

Resource Summary Report

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[ggrepel](#)

RRID:SCR_017393

Type: Tool

Proper Citation

ggrepel (RRID:SCR_017393)

Resource Information

URL: <https://cran.r-project.org/package=ggrepel>

Proper Citation: ggrepel (RRID:SCR_017393)

Description: Software tool to provide text and label geoms for ggplot2 that help to avoid overlapping text labels. Labels repel away from each other and away from data points.

Resource Type: software resource, software application, standalone software

Keywords: text, label, geoms, avoid, overlapping

Availability: Free, Available for download, Freely available

Resource Name: ggrepel

Resource ID: SCR_017393

Alternate URLs: <https://github.com/slowkow/ggrepel>

License: GNU GPL v3

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260804T043651+0000

Ratings and Alerts

No rating or validation information has been found for ggrepel.

No alerts have been found for ggrepel.

Data and Source Information

Usage and Citation Metrics

We found 50 mentions in open access literature.

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

Priego-Cubero S, et al. (2025) Evolution and diversification of the momilactone biosynthetic gene cluster in the genus *Oryza*. *The New phytologist*, 245(6), 2681.

Tercan B, et al. (2025) Protocol for assessing distances in pathway space for classifier feature sets from machine learning methods. *STAR protocols*, 6(2), 103681.

de Ocampo MP, et al. (2025) Leaf Na⁺ effects and multi-trait GWAS point to salt exclusion as the key mechanism for reproductive stage salinity tolerance in rice. *Annals of botany*, 135(5), 949.

Lin CP, et al. (2025) Spatiotemporal dynamics reveal high turnover and contrasting assembly processes in fungal communities across contiguous habitats of tropical forests. *Environmental microbiome*, 20(1), 23.

Song X, et al. (2025) Leaf functional metabolic traits reveal the adaptation strategies of larch trees along the R/B ratio gradient at the stand level. *Scientific reports*, 15(1), 19185.

Schall PZ, et al. (2025) Integrative Genotyping and Analysis of Canine Structural Variation Using Long-read and Short-read Data. *Genome biology and evolution*, 17(10).

Berger AH, et al. (2025) High-resolution transcriptional impact of AIRE: effects of pathogenic variants p.Arg257Ter, p.Cys311Tyr, and polygenic risk variant p.Arg471Cys. *Frontiers in immunology*, 16, 1572789.

Jelcic I, et al. (2025) T-bet⁺ CXCR3⁺ B cells drive hyperreactive B-T cell interactions in multiple sclerosis. *Cell reports. Medicine*, 6(3), 102027.

Wang H, et al. (2025) Phenotypic plasticity and increased infiltration of peripheral blood-derived TREM1⁺ mono-macrophages following radiotherapy in rectal cancer. *Cell reports. Medicine*, 6(1), 101887.

Peskett TR, et al. (2025) A network of P-body and Whi3 condensates adjusts cell fate decisions to cellular context. *Molecular cell*, 85(19), 3661.

Okoye GD, et al. (2025) Single-cell map of innate-like lymphocyte response to *Francisella tularensis* infection reveals interleukin-17-dependent protection by MAIT cells. *iScience*, 28(3), 111810.

Paloviita P, et al. (2025) Integrated transcriptomic analysis reveals metabolic remodeling and gene expression networks related to human 8-cell-stage embryo-like cells. *Cell reports*, 45(1), 116748.

Hoyer MJ, et al. (2024) Combinatorial selective ER-phagy remodels the ER during neurogenesis. *Nature cell biology*, 26(3), 378.

Chan M, et al. (2024) A kinase to cytokine explorer to identify molecular regulators and potential therapeutic opportunities. *eLife*, 12.

Fuchs Wightman F, et al. (2024) Influence of RNA circularity on Target RNA-Directed MicroRNA Degradation. *Nucleic acids research*, 52(6), 3358.

Zaychikova M, et al. (2024) Vic9 mycobacteriophage: the first subcluster B2 phage isolated in Russia. *Frontiers in microbiology*, 15, 1513081.

Hodonsky CJ, et al. (2024) Multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci. *Cell genomics*, 4(1), 100465.

de Wit S, et al. (2024) Heart failure-induced microbial dysbiosis contributes to colonic tumour formation in mice. *Cardiovascular research*, 120(6), 612.

Lin CP, et al. (2024) Environmental DNA-based biodiversity profiling along the Houdong River in north-eastern Taiwan. *Biodiversity data journal*, 12, e116921.

Bénéjam J, et al. (2024) Phenotyping data coupled with RNA sequencing of apple genotypes exhibiting contrasted quantitative trait loci architecture for apple scab (*Venturia inaequalis*) resistance. *Data in brief*, 56, 110778.