

Resource Summary Report

Generated by RRID on Aug 5, 2026

UpSetR

RRID:SCR_026112

Type: Tool

Proper Citation

UpSetR (RRID:SCR_026112)

Resource Information

URL: <https://github.com/hms-dbmi/UpSetR>

Proper Citation: UpSetR (RRID:SCR_026112)

Description: Software R package for visualization of intersecting sets and their properties.

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:28645171](https://pubmed.ncbi.nlm.nih.gov/28645171/)

Keywords: visualization of intersecting sets,

Funding: NHGRI R00 HG007583;
NHGRI U54HG007963;
NCI U01 CA198935

Availability: Free, Available for download, Freely available

Resource Name: UpSetR

Resource ID: SCR_026112

Alternate URLs: <https://cran.rstudio.com/web/packages/UpSetR/>

License: MIT license

Record Creation Time: 20241203T053255+0000

Record Last Update: 20260805T044554+0000

Ratings and Alerts

No rating or validation information has been found for UpSetR.

No alerts have been found for UpSetR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 72 mentions in open access literature.

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

Zhu Y, et al. (2025) In-depth analysis of 17,115 rice transcriptomes reveals extensive viral diversity in rice plants. Nature communications, 16(1), 1559.

Barnouin K, et al. (2025) Identification of mechanistic CKD biomarkers in a rat SNx kidney fibrosis model by transcriptomics and proteomics detectable in biofluids. Scientific reports, 15(1), 11200.

Fu X, et al. (2025) The baseline circulating immunophenotype characteristics associate with PD(L)-1 targeted treatment response, irae onset, and prognosis. Scientific reports, 15(1), 17450.

Crombez E, et al. (2025) The subordinate role of pseudogenization to recombinative deletion following polyploidization in angiosperms. Nature communications, 16(1), 6335.

Rask GC, et al. (2025) Seclidemstat (SP-2577) Induces Transcriptomic Reprogramming and Cytotoxicity in Multiple Fusion-Positive Sarcomas. Cancer research communications, 5(9), 1584.

Borsari B, et al. (2025) The chronODE framework for modelling multi-omic time series with ordinary differential equations and machine learning. Nature communications, 16(1), 7021.

Yassouf MY, et al. (2025) Improved transcriptome assembly and functional annotation of *Pleurodeles waltl* for regeneration research. PloS one, 20(5), e0323196.

Xu D, et al. (2025) Spatially resolved single-cell transcriptome analysis of murine *Salmonella* infection reveals the role of distal colonocytes in the inflammatory response. Gut microbes, 17(1), 2579909.

Feng Y, et al. (2025) Regional antimicrobial resistance gene flow among the One Health sectors in China. Microbiome, 13(1), 3.

Rudraprasad D, et al. (2025) RNA-Sequencing Reveals the Modulation of the NLRP3 Inflammasome by miR-223-3p in Extracellular Vesicles in Bacterial Endophthalmitis. Investigative ophthalmology & visual science, 66(4), 53.

Tang N, et al. (2025) Identification of Key Ferroptosis-Related Genes as Potential Diagnostic Biomarkers for Ischemic Stroke: Evidences from Integrated Bioinformatics Analysis and Experiments. *Cellular and molecular neurobiology*, 45(1), 97.

Zobel M, et al. (2025) A human CAGinSTEM platform for decoding HTT repeats' somatic instability links CAG interruption to HD pathology in neurons. *Cell reports*, 44(12), 116685.

Omufwoko KS, et al. (2025) Developmental transcriptomes predict adult social behaviours in the socially flexible sweat bee, *Lasioglossum baleicum*. *Molecular ecology*, 34(15), e17244.

Feng H, et al. (2025) Genome and Tissue-Specific Transcriptome of the Tropical Milkweed (*Asclepias curassavica*). *Plant direct*, 9(3), e70031.

Rodschinka G, et al. (2025) Comparative CRISPRi screens reveal a human stem cell dependence on mRNA translation-coupled quality control. *Nature structural & molecular biology*, 32(10), 1932.

Awasthi BW, et al. (2025) The network response to Egf is tissue-specific. *iScience*, 28(4), 112146.

Ver Heul AM, et al. (2025) RAG suppresses group 2 innate lymphoid cells. *eLife*, 13.

Beddows I, et al. (2024) Cell State of Origin Impacts Development of Distinct Endometriosis-Related Ovarian Carcinoma Histotypes. *Cancer research*, 84(1), 26.

Sulesky-Grieb A, et al. (2024) Stable, multigenerational transmission of the bean seed microbiome despite abiotic stress. *mSystems*, 9(11), e0095124.

Desponds E, et al. (2024) Immuno-Transcriptomic Profiling of Blood and Tumor Tissue Identifies Gene Signatures Associated with Immunotherapy Response in Metastatic Bladder Cancer. *Cancers*, 16(2).