

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 toolkit, source code, software resource

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: 20260815T183234+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 89 mentions in open access literature.

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

Fu L, et al. (2026) Genetic insights and mechanistic parallels in gestational diabetes mellitus and type 2 diabetes. *Nature communications*, 17(1), 660.

Dor?? G, et al. (2026) First draft genome of the decaploid species, *Ludwigia grandiflora* subsp. *hexapetala*, validated through gene expression. *GigaByte* (Hong Kong, China), 2026, gigabyte176.

DePuyt AE, et al. (2026) Type 1-polarized DC immunotherapeutic contains heterogeneous populations with IL-12p70 production restricted to a rare subset. *bioRxiv : the preprint server for biology*.

Chen W, et al. (2026) Integrative multi-omics reveals microbial genomic variants driving altered host-microbe interactions in autism spectrum disorder. *Cell reports. Medicine*, 7(1), 102516.

Marquardt A, et al. (2026) Transcriptome and metabolome insights into closely related upland cotton (*Gossypium hirsutum*) genotypes during differing responses to progressive soil drying. *BMC plant biology*, 26(1).

Liu Y, et al. (2026) Positive bacteria-phage interactions drive sulfamethoxazole removal. *Environmental science and ecotechnology*, 31, 100698.

Giovannini L, et al. (2026) Arbuscular mycorrhizal symbiosis in tomato roots with a diverse range of carotene accumulation. *Mycorrhiza*, 36(3).

Liu X, et al. (2026) Transcriptome-metabolome integration reveals MYB/WRKY-RGA network and phenylalanine metabolism in potato late blight resistance. *BMC plant biology*, 26(1).

Zhang J, et al. (2026) Expression and significance analyses of microRNAs in colorectal cancer. *Molecular and clinical oncology*, 24(3), 20.

Wang YY, et al. (2026) The reduced genome of *Candidatus Portiera* sp. in *Bemisia afer*: evolutionary trajectories and functional implications. *BMC genomics*, 27(1), 205.

Kiran S, et al. (2026) Segmented filamentous bacteria are worldwide human gut commensals. *Nature communications*, 17(1).

Muturi EJ, et al. (2026) Fungal Community Composition and Diversity Across Soil Depths Under Different Cover Crop Treatments. *Journal of fungi (Basel, Switzerland)*, 12(2).

Sterrett MC, et al. (2025) Comparative analyses of disease-linked missense mutations in the RNA exosome modeled in budding yeast reveal distinct functional consequences in translation. *RNA (New York, N.Y.)*, 31(7), 988.

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.

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.

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

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.

Li E, et al. (2025) Single-cell transcriptomics of ventral forebrain progenitors identifies Evf2 enhancer lncRNA-enhancer gene guidance through direct RNA binding and RNP recruitment domains. *Nature communications*, 16(1), 6902.

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.

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.