

Resource Summary Report

Generated by [kravitz2](#) on Aug 3, 2026

categoryCompare

RRID:SCR_001223

Type: Tool

Proper Citation

categoryCompare (RRID:SCR_001223)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/categoryCompare.html>

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Description: A software package for meta-analysis of high-throughput experiments using feature annotations. It calculates significant annotations (categories) in each of two (or more) feature (i.e. gene) lists, determines the overlap between the annotations, and returns graphical and tabular data about the significant annotations and which combinations of feature lists the annotations were found to be significant. Interactive exploration is facilitated through the use of RCytoscape (heavily suggested).

Abbreviations: categoryCompare

Synonyms: categoryCompare - Meta-analysis of high-throughput experiments using feature annotations

Resource Type: data analysis software, software resource, data processing software, software application

Defining Citation: [PMID:24808906](#)

Keywords: annotation, go, gene expression, multiple comparison, pathway, gene

Availability: Free, Available for download, Freely available

Resource Name: categoryCompare

Resource ID: SCR_001223

Alternate IDs: OMICS_02122

License: GNU General Public License v2

Record Creation Time: 20220129T080206+0000

Ratings and Alerts

No rating or validation information has been found for categoryCompare.

No alerts have been found for categoryCompare.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Erener S, et al. (2021) Deletion of pancreas-specific miR-216a reduces beta-cell mass and inhibits pancreatic cancer progression in mice. Cell reports. Medicine, 2(11), 100434.

Lanceta L, et al. (2021) Differential gene expression analysis of palbociclib-resistant TNBC via RNA-seq. Breast cancer research and treatment, 186(3), 677.

Lanceta L, et al. (2020) Transcriptomic Profiling Identifies Differentially Expressed Genes in Palbociclib-Resistant ER+ MCF7 Breast Cancer Cells. Genes, 11(4).

Hinderer EW, et al. (2019) Advances in gene ontology utilization improve statistical power of annotation enrichment. PloS one, 14(8), e0220728.

Klinge CM, et al. (2019) HNRNPA2/B1 is upregulated in endocrine-resistant LCC9 breast cancer cells and alters the miRNA transcriptome when overexpressed in MCF-7 cells. Scientific reports, 9(1), 9430.

Rouchka EC, et al. (2019) Dataset for dose and time-dependent transcriptional response to ionizing radiation exposure. Data in brief, 27, 104624.

Rouchka EC, et al. (2016) Transcriptional profile of immediate response to ionizing radiation exposure. Genomics data, 7, 82.

Rouchka EC, et al. (2016) Data set for transcriptional response to depletion of the Shoc2 scaffolding protein. Data in brief, 7, 770.

Riedmann C, et al. (2015) Inorganic Arsenic-induced cellular transformation is coupled with genome wide changes in chromatin structure, transcriptome and splicing patterns. BMC genomics, 16(1), 212.