

## Short Guide to the GO-tool

The GO tool provides fast access to enriched GO-terms of the [Gene Ontology \(GO\) project](http://www.geneontology.org):

“The GO defines concepts/classes used to describe gene function, and relationships between these concepts. It classifies functions along three aspects:

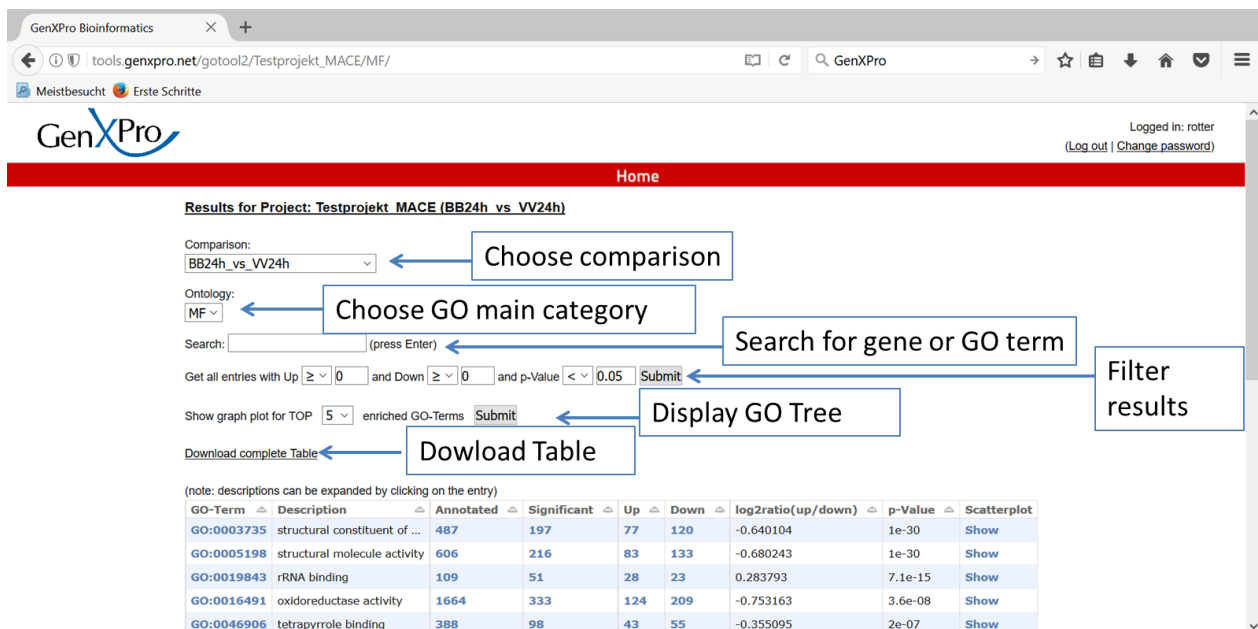
**molecular function (MF):** molecular activities of gene products

**cellular component (CC):** where gene products are active

**biological process (BP):** pathways and larger processes made up of the activities of multiple gene products.”

(From <http://www.geneontology.org>)

Our tool performs an enrichment analyses for GO terms by using a hypergeometric test (one tailed fisher’s exact test). It displays and sorts the enriched GO terms according to their p-value for likelihood of enrichment. The tool can be also be used to quickly filter for the genes involved in a specific function. On the start page, a pairwise comparison must be chosen, as well as the main category (MF; CC, BP). The tool then lists the most likely enriched GO terms and the number of genes belonging to these GO terms. The numbers can be clicked to access the genes and their expression values. Please see “Table” information below for further information. The tool also has two plotting options: the first plots the GO terms and their relation within the GO-structure (“=Tree”). The other plots the GO-associated genes in a scatter plot (see “Scatterplot” information below.



Results for Project: Testprojekt\_MACE (BB24h vs\_VV24h)

Comparison:  Choose comparison

Ontology:  Choose GO main category

Search:  (press Enter) Search for gene or GO term

Get all entries with Up  and Down  and p-Value  Submit Filter results

Show graph plot for TOP  enriched GO-Terms Submit Display GO Tree

Download complete Table Download Table

GO-Term	Description	Annotated	Significant	Up	Down	log2ratio(up/down)	p-Value	Scatterplot
GO:0003735	structural constituent of ...	487	197	77	120	-0.640104	1e-30	Show
GO:0005198	structural molecule activity	606	216	83	133	-0.680243	1e-30	Show
GO:0019843	rRNA binding	109	51	28	23	0.283793	7.1e-15	Show
GO:0016491	oxidoreductase activity	1664	333	124	209	-0.753163	3.6e-08	Show
GO:0046906	tetrapyrrole binding	388	98	43	55	-0.355095	2e-07	Show

**The Table:**

All blue colored letters and numbers contain hyperlinks. When clicking the numbers, a table is opened containing the gene lists.

**Column 1:** GO term number

**Column 2:** Description of GO Term

**Column 3:** Number of all genes that could be annotated to the GO term

**Column 4:** Number of genes belonging to the GO term that are significantly differentially expressed in the pairwise comparison ( $p$ -value 0,05 or lower).

**Column 5:** Number of genes from Column 4 that are upregulated

**Column 6:** Number of genes from Column 4 that are downregulated

**Column 7:** Log to the basis of 2 of the ratio of the number of up/down regulated genes

**Column 8:** P-value describing the likelihood for GO enrichment based on fishers exact test.

**Column 9:** Link to scatterplot

## The Scatterplot

All differentially expressed genes are represented as blue dots. The expression of the gene in the two compared samples can be delineated from position of the dots on the x and y axis. The red dots are genes belonging to the specific GO-term. When hovering over the red dots with the mouse, gene expression data, ID, name and description of the gene is displayed.

