

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: source code, software resource, software toolkit

Defining Citation: [PMID:34557218](#)

Keywords: generate Venn diagram,

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

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: 20260728T043745+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 37 mentions in open access literature.

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

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

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.

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.

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.

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.

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*.

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.

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

Krueger ME, et al. (2025) Comparative analysis of Parkinson's and inflammatory bowel disease gut microbiomes reveals shared butyrate-producing bacteria depletion. *NPJ Parkinson's disease*, 11(1), 50.

Banerjee S, et al. (2025) Quorum sensing regulation by the nitrogen phosphotransferase system in *Pseudomonas aeruginosa*. *Journal of bacteriology*, 207(8), e0004825.

Wilcox JJS, et al. (2025) The CpG Landscape of Protein Coding DNA in Vertebrates. *Evolutionary applications*, 18(5), e70101.

Zanghí G, et al. (2025) Genome-wide gene expression profiles throughout human malaria parasite liver stage development in humanized mice. *Nature microbiology*, 10(2), 569.

Falcucci S, et al. (2025) Transcriptome analysis of HPV16-positive cells expressing intrabodies targeting E6 and E7 oncoproteins to unravel intrabody antitumor activity. *Journal of translational medicine*, 23(1), 1095.

Sidhu G, et al. (2025) The transcriptomics of phenotypic nonspecificity in *Drosophila melanogaster*. *G3 (Bethesda, Md.)*, 15(11).

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.

Zhang X, et al. (2025) Benchmarking metabolic RNA labeling techniques for high-throughput single-cell RNA sequencing. *Nature communications*, 16(1), 5952.

Böttinger K, et al. (2024) "Small is beautiful" - Examining reliable determination of low-abundant therapeutic antibody glycovariants. *Journal of pharmaceutical analysis*, 14(10), 100982.

Fang M, et al. (2024) Structural and functional differences of gut microbiota in *Pomacea canaliculata* from different geographical locations and habitats. *Ecology and evolution*, 14(10), e70283.