

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

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: 20260912T200007+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 32 mentions in open access literature.

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

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in Mycobacterium tuberculosis constitutively generates subpopulations with distinct clinical phenotypes. iScience, 29(5), 115045.

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.

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.

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

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).

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

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