

Enrichment Analysis – Legends

Legends to figures

Barplots show the ten terms with the highest significance according to the adjusted FDR p-value, ordered by this field. The X-axis indicates the $-\log_{10}$ of the adjusted p-value and the Y-axis includes information relative to the category, the Ratio (count/size) and the adjusted p-value (Padj).

Note

All the graphs generated with CANTOOL are produced in PNG (600 ppp) and PDF, which can be edited for example with [Inkscape](#) or [GIMP](#).

Legends to tables

The tab-delimited tables contain the following fields:

- Category/DOSEID/GOBPID/GOCCID/GOMFID/KEGGID/PathwayID: Identifiers of the enriched term.
- Count: The gene count from the provided gene list that correspond to the category.
- ExpCount: The gene count expected within each category if no enrichment would be assumed (null distribution).
- Genes or geneID: The list of gene identifiers from the provided gene list that correspond to the category.
- OddsRatio: A measure of association between an expectation and an outcome. The OR represents the odds that an outcome will occur given a particular exposure (in this case, the user gene list), compared to the odds of the outcome occurring in the absence of that exposure (a random list of genes)
- Pvalue or pValue: P value from enrichment test.
- PvalueAdj: Adjusted p-value using [Benjamini–Hochberg](#) (BH) method.
- Qvalue: The q-value accounts for the proportion of false positives incurred (called the false discovery rate) when that particular test is called significant.
- Size: The number of genes assigned to the category.
- Term/Description: A description of the enriched pathway or route.