Mining Proteomics Data on VEuPathDB: An Exercise

Protein phosphorylation in intracellular Toxoplasma tachyzoites

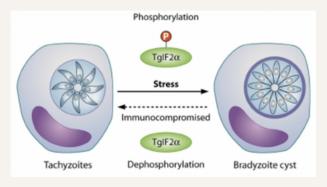


The search question



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.



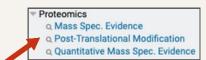
<u>Image credit</u>

What platform is best suited for this question?



This knowledgebase has data and informatics resources for Toxoplasma as well as Cyclospora, etc.

What search is best suited for this question?



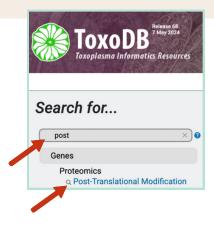
Although phosphorylated peptides can be identified by searching the appropriate experiments in the Mass Spec. Evidence search page, VEuPathDB also contains a search that specifically access proteomics data that determined post-translational modifications.

What is a possible search strategy that will answer this question?

Use **Post-Translational Modification** search in two steps- (1) identify genes that have phosphorylation events, (2) intersect that search with a micromene localization search.

1. Navigate to the appropriate search

- Navigate to <u>ToxoDB.org</u>
- From the sidebar or header, search for "post" and click on Post-Translational Modification



2. Choose appropriate experiments/ samples & parameters within the search

 Configure the search to have at least 5 phosphorylation events from all available phosphoproteomic experiments in Toxoplasma.

How many genes did you get?

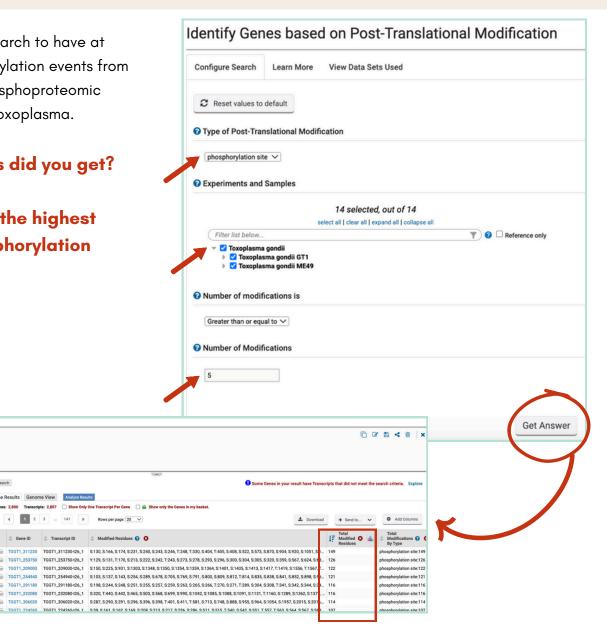
Which gene has the highest number of phosphorylation sites?

Toxoplasma phosphorylation *

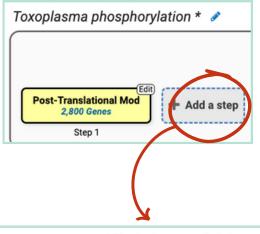
☐ Hide zero counts | ☐ Reference only

+ Add a step

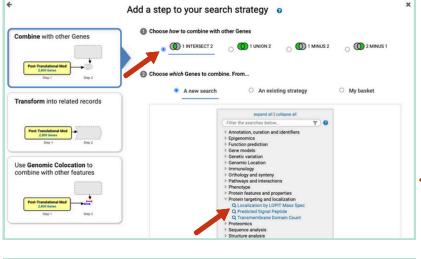
800 Genes (1,806 ortholog groups) Revise this search

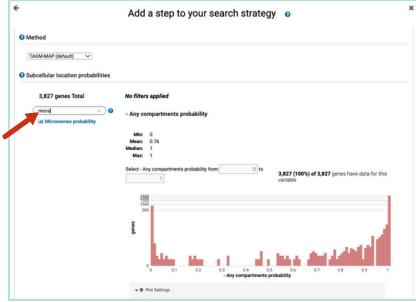


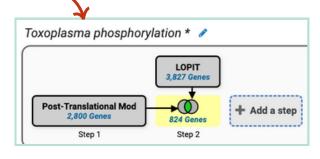
3. Add a step to your search strategy to limit to genes expressed in the microneme



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