

Gene Ontology (GO) Enrichment

In a previous exercise you identified all gene in *Cryptosporidium* species that contain a with the YXXΦ receptor signal motif:

<http://cryptodb.org/cryptodb/im.do?s=928309b4c1b9ef3f>

Look at the results for *C. muris*. Are you able to identify types of proteins that are enriched in the list just by looking? How confident are you about your conclusion? To help, you can also click on the graph icon next to the product description column to generate a word cloud of all the words in the product descriptions of your results. Is this statistical?

110 Genes from Step 2
Strategy: Proteins with endosomal/lysosomal sorting signal YXXphi and TM domain Add 110 Genes to Basket | Download 110 Genes

Click on a number in this table to limit/filter your results

All Results	Ortholog Groups	Apicomplexa			Chromerida		
		<i>Cryptosporidium</i>	<i>Gregarina</i>	<i>Chromera</i>	<i>Vitrella</i>		
		<i>C. hominis</i>	<i>C. muris</i>	<i>C. parvum</i>	<i>G. niphandrodes</i>	<i>C. velia</i>	<i>V. brassicaformis</i>
		TU502	RN66	Iowa II	Unknown strain	CCMP2878	CCMP3155
282	205	81	110	91	0	0	0

Gene Results Genome View Analyze Results **BETA**

First 1 2 3 4 5 Next Last Advanced Paging Add Columns

Gene ID	Genomic Location	Product Description
CMU_037790	DS989726: 41,920 - 43,329 (+)	hypothetical protein, conserved
CMU_038090	DS989726: 122,946 - 124,004 (-)	hypothetical protein, conserved
CMU_038180	DS989726: 142,785 - 144,212 (+)	hypothetical protein,
CMU_038270	DS989726: 163,292 - 164,866 (+)	transmembrane amir
CMU_038340	DS989726: 184,859 - 189,688 (-)	ABC transporter fam
CMU_039090	DS989726: 401,352 - 406,928 (-)	hypothetical protein
CMU_039120	DS989726: 411,042 - 412,847 (-)	hypothetical protein,
CMU_039130	DS989726: 413,143 - 416,793 (-)	hypothetical protein,
CMU_039540	DS989726: 506,535 - 506,903 (+)	hypothetical protein
CMU_039560	DS989726: 512,239 - 513,519 (+)	glycosyl transferase
CMU_041340	DS989726: 923,375 - 926,695 (-)	hypothetical protein,
CMU_041610	DS989726: 983,292 - 984,672 (+)	oxidoreductase, shor
CMU_041760	DS989726: 1,005,531 - 1,006,922 (-)	hypothetical protein,
CMU_041810	DS989726: 1,014,553 - 1,015,645 (-)	hypothetical protein,
CMU_042220	DS989726: 1,102,277 - 1,103,155 (+)	Mpv17 / PMP22 family protein
042250	DS989726: 1,109,477 - 1,112,080 (+)	zinc finger, C3HC4 type domain-containing protein

Word Cloud

Filter words by rank: 1 to 50

Sort by: Rank A-Z

conserved
 hypothetical
 protein

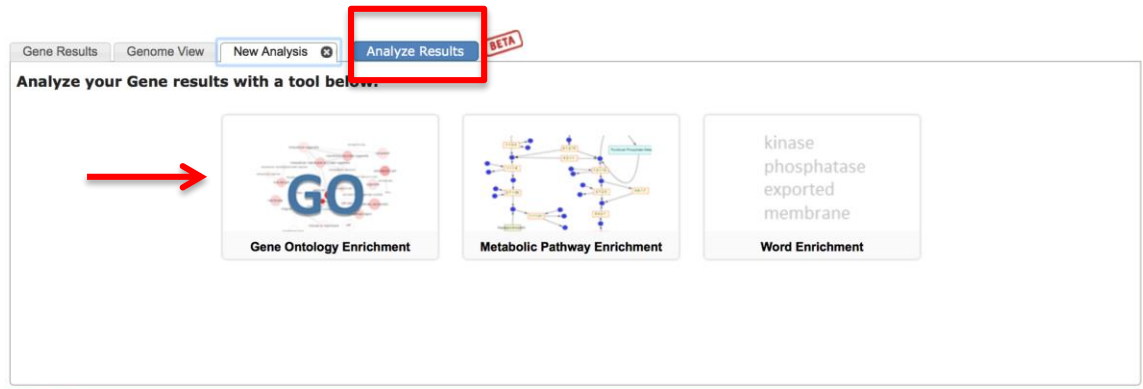
Enrichment analysis allows you to look for overrepresented features in your results. GO terms provide a structured vocabulary for product descriptions. At EuPathDB we get GO terms from the official annotation and by transferring GO terms associated with InterPro domains (using InterPro scan).

Here are some useful links with additional information:

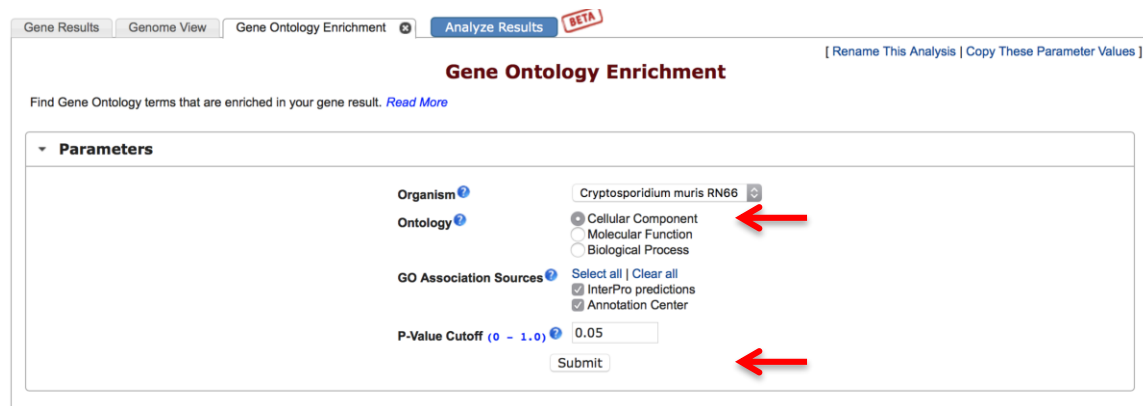
<http://geneontology.org/page/documentation>

<http://geneontology.org/page/go-enrichment-analysis>

To run a GO enrichment analysis, click on the “Analyze Results” tab then click on the GO enrichment option:



Next select “the cellular component” option and submit your analysis:



Examine your results. Do they make sense?

Gene Results | Genome View | Gene Ontology Enrichment | Analyze Results **BETA** [Rename This Analysis | Copy These Parameter Values]

Gene Ontology Enrichment

Find Gene Ontology terms that are enriched in your gene result. [Read More](#)

Parameters

Organism: Cryptosporidium muris RN66

Ontology: Cellular Component Molecular Function Biological Process

GO Association Sources: Select all | Clear all InterPro predictions Annotation Center

P-Value Cutoff (0 - 1.0): 0.05

Submit

Analysis Results: [Download Analysis Results](#)

Got a total of 11 results Filter:

This analysis result may be lost if you change your gene result. To save this analysis result, please download.

GO ID	GO Term	Genes in the bkgd with this term	Genes in your result with this term	Percent of bkgd Genes in your result	Fold enrichment	Odds ratio	P-value	Benjamini	Bonferroni
GO:0016020	membrane	271	25	9.2	4.37	8.8	1.76e-11	1.94e-10	1.94e-10
GO:0031224	intrinsic to membrane	121	18	14.9	7.05	11.23	3.82e-11	2.10e-10	4.20e-10
GO:0016021	integral to membrane	119	17	14.3	6.77	10.4	2.90e-10	1.06e-9	3.19e-9
GO:0044425	membrane part	177	18	10.2	4.82	7.46	1.18e-8	3.25e-8	1.30e-7
GO:0005575	cellular_component	870	30	3.4	1.63	2.99	4.14e-4	9.10e-4	4.55e-3
GO:0005789	endoplasmic reticulum membrane	13	3	23.1	10.93	11.66	3.83e-3	6.02e-3	4.21e-2
GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	13	3	23.1	10.93	11.66	3.83e-3	6.02e-3	4.21e-2
GO:0044432	endoplasmic reticulum part	14	3	21.4	10.15	10.82	4.58e-3	6.30e-3	5.04e-2
GO:0005783	endoplasmic reticulum	18	3	16.7	7.89	8.4	8.46e-3	1.03e-2	9.31e-2
GO:0012505	endomembrane system	33	3	9.1	4.31	4.55	3.66e-2	4.03e-2	4.03e-1
GO:0031090	organelle membrane	37	3	8.1	3.84	4.05	4.79e-2	4.79e-2	5.27e-1

Some more info on Fischer's exact test:

<http://udel.edu/~mcdonald/statfishers.html>

Some more info about Odds ratios:

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2938757/>

Some more info on false discovery rates and P value correction:

<http://brainder.org/2011/09/05/fdr-corrected-fdr-adjusted-p-values/>