VEuPathDB
Eukaryotic Pathogen, Vector & Host Informatics Resources

Mining Proteomics Data

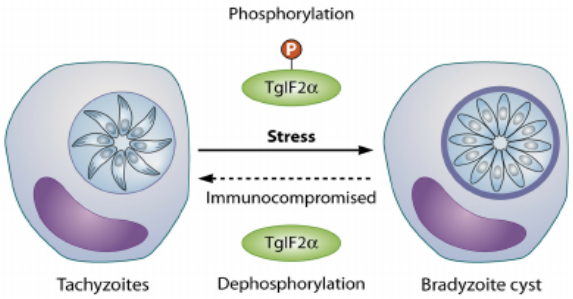
Protein phosphorylation in intracellular *Toxoplasma* tachyzoites

Learning objectives

- Explore proteomics data on VEuPathDB
- Perform a Post-Translational Modification search for genes with

Introduction

Protein phosphorylation in intracellular Toxoplasma tachyzoites is a crucial **post-translational modification** that regulates various aspects of the parasite's life cycle, including invasion, egress, motility, and adaptation to the host cell environment, primarily by controlling the activity and localization of key proteins involved in these processes. It is considered a critical mechanism for the parasite's survival and virulence within the host cell.

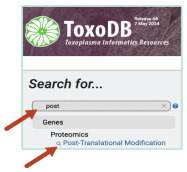


In this exercise, the goal is to **find genes with evidence of protein phosphorylation in intracellular Toxoplasma tachyzoites**.
Additionally, we want to determine how many of these phosphorylated genes are also localized to the microneme, the secretory organelle that plays a critical role in the survival and spread of the parasite.

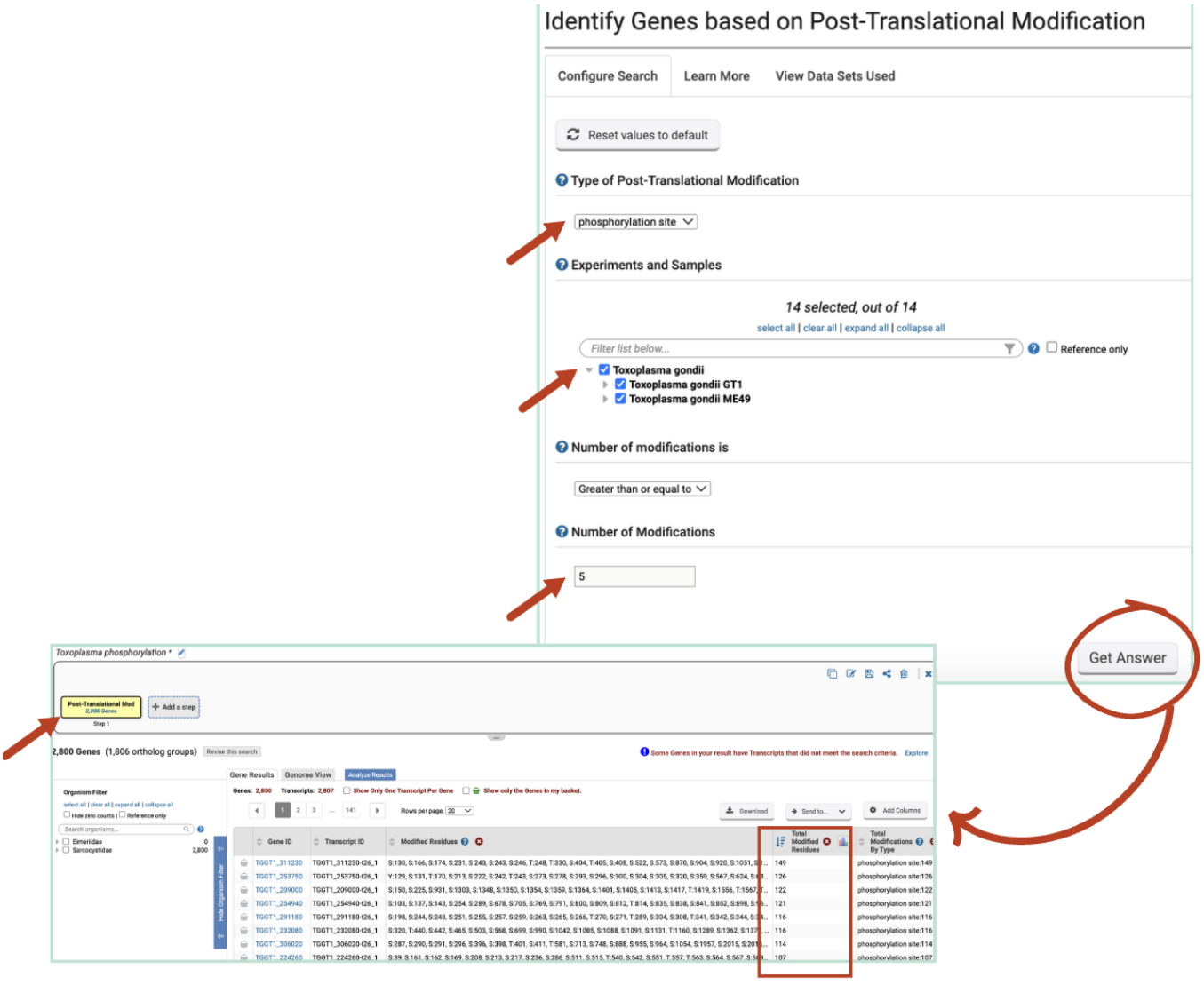
Overview of the search strategy: Use Post-Translational Modification search in two steps

- identify genes that have phosphorylation events
- intersect that search with a micromene localization search

1. Navigate to ToxoDB.org
2. From the sidebar or header, search for “post” and click on **Post-Translational Modification**

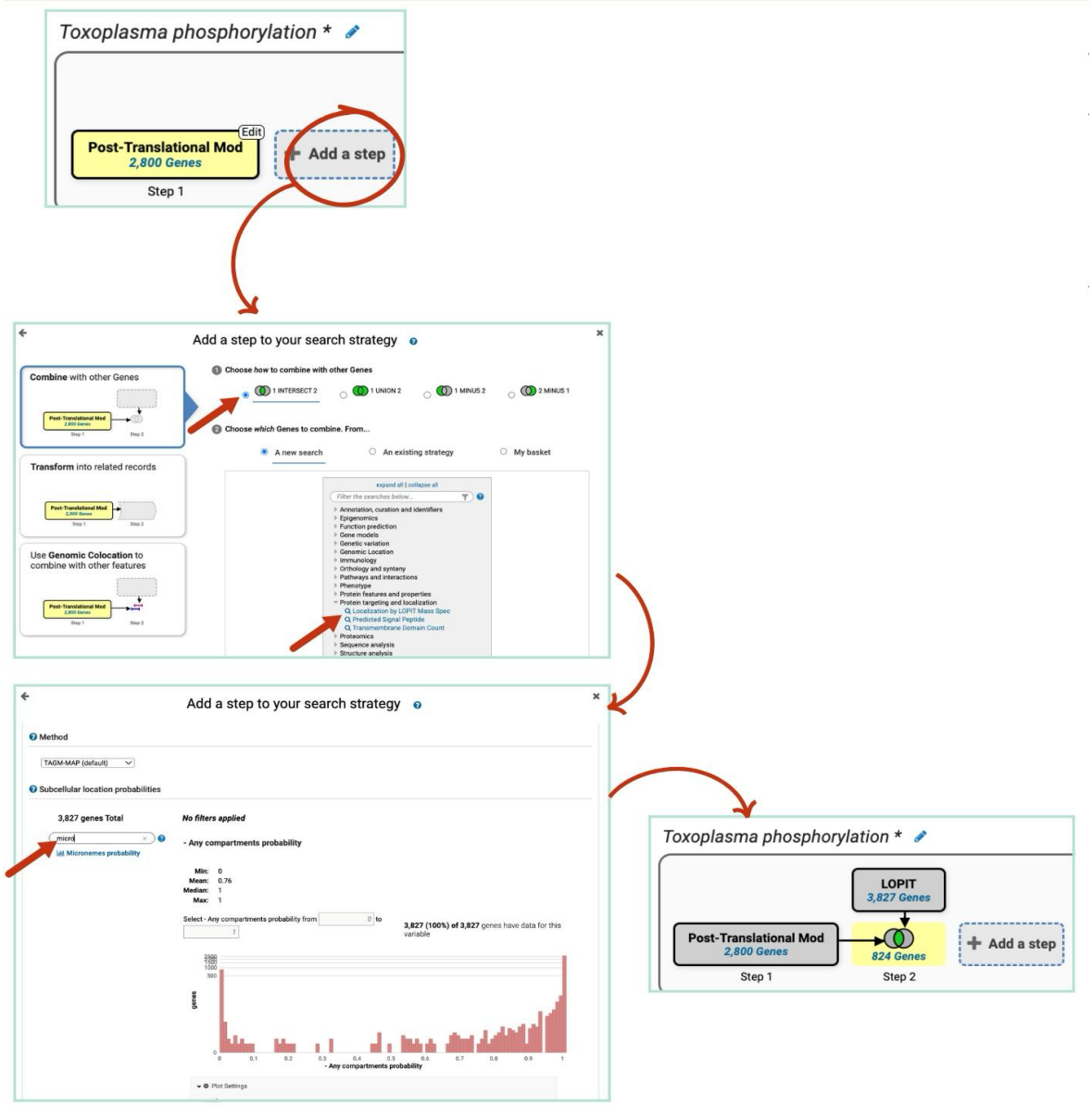


3. Configure the search to have at least 5 phosphorylation events from all available phosphoproteomic experiments in *Toxoplasma*.
   How many genes did you get? Which gene has the highest number of phosphorylation sites?



4. How many of these phosphorylated genes are also localized to the microneme organelles?

   Add a step to your search strategy to limit to genes expressed in the micronemeToxoDB has hyperLOPIT data (Hyperplexed Localisation of Organelle Proteins by Isotope Tagging), a spatial proteomics method that simultaneously captures the steady-state subcellular association of thousands of proteins. The technique reveals the probability that a protein is present in a specific cellular location (fraction). Use this data and search to find which phosphorylated genes are localized to the microneme.



How many genes did you get that are phosphorylated and that localize to the microneme?