

Resource Summary Report

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Qvalue

RRID:SCR_001073

Type: Tool

Proper Citation

Qvalue (RRID:SCR_001073)

Resource Information

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

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Description: R package that takes a list of p-values resulting from the simultaneous testing of hypotheses and estimates their q-values. It is designed to measure the proportion of false positives when a test is significant. The software is capable of generating plots for visualization. It can be applied to problems in genomics, brain imaging, astrophysics, and data mining.

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

Keywords: p value, false positive, null hypothesis, genomics, brain imaging, astrophysics, data mining, r, visualization

Availability: Free, Available for download, Freely available

Resource Name: Qvalue

Resource ID: SCR_001073

Alternate IDs: OMICS_00624

Alternate URLs: <https://github.com/jdstorey/qvalue>

License: LGPL

Record Creation Time: 20220129T080205+0000

Record Last Update: 20260728T043107+0000

Ratings and Alerts

No rating or validation information has been found for Qvalue.

No alerts have been found for Qvalue.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Zhang S, et al. (2025) Immunosequencing identifies signatures of T cell responses for early detection of nasopharyngeal carcinoma. *Cancer cell*, 43(8), 1423.

Karapouliou C, et al. (2025) HMMR has oncoprotein-like properties in neuroblastoma cells and high HMMR expression has independent prognostic potential in neuroblastomas. *Scientific reports*, 15(1), 40434.

Ni A, et al. (2025) Identifying candidate genetic variants for egg number by analyzing over 1,000 fully sequenced layers. *GigaScience*, 14.

Christensson G, et al. (2024) Spatial Multiomics Reveals Intratumoral Immune Heterogeneity with Distinct Cytokine Networks in Lung Cancer Brain Metastases. *Cancer research communications*, 4(11), 2888.

Brenes AJ, et al. (2024) Proteomic and functional comparison between human induced and embryonic stem cells. *eLife*, 13.

Lammer L, et al. (2023) Impact of social isolation on grey matter structure and cognitive functions: A population-based longitudinal neuroimaging study. *eLife*, 12.

Binh Tran TD, et al. (2023) Microbial glutamate metabolism predicts intravenous cocaine self-administration in diversity outbred mice. *Neuropharmacology*, 226, 109409.

Tran TDB, et al. (2023) The microbial community dynamics of cocaine sensitization in two behaviorally divergent strains of collaborative cross mice. *Genes, brain, and behavior*, e12845.

Chan M, et al. (2022) Novel insights from a multiomics dissection of the Hayflick limit. *eLife*, 11.

Hancock-Cerutti W, et al. (2022) ER-lysosome lipid transfer protein VPS13C/PARK23 prevents aberrant mtDNA-dependent STING signaling. *The Journal of cell biology*, 221(7).

Pickett BD, et al. (2022) Genome assembly of the roundjaw bonefish (*Albula glossodonta*), a vulnerable circumtropical sportfish. *GigaByte (Hong Kong, China)*, 2022, gigabyte44.

Brenes AJ, et al. (2021) Erosion of human X chromosome inactivation causes major remodeling of the iPSC proteome. *Cell reports*, 35(4), 109032.

Teuwen LA, et al. (2021) Tumor vessel co-option probed by single-cell analysis. *Cell reports*, 35(11), 109253.

Brenes AJ, et al. (2021) Tissue environment, not ontogeny, defines murine intestinal intraepithelial T lymphocytes. *eLife*, 10.

Goveia J, et al. (2020) An Integrated Gene Expression Landscape Profiling Approach to Identify Lung Tumor Endothelial Cell Heterogeneity and Angiogenic Candidates. *Cancer cell*, 37(1), 21.

Curtis M, et al. (2019) Fibroblasts Mobilize Tumor Cell Glycogen to Promote Proliferation and Metastasis. *Cell metabolism*, 29(1), 141.

Carazo F, et al. (2019) TranscriptAchilles: a genome-wide platform to predict isoform biomarkers of gene essentiality in cancer. *GigaScience*, 8(4).

Odamaki T, et al. (2018) Genomic diversity and distribution of *Bifidobacterium longum* subsp. *longum* across the human lifespan. *Scientific reports*, 8(1), 85.

Smith NL, et al. (2018) Developmental Origin Governs CD8⁺ T Cell Fate Decisions during Infection. *Cell*, 174(1), 117.

Drawnel FM, et al. (2017) Molecular Phenotyping Combines Molecular Information, Biological Relevance, and Patient Data to Improve Productivity of Early Drug Discovery. *Cell chemical biology*, 24(5), 624.