 | <a href="#">c2mckA_</a>  | Alignment | not modelled | 5.6 | 37 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polyprotein;<br><b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for murine2 norovirus cr6 ns1/2 protein<br><b>PDB header:</b> cell cycle                           |

|    |                         |           |              |     |    |   |
|----|-------------------------|-----------|--------------|-----|----|---|
| 55 | <a href="#">c2mmuA_</a> | Alignment | not modelled | 5.6 | 40 | <b>Chain:</b> A; <b>PDB Molecule:</b> cell division protein crga; <b>PDBTitle:</b> structure of crga, a cell division structural and regulatory protein2 from mycobacterium tuberculosis, in lipid bilayers |
| 56 | <a href="#">c5lmxA_</a> | Alignment | not modelled | 5.4 | 25 | <b>PDB header:</b> transcription<br><b>Chain:</b> A; <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa190; <b>PDBTitle:</b> monomeric rna polymerase i at 4.9 a resolution                     |
| 57 | <a href="#">c1zzaA_</a> | Alignment | not modelled | 5.3 | 21 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> stannin; <b>PDBTitle:</b> solution nmr structure of the membrane protein stannin   |
| 58 | <a href="#">c5fbfA_</a> | Alignment | not modelled | 5.2 | 30 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> nuclease s1; <b>PDBTitle:</b> s1 nuclease from aspergillus oryzae in complex with two molecules of 2'-deoxycytidine-5'-monophosphate  |
| 59 | <a href="#">c1i6hA_</a> | Alignment | not modelled | 5.2 | 25 | <b>PDB header:</b> transcription/dna-rna hybrid<br><b>Chain:</b> A; <b>PDB Molecule:</b> dna-directed rna polymerase ii largest subunit; <b>PDBTitle:</b> rna polymerase ii elongation complex              |
| 60 | <a href="#">c5fjaA_</a> | Alignment | not modelled | 5.1 | 38 | <b>PDB header:</b> transcription<br><b>Chain:</b> A; <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc1; <b>PDBTitle:</b> cryo-em structure of yeast rna polymerase iii at 4.7 a             |
| 61 | <a href="#">d1alna2</a> | Alignment | not modelled | 5.1 | 20 | <b>Fold:</b> Cytidine deaminase-like<br><b>Superfamily:</b> Cytidine deaminase-like<br><b>Family:</b> Cytidine deaminase  |