

## Evaluation of Prototypes (Wednesday 11:45 – 12:15 pm)

Please help us evaluate our new analysis tool by completing three short tasks that exercise this tool. We'll ask you to record your screen, perform some tasks and answer a short survey. Be assured that it is okay if you don't complete the tasks. Please be sure to complete the survey, even if you can't complete the tasks.

### TASK 1

Find all genes in AmoebaDB that have between 2 and 20 exons. Write down the third ID in your result list.

- Use the search [Identify Genes based on Exon Count](#)
- Third ID =

### TASK 2

Find *E. histolytica* genes that are differentially expressed (up or down) at least 5-fold in Rahman strain compared to HM1:IMSS based on RNA sequence data.

- Use the search: [Identify Genes based on RNA Seq Evidence](#)
- Use the fold change (FC) search with the data set: Transcriptomes of HM1:IMSS and Rahman strain trophozoites (Hon et al.)
- First 2 IDs =

### TASK 3

#### BACKGROUND

- The Gene Ontology (GO) is a public resource that provides a hierarchy of terms used to describe a gene's molecular function, cellular location or molecular process.
- Many genes in AmoebaDB are annotated with GO terms.
- A set of genes is *enriched* for a GO term if that term appears in the gene set more frequently than it does in the set of all genes for that organism. Typically GO enrichment is found by running a statistical tool on a set of genes.

Identify enriched molecular function gene ontology (GO) terms in your **results of TASK 2** and write down the two terms with the lowest P-value (most enriched).

- First 2 enriched Molecular Function GO terms =

### TASK 4

Please complete the following 9-question survey.

<https://www.surveymonkey.com/s/ZC6Q8F8>