

Resource Summary Report

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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](#)

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.

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

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.

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.

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

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.

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

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.

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).

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