

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

[ggvenn](#)

RRID:SCR_025300

Type: Tool

Proper Citation

ggvenn (RRID:SCR_025300)

Resource Information

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

Proper Citation: ggvenn (RRID:SCR_025300)

Description: Software R package to draw venn diagram by ggplot2.

Resource Type: software resource, software toolkit, source code

Keywords: draw venn diagram,

Availability: Free, Available for download, Freely available

Resource Name: ggvenn

Resource ID: SCR_025300

License: MIT license

Record Creation Time: 20240502T053246+0000

Record Last Update: 20260821T194324+0000

Ratings and Alerts

No rating or validation information has been found for ggvenn.

No alerts have been found for ggvenn.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Huang Q, et al. (2026) Evaluation and expression-level verification of the prognostic value of palmitoylation-related genes in ovarian cancer. *Scientific reports*, 16(1).

Shang C, et al. (2026) Integrated Single-Cell and Bulk RNA Sequencing Identifies Macrophage Heterogeneity and Mitophagy-Related Biomarkers in Idiopathic Pulmonary Fibrosis. *International journal of molecular sciences*, 27(10).

Meyer D, et al. (2026) diffMONT: predicting methylation-specific PCR biomarkers based on nanopore sequencing data for clinical application. *Bioinformatics (Oxford, England)*, 42(2).

Luo S, et al. (2026) Identification of prognostic genes associated with tolerogenic dendritic cells in gastric cancer based on transcriptomic data. *PloS one*, 21(3), e0343688.

Zeng TB, et al. (2026) SETDB1 enables development beyond cleavage stages by extinguishing the MERVL-driven two-cell totipotency transcriptional program in the mouse embryo. *eLife*, 15.

Sasidharan V, et al. (2026) Extracellular vesicles mediate stem cell signaling and systemic RNAi in planarians. *Science advances*, 12(6), eady1461.

Zhang T, et al. (2026) Identification and validation of paraptosis-related prognostic biomarkers in lung adenocarcinoma: An observational study based on transcriptomics and clinical outcomes. *Medicine*, 105(8), e47724.

Zhao X, et al. (2026) Identification and validation of mitochondrial metabolism-related biomarkers in coronary heart disease. *Medicine*, 105(7), e47595.

Xu R, et al. (2026) Identification of mitochondria metabolism-related biomarkers associated with the development of rheumatoid arthritis using bioinformatics: An observational study. *Medicine*, 105(2), e44435.

Yang R, et al. (2026) Identification of Biomarkers Associated With Copper Metabolism in Ischemic Stroke Through Bulk RNA Sequencing and Mendelian Randomization Analysis. *Cellular and molecular neurobiology*, 46(1).

Ting W, et al. (2026) Identification of NF- κ B pathway-related biomarkers in myocardial ischemia-reperfusion injury: based on transcriptomics analysis and RT-qPCR validation. *Scientific reports*, 16(1).

Valdez-Palomares F, et al. (2026) Human fecal transplantation from stunted children promotes metabolic dysfunction in mice fed with a high-fat and high-fructose corn syrup diet. *Gut microbes*, 18(1), 2651984.

Gong X, et al. (2026) Location and growth period influence the bioactive compounds of *Angelica sinensis* (Oliv.) diels: multi-omics insights. *BMC plant biology*, 26(1).

Genebrier S, et al. (2026) Granzyme B-expressing regulatory B cells share the same origin as conventional blood B cells. *Biochemistry and biophysics reports*, 46, 102594.

Li N, et al. (2026) Exploration of m7G-related immune genes and construction of a prognostic risk model in gastric cancer. *Scientific reports*, 16(1).

Shen P, et al. (2026) High RMI1 expression is associated with cancer cell progression and poor prognosis in prostate cancer. *Oncology reports*, 55(4).

Heraghty SD, et al. (2026) Sequencing, annotation and analysis of the genome of *Oxycarenus hyalinipennis*, the cotton seed bug. *Life science alliance*, 9(8).

Zhao T, et al. (2026) Identification of key macrophage-related genes in systemic sclerosis-associated interstitial lung disease based on single-cell and bulk transcriptomic data. *PLoS one*, 21(3), e0344166.

LaBuda SE, et al. (2026) Characterizing the Discordance between AT-Rich Interacting Domain 1A Protein and Genotype in Endometrioid-Type Endometrial Tumors. *The American journal of pathology*, 196(7), 1530.

Sun M, et al. (2025) Transcriptome combined with Mendelian randomization to identify key genes related to polyamine metabolism in childhood obesity and elucidate their molecular regulatory mechanisms. *Scientific reports*, 15(1), 17799.