LeptoDB User guide

• **LeptoDB Overview**

  The LeptoDB database is a single window architecture modelled using heterogeneous data as a core resource for *Leptospira* research community.

• ***Leptospira* Genomes**

  The list contains 23 species and their Genomes.
• **Genomes:**
To access the details; (1) Organism Name (2) Strain (3) Assembly Status (4) Replicons (5) Genome size (6) GC% (7) Genes (8) Proteins.

• **Gene/Protein:**
This tab will display organism list. Click on organism name for genome features (Gene, Protein, cds, tRNA, rRNA, ncRNA, Protein)
• **Epitope**: get the protein specific Assay information

<table>
<thead>
<tr>
<th>Protein (Antigen) name</th>
<th>Epitope</th>
<th>T cell Assay</th>
<th>B cell Assay</th>
<th>MHC-Ii/ii Assay</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chaperonin 30/Cytoplasm</td>
<td>2</td>
<td>-</td>
<td>3</td>
<td>-</td>
</tr>
<tr>
<td>Heavy metal efflux pump</td>
<td>1</td>
<td>-</td>
<td>1</td>
<td>-</td>
</tr>
<tr>
<td>Hypothetical protein</td>
<td>9</td>
<td>-</td>
<td>2</td>
<td>-</td>
</tr>
<tr>
<td>Leucine rich repeat protein</td>
<td>1</td>
<td>-</td>
<td>2</td>
<td>-</td>
</tr>
<tr>
<td>LPS/LPS</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>-</td>
</tr>
<tr>
<td>Major outer membrane protein</td>
<td>8</td>
<td>18</td>
<td>24</td>
<td>-</td>
</tr>
<tr>
<td>Outer membrane lipoprotein</td>
<td>2</td>
<td>4</td>
<td>5</td>
<td>-</td>
</tr>
<tr>
<td>Putative outer membrane protein</td>
<td>1</td>
<td>-</td>
<td>1</td>
<td>-</td>
</tr>
<tr>
<td>Putative surface protein</td>
<td>3</td>
<td>11</td>
<td>6</td>
<td>-</td>
</tr>
</tbody>
</table>

• **Primer**: Gene Specific primer information is available here
• **Genomic Islands:**
Select a particular organism name from drop down for picking predicted Genomic Islands information

![Genomic Islands](image)

• **CRISPR/Cas:** *Leptospira* specific predicted CRISPR/Cas data is available

![CRISPR/Cas](image)
• **3D Structure:** *Leptospira* specific predicted 3D Structure of Proteins

![LeptoDB : Leptospirosis Database](image1)

• **Analysis Tools: JBrowse**
  Genome navigation can be done using "JBrowse " which allows dynamic visualisation of annotations. Track is available for genome. The panel at the upper end shows the ruler to move through along with the reference sequence. Different annotation features are shown with distinct colours.

![LeptoDB : Leptospirosis Database](image2)
• **Analysis Tools: Jmol**
  Jmol has been integrated for 3D structure visualization of proteins
- **Analysis Tools: BLAST**
  To align and find homologous or similar sequences against *Leptospira* genomes and genes
BLAST Results in Tabular Format

### Analysis Tools: MUSCLE
User is allowed to interactively use the MUSCLE tool to visualize multiple sequence alignment and analysing the features.
Result of MUSCLE
- **Download options:**

![Download options](image)