

## My Organism Preferences

**Note:** this exercise uses VEuPathDB.org as an example database, but the same functionality is available on all VEuPathDB resources.

### Learning objectives:

- Navigate to the My Organism Preferences page
- Set your organism preferences
- Enable and disable the My Organism Preferences tool

The My Organism Preferences feature allows you to cherry-pick any combination of organisms you might be interested in. Enabling this feature applies your organism preferences globally across the site, resulting in a filtered view to help focus your work. Search menus and tools will reflect only your chosen organisms and only search data associated with your chosen organisms. The goal of this exercise is to set your organism preferences to include Apicomplexa and Oomycetes and exclude all other organisms in the database.

The screenshot shows the VEuPathDB website interface. At the top, there is a navigation bar with the VEuPathDB logo, release information (Release 59, 30 Aug 2022), a site search box, and a list of navigation links: My Strategies, Searches, Tools, My Workspace, Data, About, Help, and Contact Us. A red box highlights the 'My Organism Preferences (646 of 646)' link, which is accompanied by a gear icon and a toggle switch labeled 'enabled'. Below the navigation bar, the main content area is divided into two sections. On the left, there is a 'Search for...' sidebar with a filter dropdown and a list of search categories: Genes, Organisms, Popset Isolate Sequences, Genomic Sequences, Genomic Segments, and ESTs. On the right, there is an 'Overview of Resources and Tools' section with icons for Take a Tour, Getting Started, Search Strategies, Genome Browser, Transcriptomic Resources, Phenotypic Data, and Analyze My Data. Below this, there is a 'Getting Started' section with a brief introduction to VEuPathDB and a 'SITE SEARCH' section with instructions on how to use the site search box.

1. Navigate to “My Organism Preferences” link at the top right of the page.
  - a. The next page displays the current organism preferences selection. If you haven’t set these preferences before you should see all VEuPathDB organisms chosen by default.
  - b. Click on the clear all option, then select the Apicomplexa and Oomycota checkboxes. Notice that the panel on the right updates automatically with your selection from the left.
  - c. Once you are satisfied with your selection, click on the Apply button to activate your organism preferences.

## My Organism Preferences

Set your **My Organism Preferences** to limit the organisms you see throughout VEuPathDB.

Choose organisms to keep Apply X

select all | clear all | expand all | collapse all

Type a taxonomic name

☐ Amoebozoa

☒ Apicomplexa

☐ Chromeraceae

☐ Euglenozoa

☐ Fornicata

☐ Fungi

☐ Heterolobosea

☐ Metazoa

☒ Oomycota

☐ Parabasalia

☐ Preaxostyla

☐ Vitrellaceae

select all | clear all | expand all | collapse all

Show only reference organisms

### Preview of My Organism Preferences (157 of 646)

VEuPathDB will restrict the organisms it displays, throughout the site, to those you have chosen, as shown below.

- Apicomplexa
  - Aconoidasida
    - Haemosporida
      - Haemoproteidae
        - Haemoproteus tartakovskyi strain SISKIN1 [Reference]
      - Plasmodiidae
        - Hepatocystis sp. ex Piliocolobus tephrosceles 2019 [Reference]
        - Plasmodium
          - Plasmodium adleri G01 [Reference]
          - Plasmodium berghei ANKA [Reference]
          - Plasmodium bilcollinsi G01 [Reference]
          - Plasmodium blacklocki G01 [Reference]
          - Plasmodium chabaudi chabaudi [Reference]
          - Plasmodium coatneyi Hackeri [Reference]
          - Plasmodium cynomolgi
            - Plasmodium cynomolgi strain B
            - Plasmodium cynomolgi strain M [Reference]
          - Plasmodium falciparum
            - Plasmodium falciparum 3D7 [Reference]

- Explore how the My Organism Preference affects your experience on VEuPathDB. For example, navigate to the “RNA-Seq Evidence” search page. Click on the searches menu item then search for RNAseq. Next click on the RNA-Seq Evidence to go to that search page. Examine the available datasets. They should all be from organisms set in your preferences.

Site search, e.g. P1307\_1103400 or Reductase or binding protein

My Strategies **Searches** Tools My Workspace Data About Help Contact Us

it the organisms you see

Genes

Transcriptomics

[RNA-Seq Evidence](#)

ism Preferences

## Identify Genes based on RNA-Seq Evidence

Legend: ☒ Coexpression ☒ Quantitative Phenotype ☒ Similarity ☒ Splice Site Loc ☒ Differential Expression ☒ Fold Change ☒ MetaCycle ☒ Percentile ☒ SenseAntisense

Filter Data Sets:  100 rows

Organism	Data Set	Choose a Search
<i>Babesia</i> sp. Xinjiang Xinjiang <i>Naegleria fowleri</i> strain Ty	Trophozoite Transcriptome (Nfow) (Zysset-Burri et al.)	<input type="checkbox"/> P
<i>Babesia</i> sp. Xinjiang Xinjiang <i>Naegleria fowleri</i> strain Ty	Merozoite transcriptome (Guan et al.)	<input type="checkbox"/> P
<i>Besnoitia besnoiti</i> strain Bb-Ge1	Tachyzoite and tissue cyst transcriptomes (Ramakrishnan et al.)	<input type="checkbox"/> FC <input type="checkbox"/> P <input type="checkbox"/> SA
<i>Cryptosporidium hominis</i> TU502	Transcriptome of <i>C. hominis</i> oocysts (Widmer 2018)	<input type="checkbox"/> P
<i>Cryptosporidium parvum</i> Iowa II	Transcriptome of oocyst and intracellular stages (Widmer et al.)	<input type="checkbox"/> FC <input type="checkbox"/> P <input type="checkbox"/> SA
<i>Cryptosporidium parvum</i> Iowa II	Transcriptome of <i>C. parvum</i> intracellular stages (Widmer et al.)	<input type="checkbox"/> DE <input type="checkbox"/> FC <input type="checkbox"/> P <input type="checkbox"/> SA
<i>Cryptosporidium parvum</i> Iowa II	Transcriptome of <i>C. parvum</i> sporozoites treated with GalNAc (Widmer 2018)	<input type="checkbox"/> FC <input type="checkbox"/> P <input type="checkbox"/> SA

3. Try toggling the “My Organism Preferences” switch (hint, just click on it to deactivate or activate). What happens to the list of datasets?

## Identify Genes based on RNA-Seq Evidence

Filter Data Sets:  Legend: ☒ Similarity ☒ Splice Site Loc ☒ Differential Expression ☒ Fold Change ☒ MetaCycle ☒ Percentile ☒ SenseAntisense

Organism	Data Set	Choose a Search
<i>Acanthamoeba castellanii</i> str. Neff	Trophozoite transcriptome of <i>A. castellanii</i> (Wojtkawska et al.)	<input type="checkbox"/> P
<i>Aedes aegypti</i> LVP_AGWG	Mating-induced transcriptome changes in the reproductive tract of female <i>Aedes aegypti</i> (Alfonso-Parra et al 2016)	<input type="checkbox"/> FC <input type="checkbox"/> P
<i>Aedes aegypti</i> LVP_AGWG	Filarial worm-mosquito interactions (Choi et al 2014)	<input type="checkbox"/> DE <input type="checkbox"/> FC <input type="checkbox"/> P
<i>Aedes aegypti</i> LVP_AGWG	Male versus female carcass transcriptomes (Jiang et al 2015)	<input type="checkbox"/> DE <input type="checkbox"/> FC <input type="checkbox"/> P <input type="checkbox"/> SA
<i>Aedes aegypti</i> LVP_AGWG	Aag2 cells infected with blue tongue or Schmallenberg virus (Schnettler et al 2013)	<input type="checkbox"/> FC <input type="checkbox"/> P <input type="checkbox"/> SA
<i>Aedes aegypti</i> LVP_AGWG	Transcriptional profiling of <i>Aedes aegypti</i> spermathecal-related genes (Pascini et al 2020)	<input type="checkbox"/> FC <input type="checkbox"/> P