

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 organism preferences page
- Set your organism preferences
- Toggle the organism preferences enable/disable switch

The My Organism Preferences feature allows you to cherry-pick any combination of organisms you might be interested. Enabling this feature applies your organism preferences globally across the site resulting in a filtered view to help focus your work.

The screenshot shows the VEuPathDB website interface. At the top, the header includes the VEuPathDB logo, release information (Release 55, 2 Dec 2021), a search bar, and navigation links: My Strategies, Searches, Tools, My Workspace, Data, About, Help, and Contact Us. A red box highlights the 'My Organism Preferences (573 of 573)' link, which is accompanied by a gear icon and a toggle switch labeled 'enabled'. Below the header, the main content area is divided into a left sidebar with search filters (Genes, Organisms, Popset Isolate Sequences, Genomic Sequences, Genomic Segments, ESTs) and a central 'Overview of Resources and Tools' section. The 'Getting Started' section in the center provides instructions on how to use the site search. The footer contains logos for BRC and NIAID, copyright information for 2021 The VEuPathDB Project Team, and a 'COMMUNITY CHAT' button.

The goal of this exercises is to set your organism preferences to include Apicomplexa and Oomycetes and exclude all other organisms in the database.

1. Click on the “My Organism Preferences” link at the top right of the page.

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2. The next page displays the current organism preferences selection. If you haven't set these preferences before you should see the default selection which is all organisms in

VEuPathDB Release 55
2 Dec 2021

Site search, e.g. PF3D7_1133400 or *reductase or *binding protein

My Strategies Searches Tools My Workspace Data About Help Contact Us

My Organism Preferences (573 of 573) enabled

My Organism Preferences

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

Choose organisms to keep

select | **clear all** | expand all | collapse all

Type a taxonomic name

Show only reference organisms

- ☒ Amoebozoa
- ☒ Apicomplexa
- ☒ Chromeraceae
- ☒ Euglenozoa
- ☒ Fornicata
- ☒ Fungi
- ☒ Heterolobosea
- ☒ Metazoa
- ☒ Oomycota
- ☒ Parabasalida
- ☒ Preaxostyla
- ☒ Vitrellaceae

select all | clear all | expand all | collapse all

Display a menu

My Organism Preferences (573 of 573)

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

- Amoebozoa
 - Discosea
 - Acanthamoeba astronyxis Unknown [Reference]
 - Acanthamoeba castellanii
 - Acanthamoeba castellanii Ma
 - Acanthamoeba castellanii str. Neff [Reference]
 - Acanthamoeba culbertsoni A1 [Reference]
 - Acanthamoeba lenticulata PD25 [Reference]
 - Acanthamoeba lugdunensis L3a [Reference]
 - Acanthamoeba mauritanensis 1652 [Reference]
 - Acanthamoeba palestinensis Reich [Reference]
 - Acanthamoeba quina VII3 [Reference]
 - Acanthamoeba rhyodes Singh [Reference]
 - Acanthamoeba sp.
 - Acanthamoeba sp. Galka [Reference]
 - Acanthamoeba sp. Incertae sedis
 - Acanthamoeba sp. T4b-type
 - Acanthamoeba triangularis SH621 [Reference]
 - Eusea
 - Entamoebidae
 - Entamoeba dispar SAW760 [Reference]
 - Entamoeba histolytica
 - Entamoeba histolytica HM-1:IMSS [Reference]

COMMUNITY CHAT

the database.

-
-
3. Click on the clear all option, then select the Apicomplexa and Oomycota checkboxes. Notice that the panel on the right update automatically with your selection from the left.
4. Once you are satisfied with your selection, click on the Apply button to activate your organism preferences.
5. Explore how the My Organism Preference affects your experience on VEuPathDB. For example, try navigating to the “RNA-Seq Evidence” search page. Click on the searches menu item then search for RNAseq. Next click on the RNA-Seq Evidence

Site search, e.g. PF3D7_1133400 or *reductase or *binding protein

Set Ch

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

it the organisms you see

rnas

Genes

Transcriptomics

[RNA-Seq Evidence](#)

ism Preferences

Plasmodium falciparum 708

Plasmodium falciparum 708

6. Examine the available datasets. They should all be from organisms set in your

Identify Genes based on RNA-Seq Evidence

Filter Data Sets:

Legend:

Similarity

SSL

Splice Site Loc

DE

Differential Expression

FC

Fold Change

MC

MetaCycle

P

Percentile

SA

SenseAntisense

Organism	Data Set	Choose a Search			
<i>Babesia bovis</i> T2Bo	Transcriptome during development (Ueti et al.) NEW	<div>DE</div>	<div>FC</div>	<div>P</div>	<div>SA</div>
<i>Babesia</i> sp. Xinjiang Xinjiang	Merozoite transcriptome (Guan et al.)			<div>P</div>	
<i>Besnoitia besnoiti</i> strain Bb-Ger1	Tachyzoite and tissue cyst transcriptomes (Ramakrishnan et al.)	<div>FC</div>		<div>P</div>	<div>SA</div>
<i>Cryptosporidium hominis</i> TU502	Transcriptome of <i>C. hominis</i> oocysts (Widmer 2018)			<div>P</div>	
<i>Cryptosporidium parvum</i> Iowa II	Transcriptome of oocyst and intracellular stages (Widmer et al.)	<div>FC</div>		<div>P</div>	<div>SA</div>
<i>Cryptosporidium parvum</i> Iowa II	Transcriptome of <i>C. parvum</i> intracellular stages (Widmer et al.)	<div>DE</div>	<div>FC</div>	<div>P</div>	<div>SA</div>
<i>Cryptosporidium parvum</i> Iowa II	Transcriptome of <i>C. parvum</i> sporozoites treated with GalNAc (Widmer 2018)	<div>FC</div>		<div>P</div>	<div>SA</div>

preferences.

7. 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: <input type="text"/>		Legend: <input checked="" type="checkbox"/> S Similarity <input checked="" type="checkbox"/> SSL Splice Site Loc <input checked="" type="checkbox"/> DE Differential Expression <input checked="" type="checkbox"/> FC Fold Change <input checked="" type="checkbox"/> MC MetaCycle <input checked="" type="checkbox"/> P Percentile <input checked="" type="checkbox"/> SA 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="button" value="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 checked="" type="button" value="FC"/>			<input type="button" value="P"/>
<i>Aedes aegypti</i> LVP_AGWG	Filarial worm-mosquito interactions (Choi et al 2014)		<input checked="" type="button" value="DE"/>	<input checked="" type="button" value="FC"/>		<input type="button" value="P"/>
<i>Aedes aegypti</i> LVP_AGWG	Male versus female carcass transcriptomes (Jiang et al 2015)		<input checked="" type="button" value="DE"/>	<input checked="" type="button" value="FC"/>		<input type="button" value="P"/> <input checked="" type="button" value="SA"/>
<i>Aedes aegypti</i> LVP_AGWG	Aag2 cells infected with blue tongue or Schmallenberg virus (Schnettler et al 2013)			<input checked="" type="button" value="FC"/>		<input type="button" value="P"/> <input checked="" type="button" value="SA"/>
<i>Aedes aegypti</i> LVP_AGWG	Transcriptional profiling of <i>Aedes aegypti</i> spermathecal-related genes (Pascini et al 2020)			<input checked="" type="button" value="FC"/>		<input type="button" value="P"/>