

Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

ErmineJ

RRID:SCR_006450

Type: Tool

Proper Citation

ErmineJ (RRID:SCR_006450)

Resource Information

URL: <http://bioinformatics.ubc.ca/ermineJ/>

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Description: Data analysis software for gene sets in expression microarray data or other genome-wide data that results in rankings of genes. A typical goal is to determine whether particular biological pathways are doing something interesting in the data. The software is designed to be used by biologists with little or no informatics background. A command-line interface is available for users who wish to script the use of ermineJ. Major features include: * Implementation of multiple methods for gene set analysis: ** Over-representation analysis ** A resampling-based method that uses gene scores ** A rank-based method that uses gene scores ** A resampling-based method that uses correlation between gene expression profiles (a type of cluster-enrichment analysis). * Gene sets receive statistical scores (p-values), and multiple test correction is supported. * Support of the Gene Ontology terminology; users can choose which aspects to analyze. * User files use simple text formats. * Users can modify gene sets or create new ones. * The results can be visualized within the software. * It is simple to compare multiple analyses of the same data set with different settings. * User-definable hyperlinks are provided to external sites to allow more efficient browsing of the results. * For programmers, there is a command line interface as well as a simple application programming interface that can be used to plug ermineJ functionality into your own code Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: ermineJ

Synonyms: ermineJ: Gene Ontology analysis for high-throughput data

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

Defining Citation: [PMID:16280084](#)

Keywords: microarray, gene ontology, analysis, high-throughput, gene, gene expression, statistical analysis, term enrichment, genome

Availability: Free for academic use

Resource Name: ErmineJ

Resource ID: SCR_006450

Alternate IDs: nif-0000-07758

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260801T042625+0000

Ratings and Alerts

No rating or validation information has been found for ErmineJ.

No alerts have been found for ErmineJ.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 50 mentions in open access literature.

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

Zhao T, et al. (2025) Choroid plexus organoids reveal mechanisms of Streptococcus suis translocation at the blood-cerebrospinal fluid barrier. Fluids and barriers of the CNS, 22(1), 14.

McAfee A, et al. (2025) Western red cedar (Thuja plicata) beehives have no impact on honey bee (Apis mellifera) overwintering colony survival or detoxification enzyme expression. PloS one, 20(4), e0318764.

McAfee A, et al. (2024) Conserved and Unique Protein Expression Patterns Across Reproductive Stage Transitions in Social Hymenopteran Queens. Molecular ecology, 33(23), e17568.

Das SC, et al. (2023) Altered transcriptomes, cell type proportions, and dendritic spine morphology in hippocampus of suicide deaths. medRxiv : the preprint server for health sciences.

López Nadal A, et al. (2023) Omics and imaging combinatorial approach reveals butyrate-induced inflammatory effects in the zebrafish gut. Animal microbiome, 5(1), 15.

Ryan CP, et al. (2022) Immune cell type and DNA methylation vary with reproductive status in women: possible pathways for costs of reproduction. *Evolution, medicine, and public health*, 10(1), 47.

Le Dour C, et al. (2022) Actin-microtubule cytoskeletal interplay mediated by MRTF-A/SRF signaling promotes dilated cardiomyopathy caused by LMNA mutations. *Nature communications*, 13(1), 7886.

Arnatkeviciute A, et al. (2021) Genetic influences on hub connectivity of the human connectome. *Nature communications*, 12(1), 4237.

McAfee A, et al. (2021) Trade-offs between sperm viability and immune protein expression in honey bee queens (*Apis mellifera*). *Communications biology*, 4(1), 48.

Vignier N, et al. (2021) The non-muscle ADF/cofilin-1 controls sarcomeric actin filament integrity and force production in striated muscle laminopathies. *Cell reports*, 36(8), 109601.

McAfee A, et al. (2020) Candidate stress biomarkers for queen failure diagnostics. *BMC genomics*, 21(1), 571.

Saha C, et al. (2020) *Campylobacter jejuni* Cas9 Modulates the Transcriptome in Caco-2 Intestinal Epithelial Cells. *Genes*, 11(10).

Uthicke S, et al. (2019) Little evidence of adaptation potential to ocean acidification in sea urchins living in "Future Ocean" conditions at a CO₂ vent. *Ecology and evolution*, 9(17), 10004.

Zhuang B, et al. (2019) Mega-Analysis of Gene Expression in Mouse Models of Alzheimer's Disease. *eNeuro*, 6(6).

De Wit P, et al. (2018) Gene expression correlated with delay in shell formation in larval Pacific oysters (*Crassostrea gigas*) exposed to experimental ocean acidification provides insights into shell formation mechanisms. *BMC genomics*, 19(1), 160.

Iovinella I, et al. (2018) Proteomic analysis of chemosensory organs in the honey bee parasite *Varroa destructor*: A comprehensive examination of the potential carriers for semiochemicals. *Journal of proteomics*, 181, 131.

Arnatkeviciute A, et al. (2018) Hub connectivity, neuronal diversity, and gene expression in the *Caenorhabditis elegans* connectome. *PLoS computational biology*, 14(2), e1005989.

Lussier AA, et al. (2018) Prenatal Alcohol Exposure: Profiling Developmental DNA Methylation Patterns in Central and Peripheral Tissues. *Frontiers in genetics*, 9, 610.

Ohde T, et al. (2018) Rhinoceros beetle horn development reveals deep parallels with dung beetles. *PLoS genetics*, 14(10), e1007651.

Wilson SL, et al. (2018) Mining DNA methylation alterations towards a classification of placental pathologies. *Human molecular genetics*, 27(1), 135.