

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 analysis software, data processing software, software application, software resource

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://pantano.github.io/DEGreport>

License: MIT License

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260919T195400+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 22 mentions in open access literature.

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

Gyles TM, et al. (2026) Transcriptional profiles of antidepressant resistance across the corticolimbic pathway of chronically stressed mice. *Neuropsychopharmacology* : official publication of the American College of Neuropsychopharmacology, 51(7), 1279.

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

Lamon S, et al. (2026) The transcriptomic signature of age and sex is not conserved in human primary myotubes. *Skeletal muscle*, 16(1).

Gyles TM, et al. (2026) A shared transcriptional network in the nucleus accumbens supports resilience to chronic stress across sex. *bioRxiv* : the preprint server for biology.

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.

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 glauca*. *Genome biology and evolution*, 17(3).

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

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.

Oliveira LFS, et al. (2024) Cataloguing the postnatal small intestinal transcriptome during the first postnatal month. *bioRxiv* : the preprint server for biology.

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.

Liu T, et al. (2023) Genome-Wide Characterization of TAZ Binding Sites in Mammary Epithelial Cells. *Cancers*, 15(19).

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

Pernas S, et al. (2022) Early on-treatment transcriptional profiling as a tool for improving pathological response prediction in HER2-positive inflammatory breast cancer. *Therapeutic advances in medical oncology*, 14, 17588359221113269.

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).