

Resource Summary Report

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ggVennDiagram

RRID:SCR_026950

Type: Tool

Proper Citation

ggVennDiagram (RRID:SCR_026950)

Resource Information

URL: <https://cran.r-project.org/web/packages/ggVennDiagram/readme/README.html>

Proper Citation: ggVennDiagram (RRID:SCR_026950)

Description: Software R package to generate Venn diagram.'ggplot2' implement of Venn Diagram.

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:34557218](#)

Keywords: generate Venn diagram,

Funding: Fundamental Research Funds for the Central Universities ;
National Key Research Program of China ;
National Natural Science Foundation of China ;
Royal Society-Newton Advanced Fellowship ;
Wuhan Applied Foundational Frontier Project

Availability: Free, Available for download, Freely available

Resource Name: ggVennDiagram

Resource ID: SCR_026950

Alternate URLs: <https://github.com/gaospecial/ggVennDiagram>

License: GNU GPL v3

Record Creation Time: 20250517T055756+0000

Record Last Update: 20260829T183458+0000

Ratings and Alerts

No rating or validation information has been found for ggVennDiagram .

No alerts have been found for ggVennDiagram .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Amin MHF, et al. (2026) Haplotype-level analysis of environmental DNA metabarcoding revealed the biogeography and phylogeography of freshwater fishes in Korean Peninsula. Scientific reports, 16(1), 6955.

Witkowski RJ, et al. (2026) A Volatile Cue From a Specialist Herbivore Primes Gene Expression Against Biotic Stress in Tall Goldenrod (*Solidago altissima* L.). Plant, cell & environment, 49(3), 1424.

Mäkinen M, et al. (2026) Transcriptomics analysis identifies folding and secretion related genes for improving monoclonal antibody production in *Thermothelomyces heterothallica* C1. Microbial cell factories, 25(1).

Bigger-Allen AA, et al. (2026) Integrated transcriptomic and proteomic analyses identify novel biomarkers of bladder outlet obstruction. bioRxiv : the preprint server for biology.

Fan H, et al. (2026) Inhaled Angiopoietin-Like 4 Antisense Oligonucleotide Therapy for Lung Injury and Fibrosis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(23), e01909.

Aron E, et al. (2026) Single-cell immunophenotyping identifies CD8+GZMK+IFNG+ T cells as a key immune population in cutaneous Lyme disease. JCI insight, 11(4).

Yang J, et al. (2026) Decoding clone evolution in HER2 amplified breast cancer through single-cell and spatial transcriptomics analysis of copy number variations. Scientific reports, 16(1).

Baril T, et al. (2026) MycoMobilome: a community-focused non-redundant database of transposable element consensus sequences for the fungal kingdom. NAR genomics and bioinformatics, 8(1), lqag026.

Qu X, et al. (2026) Exploring the shared gene signatures between rheumatoid arthritis and type 2 diabetes and their implication for drug repositioning on bioinformatics analysis. Medicine, 105(9), e47809.

Ojo OA, et al. (2025) Gfi1 controls the formation of effector-like CD8+ T cells during chronic infection and cancer. Nature communications, 16(1), 4542.

Hernández-Becerril DU, et al. (2025) Diversity and distribution of the eukaryotic picoplankton in the oxygen minimum zone of the tropical Mexican Pacific. *Journal of plankton research*, 47(2), fbae083.

Kgoadi K, et al. (2025) Alveolar macrophages from persons with HIV mount impaired TNF signaling networks to *M. tuberculosis* infection. *Nature communications*, 16(1), 2397.

Ribeyre Z, et al. (2025) De novo transcriptome assembly and discovery of drought-responsive genes in white spruce (*Picea glauca*). *PloS one*, 20(1), e0316661.

Cassens J, et al. (2025) Whole Genome Sequencing Reveals Clade-Specific Genetic Variation in Blacklegged Ticks. *Ecology and evolution*, 15(2), e70987.

Manrique-de-la-Cuba MF, et al. (2025) Cold adaptation and horizontal gene transfer shape Antarctic sponge microbiomes. *Microbiome*, 13(1), 243.

Bargmann T, et al. (2025) Activation of CD8⁺ T Cells in the Human Ex Vivo Lung Tumor Microenvironment Using Anti-CD3/CD28 and Nivolumab. *European journal of immunology*, 55(9), e70060.

Banerjee S, et al. (2025) Quorum sensing regulation by the nitrogen phosphotransferase system in *Pseudomonas aeruginosa*. *bioRxiv : the preprint server for biology*.

Aron E, et al. (2025) Single cell immunophenotyping identifies CD8⁺ GZMK⁺ IFNG⁺ T cells as a key immune population in cutaneous Lyme disease. *bioRxiv : the preprint server for biology*.

Khoo LY, et al. (2025) Integrated multi-sample transcriptomic analysis of COVID-19 patients against controls using a bioinformatics pipeline. *Scientific reports*, 15(1), 19644.

Gil-Gomez A, et al. (2025) Proteome remodeling in the zoospore-to-vegetative cell transition of the stramenopile *Aurantiochytrium limacinum* reveals candidate ectoplasmic network proteins. *PloS one*, 20(7), e0326651.