

Mining Proteomics Data

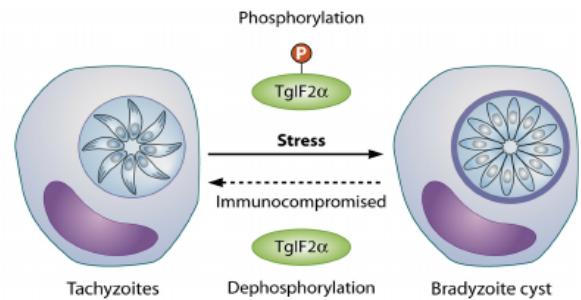
Protein phosphorylation in intracellular *Toxoplasma* tachyzoites

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.



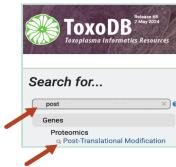
In this exercise, the goal is to **find genes with evidence of protein phosphorylation in intracellular *Toxoplasma* tachyzoites**.

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 microneme 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?

Identify Genes based on Post-Translational Modification

Configure Search Learn More View Data Sets Used

Reset values to default

Type of Post-Translational Modification: phosphorylation site

Experiments and Samples: 14 selected, out of 14

Filter list below... select all | clear all | expand all | collapse all

Toxoplasma gondii Toxoplasma gondii GT1 Toxoplasma gondii ME49

Number of modifications is: Greater than or equal to 5

Number of Modifications: 5

Get Answer

Post-Translational Mod 2,800 genes + Add a step

Gene Results Genome View Analyze Results

Some Genes in your result have Transcripts that did not meet the search criteria. Explore

Organism Filter: select all | clear all | expand all | collapse all | Hide zero count | Reference only | Search organisms...

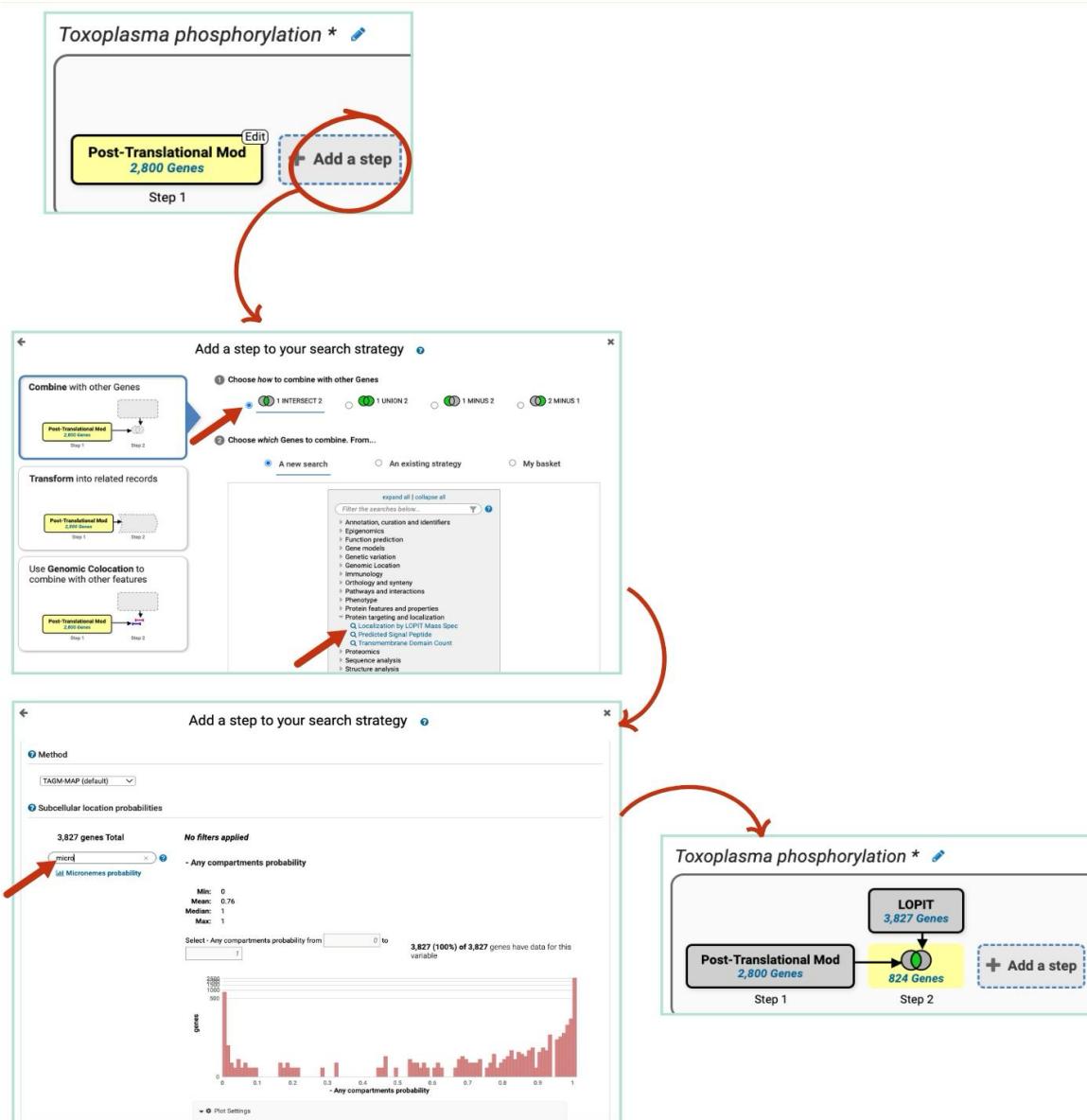
2,800 Genes (1,806 ortholog groups) Revise this search

Gene ID Transcript ID Modified Residues

Gene ID	Transcript ID	Modified Residues	Total Modified Residues
TGGT1_311230	TGGT1_311230-26_1	S:130, S:166, S:174, S:231, S:240, S:243, S:246, T:248, T:330, S:404, T:405, S:408, S:522, S:573, S:870, S:904, S:920, S:1051, S:126	149
TGGT1_23570	TGGT1_23570-26_1	Y:129, S:131, T:170, S:213, S:222, S:242, T:243, S:273, S:278, S:293, S:296, S:300, S:304, S:305, S:320, S:339, S:367, S:424, S:431, S:432	126
TGGT1_23900	TGGT1_23900-26_1	S:150, S:225, S:291, S:303, S:348, S:350, S:1354, S:1359, S:1364, S:1401, S:1405, S:1413, S:1417, T:1419, S:1556, T:1567, T:1568	122
TGGT1_234940	TGGT1_234940-26_1	S:103, S:137, S:143, S:254, S:259, S:278, S:705, S:746, S:791, S:803, S:812, S:814, S:835, S:841, S:852, S:896, S:915, S:121	149
TGGT1_239110	TGGT1_239110-26_1	S:198, S:244, S:248, S:251, S:255, S:257, S:259, S:261, S:265, T:270, S:271, T:289, S:304, T:341, S:342, S:344, S:404, S:405, S:406, S:407, S:408, S:409, S:410, S:411	116
TGGT1_232080	TGGT1_232080-26_1	S:320, T:440, S:442, S:445, S:503, S:568, S:690, S:1042, S:1085, S:1098, S:1199, S:1131, T:1160, S:1289, S:1302, S:1377, S:1378	116
TGGT1_306600	TGGT1_306600-26_1	S:287, S:290, S:291, S:296, S:336, S:398, T:401, S:411, T:581, S:713, S:748, S:830, S:955, S:994, S:1054, S:1067, S:2015, S:2016, S:2017	114
TGGT1_224260	TGGT1_224260-26_1	S:99, S:161, S:162, S:169, S:208, S:213, S:217, S:226, S:511, T:546, S:542, S:551, T:557, S:563, S:944, S:567, S:569, S:570	107

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 microneme. 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?