

Resource Summary Report

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ggsignif

RRID:SCR_023047

Type: Tool

Proper Citation

ggsignif (RRID:SCR_023047)

Resource Information

URL: <https://CRAN.R-project.org/package=ggsignif>

Proper Citation: ggsignif (RRID:SCR_023047)

Description: Software package to indicate if two groups are significantly different. Used to add significance brackets to ggplots.

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

Keywords: indicate if two groups are significantly different, add significance brackets

Availability: Free, Available for download, Freely available

Resource Name: ggsignif

Resource ID: SCR_023047

Alternate URLs: <https://github.com/const-ae/ggsignif>

License: GPL v3

Record Creation Time: 20221215T050202+0000

Record Last Update: 20260728T043648+0000

Ratings and Alerts

No rating or validation information has been found for ggsignif.

No alerts have been found for ggsignif.

Data and Source Information

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Pflughaupt P, et al. (2025) Prior knowledge on context-driven DNA fragmentation probabilities can improve de novo genome assembly algorithms. BMC bioinformatics, 26(1), 245.

Olweny G, et al. (2025) Protocol for identifying Mycobacterium tuberculosis infection status through airway microbiome profiling. STAR protocols, 6(1), 103574.

Teng ZJ, et al. (2025) Inositol phosphates as an overlooked phosphorous source in marine ecosystems. The ISME journal, 19(1).

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1 charts the structural landscape of human early endosome complexes. Nature, 643(8070), 252.

Awasthi BW, et al. (2025) The network response to Egf is tissue-specific. iScience, 28(4), 112146.

Selma-Royo M, et al. (2024) Birthmode and environment-dependent microbiota transmission dynamics are complemented by breastfeeding during the first year. Cell host & microbe, 32(6), 996.

Giovannetti M, et al. (2024) SIN-3 transcriptional coregulator maintains mitochondrial homeostasis and polyamine flux. iScience, 27(5), 109789.

Yang B, et al. (2024) Identification of ferroptosis-related gene signature for tuberculosis diagnosis and therapy efficacy. iScience, 27(7), 110182.

Ares-Arroyo M, et al. (2023) Origins of transfer establish networks of functional dependencies for plasmid transfer by conjugation. Nucleic acids research, 51(7), 3001.

Zhao J, et al. (2023) Changes in m6A RNA methylation are associated with male sterility in wolfberry. BMC plant biology, 23(1), 456.

Elizabeth Deeter M, et al. (2023) Accelerated abdominal lipid depletion from pesticide treatment alters honey bee pollen foraging strategy, but not onset, in worker honey bees. The Journal of experimental biology, 226(7).

Wang W, et al. (2023) Integration of high-throughput phenotyping, GWAS, and predictive models reveals the genetic architecture of plant height in maize. Molecular plant, 16(2), 354.

Midha AD, et al. (2023) Organ-specific fuel rewiring in acute and chronic hypoxia redistributes glucose and fatty acid metabolism. Cell metabolism, 35(3), 504.

Salimi A, et al. (2023) InterOpt: Improved gene expression quantification in qPCR experiments using weighted aggregation of reference genes. *iScience*, 26(10), 107945.