

## Exploring the Gene Page

**Note:** this exercise uses ToxoDB (<https://ToxoDB.org>) as an example database, but the same functionality is available on all VEuPathDB resources.

### Learning objectives

- Become familiar with the information in gene pages
- Navigate to and from the gene pages
- Use the contents section of the gene page
- Interact with gene page subsections

1. **Navigation to a Gene page:** For this exercise visit the gene page for TGME49\_222020 (phosphoglycerate kinase PGKII). How did you get to this gene? (hint: use the site search to retrieve the gene page link, then click on the gene ID in the results.)

Genes matching **TGME49\_222020**

1 - 1 of 1

Filter results: Hide zero counts

Genome: 1

Genes: 1

Filter Gene fields: select all | clear all

Gene ID: 1

Filter organisms: select all | clear all | expand all | collapse all

Gene - **TGME49\_222020** phosphoglycerate kinase PGKII

Gene name or symbol: PGKII

Organism: Toxoplasma gondii ME49

Fields matched: Gene ID

### 2. Explore the top section of the gene page

- a. What information is in this section?
- b. Can you easily find which chromosome this gene is located on?
- c. Is this gene protein coding?
- d. What do the shortcuts do?

Add to basket Add to favorites Download Gene

**TGME49\_222020** phosphoglycerate kinase PGKII

**Name:** PGKII  
**Gene Type:** protein coding gene  
**Biotype Classification:** protein\_coding  
**Chromosome:** II  
**Location:** TGME49\_chrl:761,396..767,399(+)

**Species:** *Toxoplasma gondii*  
**Strain:** ME49  
**Status:** Reference Strain

Add the first user comment  
View and update community annotations in Apollo

#### Shortcuts

Synteny Alignments Phenotype SNPs

Transcriptomics Protein Features Proteomics

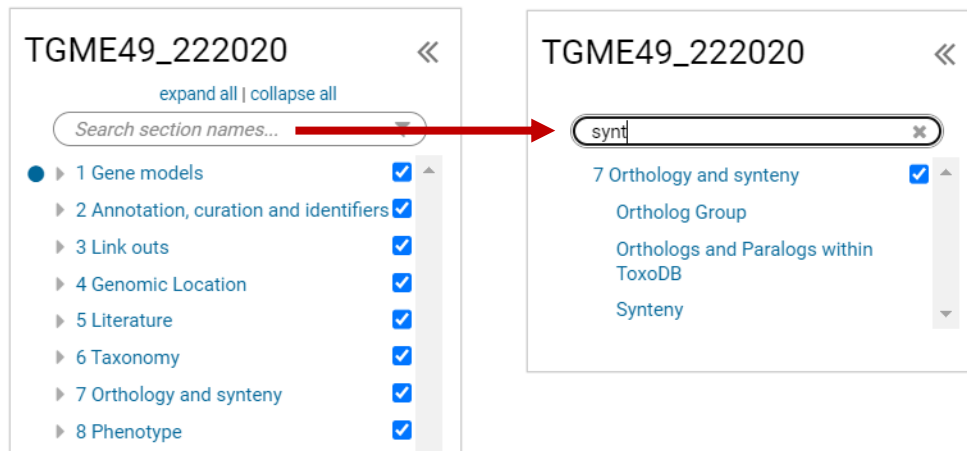
1 data sets

Also see TGME49\_222020 in the Genome Browser or Protein Browser

e. How long is the transcript? You can determine transcript length by expanding the Transcripts table.

► Transcripts

a. Navigate to the synteny section. Does *Cyclospora cayetanensis* isolate NF1\_C8 share synteny in this region?



- b. Navigate to the Transcript Expression table and open the row for the experiment called “mRNA Illumina sequences from 4 different mouse cell types infected with T. gondii and aligned to the ME49 Genome.” (Notice the filter box at the top of the table)
  - i. What data type was used to produce this data?
  - ii. In what cell type does this gene have the highest expression level?
  - iii. Open the Data table for this experiment. What is the TPM expression value for unique reads mapped to the Neurons?

5. **Run an alignment of selected protein sequences.** The Orthologs and Paralogs in ToxoDB table shows all orthologs for TGME49\_222020. This table is also a tool for running Clustal Omega on protein, CDS and genomic sequence for this gene and the orthologs you choose from the table. Within all VEuPathDB sites, OrthoMCL is used to determine orthology.

- a. Expand the “Orthologs and Paralogs in ToxoDB” section.
- b. Select a few genes from the table using the checkbox.
- c. Scroll to the bottom of the table and click on the Run Clustal Omega button.

<input type="checkbox"/>	TGVEG_222020	phosphoglycerate kinase PGKII	Toxoplasma gondii VEG	no	yes	no
<input checked="" type="checkbox"/>	TGVEG_318230	phosphoglycerate kinase PGKI	Toxoplasma gondii VEG	no	no	no
<input checked="" type="checkbox"/>	TGP89_222020	phosphoglycerate kinase PGKII	Toxoplasma gondii p89	no	yes	no
<input checked="" type="checkbox"/>	TGP89_318230	phosphoglycerate kinase PGKI	Toxoplasma gondii p89	no	no	no

Check All Uncheck All

Select sequence type for Clustal Omega multiple sequence alignment:

Please note: selecting a large flanking region or a large number of sequences will take several minutes to align.

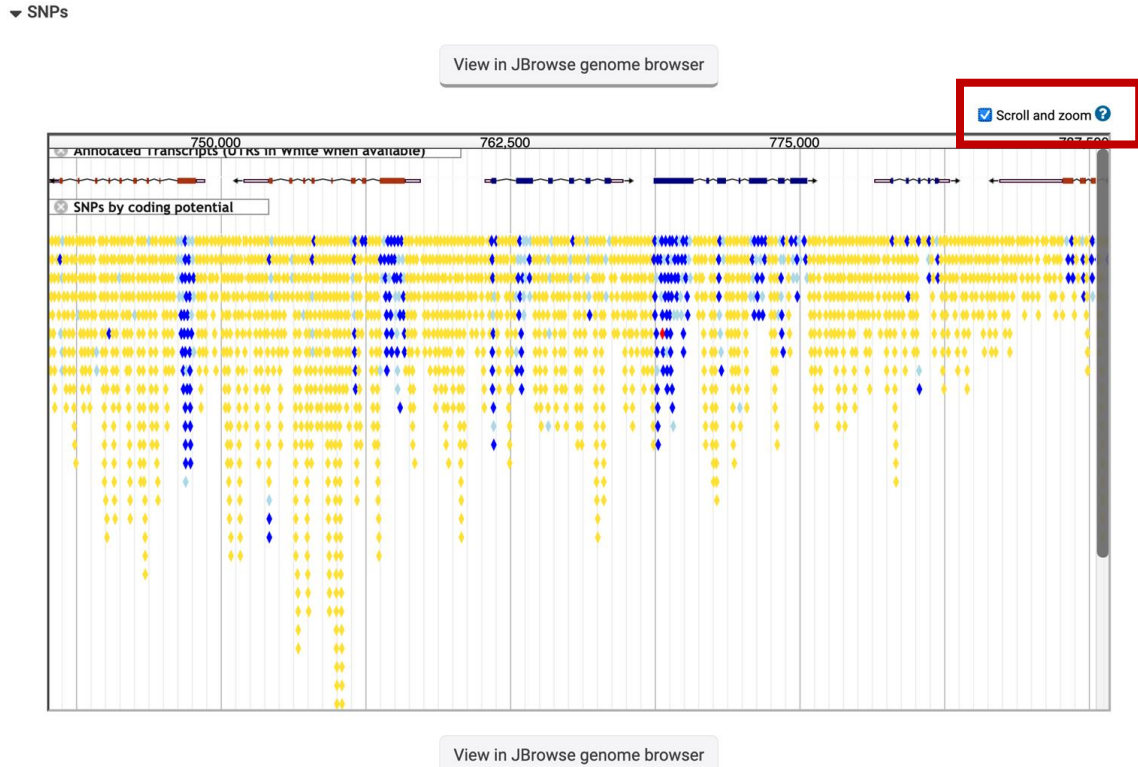
☒ Protein ☐ CDS (spliced) ☐ Genomic

Output format: Mismatches highlighted

Run Clustal Omega for selected genes

## 6. Explore the genetic variation section

The genetic variation section contains a graphic and a tool for aligning isolate sequences within the region of the gene. Go to the Genetic variation section of the gene page and expand the SNP section. Notice that by default you cannot scroll within the embedded browser window. To enable scrolling, select the “Scroll and Zoom” check box in the upper right-hand side of the browser window. To scroll down within the browser window, click and drag or use two-finger scrolling. You can also double click in an area to zoom in.



SNP color code: Dark blue (non-synonymous), light blue (synonymous), Yellow (non-coding), Red (nonsense). What kind of SNPs are in this gene? Can you see any non-synonymous SNPs? How does this compare to the neighboring genes?

## 7. Explore other sections of the gene page.

Feel free to scroll around the gene page and ask questions for clarification. Here are some questions you may want to ask about this gene:

- Is there evidence that this protein is phosphorylated? (hint: go to the proteomics section and expand the Post Translational Modification section).
- Where is the protein localized? (hint: go to the Protein Targeting and Localization section and expand the cellular localization section).
- Is there any phenotypic data available for this gene? (hint: go to the Phenotype section and expand its subsections).

- d. What other RNA-Seq data available for this gene? (hint: go to the Transcriptomics section and expand the subsections called RNA-Seq transcription summary and Transcript Expression).