

Resource Summary Report

Generated by PRECISE-TBI on Sep 9, 2026

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: 20260905T133535+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 [PRECISE-TBI](#) .

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.

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.

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).

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.

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).

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.

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*.

Banerjee S, et al. (2025) Quorum sensing regulation by the nitrogen phosphotransferase system in *Pseudomonas aeruginosa*. *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.

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

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.