Dear Colleague,

We recently released a new version of TriTrypDB which includes new data and functionality.

New Data:

- *T. brucei* protein palmitoylation data (**Emmer *et. al.***).

- To search this data, go to the "**Identify Genes based on Mass Spec. Evidence**" and select "Procyclic form palmitoylated proteins (Emmer et al.)" under *Trypanosoma brucei.* This search will return all genes that have mass spec palmitoylation evidence.

- Mass spec data can also be visualized in the protein section of gene pages (for example, scroll down to the "Protein" section of **this gene page**) and in the **genome browser**. Mousing over peptide graphics displays additional peptide and modification site information.

- Single nucleotide polymorphism (SNP) calls based on high throughput sequencing data of *T. brucei* 927 and 427 provided by George Cross. Genes with SNPs can be identified based on their type (synonymous, nonsynonymous, etc.), their frequency and/or their depth of coverage.

- To search this data click on "**Identify Genes based on HTS SNP Characteristics**" under the heading "Population Biology".

- SNP data is represented as a table on gene pages. For example, if you visit the gene page for **Tb927.1.1740**, you can view a table under the heading "SNPs summary" which includes information about the SNPs found in this gene based on this comparison.

- An additional view of SNPs is available in the **genome browser** where SNPs can be visualized based on their coding potential (represented as colored diamonds). Mousing over the diamonds reveals a popup with additional information about the SNP at that specific location. Also, the mouse over includes a link to the **SNP record page** with additional information.

- The actual sequence reads in a particular region can be **visualized in gbrowse** by turning on the "Sequence Reads" track under the heading "High Throughput Sequencing (HTS) SNPs".

- Transcriptome-wide mRNA degradation data for *T. brucei* (**Manful *et. al.***). This data is represented on gene pages in graphical (fold change and percentile) and tabular (raw data) formats. To see this data visit any *T. brucei* gene page (**for example Tb927.8.620**) and scroll down to the section called "*T. brucei* RNA Sequence of transcriptome-wide mRNA degradation" under "Expression".

- *Leishmania tarentolae* Parrot-TarII genome sequence and annotation (**Raymond *et. al.***). Chromosome sequence and annotations for *Leishmania tarentolae* are provided by the CIHR Group on host pathogen interactions (Marc Ouellette, Jacques Corbeil, Barbara Papadopoulou, Michel J. Tremblay, Frédéric Raymond, Sébastien Boisvert from Université Laval, and Martin Olivier from McGill University).

- Genes may be queried based on gene IDs, text terms, EC numbers, GO terms, sequence features (length, introns, signal sequences, Pfam domains), etc.
- Genes and sequences may also be interrogated based on BLAST similarity, user-defined motifs, etc.
- Gene pages and synteny data are also available.

- Draft assemblies of the genome sequences from the Trypanosomatid sequencing white paper. This data is graciously provided prepublication and full credit and data usage information is available by clicking on the sequence name:

- *Endotrypanum monterogeii strain LV88*
- *Leishmania major strain LV39c5*
- *Leishmania panamensis strain L13*

- Genomic sequence data is available under the heading "Genomic Sequences" on the home page and may be searched by **species**, **genomic sequence IDs** and **BLAST**.

- Additionally, genomic sequence data may be downloaded from the **TriTrypDB download directory**.

- **New Gene IDs** -- *T. cruzi* IDs have been truncated by GeneDB to make them more user friendly. Old IDs have been mapped to the new ones (ie. you can search with either old or new IDs). Currently the old ID is displayed with the new gene ID on gene pages (old ID/new ID). In a future release the only the new IDs will be displayed at the top of the page.
New   **functionality:**

- The genome browser has been updated. This newer version includes several improvements and functionalities. **A tutorial** highlighting some of the new features is also available.

- A new column analysis tool is now available that allows you to generate a word cloud or histogram based on the data in result columns. To access this feature, run any search that returns a list of results then click on the icon next to the product description column name. This will reveal a popup with the option to select "Word Cloud". Look for this analysis feature to be activated on additional columns in future releases.

- Several new tutorials have been generated:
- **The genome browser.**
- **Customizing restriction sites in the genome browser.**
- **Identifying isolates based on geographic location.**
- **Dealing with invalid IDs and search strategies.**
- **Using the orthology phylogenetic profile search.**

  Note: Our bimonthly database releases incorporate new data and correct old data when necessary. Changes in annotation and new experimental data may slightly alter your search results by increasing or decreasing the number of hits. When search parameters change with a new release, we invalidate (Ø) the search and ask you to rerun it. When IDs are updated or removed, we map the old IDs to the new ones, remove the old IDs from your Basket, and leave your Favorites page alone.