



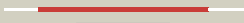
















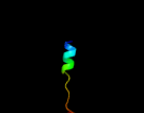


# Phyre2

|               |                                |
|---------------|--------------------------------|
| Email         | spiwokv@vscht.cz               |
| Description   | tbn1                           |
| Date          | Sun Oct 7 15:47:42<br>BST 2018 |
| Unique Job ID | 888c645d580a078d               |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c3sngA_</a> | <br>Alignment   |    | 100.0      | 100    | <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)       |
| 2  | <a href="#">c3w52A_</a> | <br>Alignment   |    | 100.0      | 54     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease 2;<br><b>PDBTitle:</b> zinc-dependent bifunctional nuclease   |
| 3  | <a href="#">dlak0a_</a> | <br>Alignment   |    | 100.0      | 29     | <b>Fold:</b> Phospholipase C/P1 nuclease<br><b>Superfamily:</b> Phospholipase C/P1 nuclease<br><b>Family:</b> P1 nuclease  |
| 4  | <a href="#">c5fbfA_</a> | <br>Alignment   |    | 100.0      | 29     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nuclease s1;<br><b>PDBTitle:</b> s1 nuclease from aspergillus oryzae in complex with two molecules of2 2'-deoxycytidine-5'-monophosphate |
| 5  | <a href="#">dlah7a_</a> | <br>Alignment |  | 100.0      | 15     | <b>Fold:</b> Phospholipase C/P1 nuclease<br><b>Superfamily:</b> Phospholipase C/P1 nuclease<br><b>Family:</b> Phospholipase C  |
| 6  | <a href="#">dlkhoal</a> | <br>Alignment |  | 98.5       | 17     | <b>Fold:</b> Phospholipase C/P1 nuclease<br><b>Superfamily:</b> Phospholipase C/P1 nuclease<br><b>Family:</b> Phospholipase C  |
| 7  | <a href="#">dlolpa1</a> | <br>Alignment |  | 98.4       | 19     | <b>Fold:</b> Phospholipase C/P1 nuclease<br><b>Superfamily:</b> Phospholipase C/P1 nuclease<br><b>Family:</b> Phospholipase C  |
| 8  | <a href="#">clolpB_</a> | <br>Alignment |  | 97.4       | 18     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alpha-toxin;<br><b>PDBTitle:</b> alpha toxin from clostridium absonum  |
| 9  | <a href="#">clgygA_</a> | <br>Alignment |  | 97.3       | 21     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase c;<br><b>PDBTitle:</b> r32 closed form of alpha-toxin from clostridium perfringens2 strain cer89I43                        |
| 10 | <a href="#">dlcalal</a> | <br>Alignment |  | 97.0       | 18     | <b>Fold:</b> Phospholipase C/P1 nuclease<br><b>Superfamily:</b> Phospholipase C/P1 nuclease<br><b>Family:</b> Phospholipase C  |
| 11 | <a href="#">c4xpmA_</a> | <br>Alignment |  | 40.4       | 30     | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein meh1;<br><b>PDBTitle:</b> crystal structure of ego-tc  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 12 | <a href="#">c2gq1A_</a> | Alignment |              | 16.9 | 8  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fructose-1,6-bisphosphatase;<br><b>PDBTitle:</b> crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions   |
| 13 | <a href="#">c2rhsB_</a> | Alignment |              | 15.3 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain;<br><b>PDBTitle:</b> phers from staphylococcus haemolyticus- rational protein engineering2 and inhibitor studies   |
| 14 | <a href="#">c3d0wD_</a> | Alignment |              | 14.2 | 12 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> D: <b>PDB Molecule:</b> yflh protein;<br><b>PDBTitle:</b> crystal structure of yflh protein from bacillus subtilis. northeast2 structural genomics consortium target sr326  |
| 15 | <a href="#">c1fpvA_</a> | Alignment |              | 10.4 | 17 | <b>PDB header:</b> virus<br><b>Chain:</b> A: <b>PDB Molecule:</b> feline panleukopenia virus (strain b) viral<br><b>PDBTitle:</b> structure determination of feline panleukopenia virus empty2 particles  |
| 16 | <a href="#">c5fugl_</a> | Alignment |              | 9.6  | 45 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> I: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 72 homolog;<br><b>PDBTitle:</b> crystal structure of a human yl1-h2a.z-h2b complex  |
| 17 | <a href="#">d2qzga1</a> | Alignment |              | 9.6  | 18 | <b>Fold:</b> Bromodomain-like<br><b>Superfamily:</b> Ta0600-like<br><b>Family:</b> Ta0600-like  |
| 18 | <a href="#">c2eouA_</a> | Alignment |              | 9.6  | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 473;<br><b>PDBTitle:</b> solution structure of the c2h2 type zinc finger (region 370-2 400) of human zinc finger protein 473  |
| 19 | <a href="#">c2g8gA_</a> | Alignment |              | 9.5  | 22 | <b>PDB header:</b> virus<br><b>Chain:</b> A: <b>PDB Molecule:</b> capsid;<br><b>PDBTitle:</b> structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4   |
| 20 | <a href="#">c4p71B_</a> | Alignment |              | 9.0  | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanine--trna ligase beta subunit;<br><b>PDBTitle:</b> apo phers from p. aeruginosa  |
| 21 | <a href="#">d1jcb6</a>  | Alignment | not modelled | 8.0  | 35 | <b>Fold:</b> PheT/TiIS domain<br><b>Superfamily:</b> PheT/TiIS domain<br><b>Family:</b> B3/B4 domain of PheRS, PheT   |
| 22 | <a href="#">c3h3gB_</a> | Alignment | not modelled | 7.9  | 45 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> parathyroid hormone-related protein;<br><b>PDBTitle:</b> crystal structure of the extracellular domain of the human parathyroid2 hormone receptor (pth1r) in complex with parathyroid hormone-related3 protein (pthrp) |
| 23 | <a href="#">d2qsba1</a> | Alignment | not modelled | 7.9  | 22 | <b>Fold:</b> Bromodomain-like<br><b>Superfamily:</b> Ta0600-like<br><b>Family:</b> Ta0600-like  |
| 24 | <a href="#">c3ikoC_</a> | Alignment | not modelled | 7.5  | 9  | <b>PDB header:</b> structural protein, protein transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> nucleoporin nup84;<br><b>PDBTitle:</b> crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoporin complex   |
| 25 | <a href="#">c4qc8A_</a> | Alignment | not modelled | 7.4  | 15 | <b>PDB header:</b> virus<br><b>Chain:</b> A: <b>PDB Molecule:</b> vp2;<br><b>PDBTitle:</b> structural annotation of pathogenic bovine parvovirus-1  |
| 26 | <a href="#">d1m5ha1</a> | Alignment | not modelled | 7.3  | 29 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase<br><b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase   |
| 27 | <a href="#">d1mvma_</a> | Alignment | not modelled | 7.3  | 11 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> ssDNA viruses<br><b>Family:</b> Parvoviridae-like VP   |
| 28 | <a href="#">d1spia_</a> | Alignment | not modelled | 6.9  | 17 | <b>Fold:</b> Carbohydrate phosphatase<br><b>Superfamily:</b> Carbohydrate phosphatase<br><b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like   |

|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
| 29 | <a href="#">c1zgxA_</a> | Alignment | not modelled | 6.8 | 12 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> guanylyl-specific ribonuclease sa;<br><b>PDBTitle:</b> crystal structure of ribonuclease mutant  |
| 30 | <a href="#">c5chlA_</a> | Alignment | not modelled | 6.8 | 45 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 72 homolog;<br><b>PDBTitle:</b> structural basis of h2a.z recognition by y11 histone chaperone2 component of srcap/swr1 chromatin remodeling complex |
| 31 | <a href="#">d1bk4a_</a> | Alignment | not modelled | 6.6 | 14 | <b>Fold:</b> Carbohydrate phosphatase<br><b>Superfamily:</b> Carbohydrate phosphatase<br><b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like  |
| 32 | <a href="#">d1c8da_</a> | Alignment | not modelled | 6.4 | 17 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> ssDNA viruses<br><b>Family:</b> Parvoviridae-like VP  |
| 33 | <a href="#">d1bh9a_</a> | Alignment | not modelled | 6.4 | 25 | <b>Fold:</b> Histone-fold<br><b>Superfamily:</b> Histone-fold<br><b>Family:</b> TBP-associated factors, TAFs   |
| 34 | <a href="#">c4g0rA_</a> | Alignment | not modelled | 6.3 | 17 | <b>PDB header:</b> virus/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein vp1;<br><b>PDBTitle:</b> structural characterization of h-1 parvovirus: comparison of2 infectious virions to replication defective particles                                      |
| 35 | <a href="#">c3kieF_</a> | Alignment | not modelled | 6.3 | 22 | <b>PDB header:</b> virus<br><b>Chain:</b> F: <b>PDB Molecule:</b> capsid protein vp1;<br><b>PDBTitle:</b> crystal structure of adeno-associated virus serotype 3b  |
| 36 | <a href="#">d1lp3a_</a> | Alignment | not modelled | 6.2 | 22 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> ssDNA viruses<br><b>Family:</b> Parvoviridae-like VP  |
| 37 | <a href="#">d2b0la1</a> | Alignment | not modelled | 6.0 | 13 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> CodY HTH domain   |
| 38 | <a href="#">d2ebfx2</a> | Alignment | not modelled | 5.9 | 30 | <b>Fold:</b> EreA/ChaN-like<br><b>Superfamily:</b> EreA/ChaN-like<br><b>Family:</b> PMT domain-like  |
| 39 | <a href="#">c2fhyL_</a> | Alignment | not modelled | 5.8 | 11 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> L: <b>PDB Molecule:</b> fructose-1,6-bisphosphatase 1;<br><b>PDBTitle:</b> structure of human liver fpbase complexed with a novel benzoxazole as2 allosteric inhibitor   |
| 40 | <a href="#">d1ftaa_</a> | Alignment | not modelled | 5.8 | 11 | <b>Fold:</b> Carbohydrate phosphatase<br><b>Superfamily:</b> Carbohydrate phosphatase<br><b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like  |
| 41 | <a href="#">c21liA_</a> | Alignment | not modelled | 5.7 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> hltf protein;<br><b>PDBTitle:</b> nmr structure of the hltf hiran domain   |
| 42 | <a href="#">d1d9qa_</a> | Alignment | not modelled | 5.7 | 11 | <b>Fold:</b> Carbohydrate phosphatase<br><b>Superfamily:</b> Carbohydrate phosphatase<br><b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like  |
| 43 | <a href="#">c3nttA_</a> | Alignment | not modelled | 5.6 | 11 | <b>PDB header:</b> virus<br><b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein;<br><b>PDBTitle:</b> structural insights of adeno-associated virus 5. a gene therapy vector2 for cystic fibrosis  |
| 44 | <a href="#">c1k3vA_</a> | Alignment | not modelled | 5.5 | 22 | <b>PDB header:</b> virus<br><b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein vp2;<br><b>PDBTitle:</b> porcine parvovirus capsid  |
| 45 | <a href="#">d1k3va_</a> | Alignment | not modelled | 5.5 | 22 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> ssDNA viruses<br><b>Family:</b> Parvoviridae-like VP  |
| 46 | <a href="#">d1s58a_</a> | Alignment | not modelled | 5.5 | 12 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> ssDNA viruses<br><b>Family:</b> Parvoviridae-like VP  |
| 47 | <a href="#">d1nuwa_</a> | Alignment | not modelled | 5.3 | 14 | <b>Fold:</b> Carbohydrate phosphatase<br><b>Superfamily:</b> Carbohydrate phosphatase<br><b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like  |
| 48 | <a href="#">c3pc0D_</a> | Alignment | not modelled | 5.1 | 31 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> phenylalanyl-trna synthetase, beta chain;<br><b>PDBTitle:</b> crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp                                      |