

Resource Summary Report

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DEGreport

RRID:SCR_018941

Type: Tool

Proper Citation

DEGreport (RRID:SCR_018941)

Resource Information

URL: <https://bioconductor.org/packages/DEGreport/>

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Description: Software R package for creation of HTML report of differential expression analyses of count data. Integrates some of code mentioned in DESeq2 and edgeR vignettes, and reports ranked list of genes according to fold changes mean and variability for each selected gene.

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

Keywords: HTML report creation, differential expression analyses, count data, code integration, gene list report

Availability: Free, Available for download, Freely available

Resource Name: DEGreport

Resource ID: SCR_018941

Alternate URLs: <http://lpantano.github.io/DEGreport>

License: MIT License

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260805T044426+0000

Ratings and Alerts

No rating or validation information has been found for DEGreport.

No alerts have been found for DEGreport.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Thomas WR, et al. (2026) Dynamic metabolic and molecular changes during seasonal shrinking in *Sorex araneus*. *Genome research*, 36(1), 61.

Arenillas C, et al. (2025) Convergent Genetic Adaptation in Human Tumors Developed Under Systemic Hypoxia and in Populations Living at High Altitudes. *Cancer discovery*, 15(5), 1037.

Bonzi LC, et al. (2025) Matching maternal and paternal experiences underpin molecular thermal acclimation. *Molecular ecology*, 34(15), e17328.

Leung C, et al. (2025) Past environments modulate response to fluctuating temperatures in a marine fish species, *Sebastes fasciatus*. *The Journal of experimental biology*, 228(21).

Ostovar T, et al. (2025) Differential Gene Expression and Unbalanced Homeolog Expression Bias in 4 Million-Year-Old Allopolyploids of *Nicotiana* Section *Repandae*. *Genome biology and evolution*, 17(3).

Huffmyer AS, et al. (2025) Shifts and critical periods in coral metabolism reveal energetic vulnerability during development. *Current biology : CB*, 35(12), 2858.

Stomper J, et al. (2025) Sex differences in DNMT3A-mutant clonal hematopoiesis and the effects of estrogen. *Cell reports*, 44(4), 115494.

Cho HM, et al. (2024) Transcriptome analysis of cynomolgus macaques throughout their lifespan reveals age-related immune patterns. *npj aging*, 10(1), 30.

Holzgruber J, et al. (2024) Type I interferon signaling induces melanoma cell-intrinsic PD-1 and its inhibition antagonizes immune checkpoint blockade. *Nature communications*, 15(1), 7165.

Sung S, et al. (2023) Distinct characteristics of two types of alternative lengthening of telomeres in mouse embryonic stem cells. *Nucleic acids research*, 51(17), 9122.

Pi??a JO, et al. (2023) Multimodal spatiotemporal transcriptomic resolution of embryonic palate osteogenesis. *Nature communications*, 14(1), 5687.

Ta AC, et al. (2022) Temporal and spatial transcriptomic dynamics across brain development in *Xenopus laevis* tadpoles. *G3 (Bethesda, Md.)*, 12(1).

Hempel PP, et al. (2021) RNA-Seq Reveals that Light and Darkness Are Different Stimuli in Freshwater Heterotrophic Actinobacteria. *Frontiers in microbiology*, 12, 739005.

Fourman LT, et al. (2020) Effects of tesamorelin on hepatic transcriptomic signatures in HIV-associated NAFLD. *JCI insight*, 5(16).

Gyuris A, et al. (2019) Physical and Molecular Landscapes of Mouse Glioma Extracellular Vesicles Define Heterogeneity. *Cell reports*, 27(13), 3972.

Pavkovic M, et al. (2019) Multi omics analysis of fibrotic kidneys in two mouse models. *Scientific data*, 6(1), 92.