

Resource Summary Report

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ComplexHeatmap

RRID:SCR_017270

Type: Tool

Proper Citation

ComplexHeatmap (RRID:SCR_017270)

Resource Information

URL: <https://bioconductor.org/packages/release/bioc/html/ComplexHeatmap.html>

Proper Citation: ComplexHeatmap (RRID:SCR_017270)

Description: Software package to arrange multiple heatmaps and support various annotation graphics. Used to visualize associations between different sources of data sets and to reveal potential patterns.

Resource Type: data analysis software, data processing software, data visualization software, software application, software resource

Defining Citation: [PMID:27207943](#)

Keywords: arrange, multiple, heatmap, visualize, data, pattern, genomic, dataset, bio.tools

Funding: BMBF ;
German Cancer Research Center-Heidelberg Center for Personalized Oncology

Availability: Free, Available for download, Freely available

Resource Name: ComplexHeatmap

Resource ID: SCR_017270

Alternate IDs: biotools:complexheatmap

Alternate URLs: <https://github.com/jokergoo/ComplexHeatmap>,
<https://bio.tools/complexheatmap>

License: MIT licence

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260912T200020+0000

Ratings and Alerts

No rating or validation information has been found for ComplexHeatmap.

No alerts have been found for ComplexHeatmap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3949 mentions in open access literature.

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

Leelatian N, et al. (2026) DNA damage response profile distinguishes poor-acting gliomas with shared methylome signatures. *Neuro-oncology*, 28(1), 117.

Zhu G, et al. (2026) Exploration Biomarkers for Recurrence of Hepatocellular Carcinoma After Liver Transplantation Based on Bioinformatics Analysis. *Biochemical genetics*, 64(3), 3896.

Kurt F, et al. (2026) A Phase-Dependent Model of Sorghum (*Sorghum bicolor*) Cold Acclimation: Integrating Multi-Layered Networks and Alternative Splicing Signatures. *Biology*, 15(7).

Fan X, et al. (2026) TRIM28 orchestrates SUMO-ubiquitin crosstalk to stabilize PPARG and drive bladder cancer progression. *Cell death & disease*, 17(1).

Qiu X, et al. (2026) Identification and validation of a novel ferroptosis-related gene signature associated with inherited retinal degeneration in Rd10 mice. *Scientific reports*, 16(1), 6992.

Zheng Y, et al. (2026) Development and validation of a robust cuproptosis related signature for primary glioma via machine learning aided by loop training and validation. *Discover oncology*, 17(1), 245.

Brown LP, et al. (2026) Metagenomic Assessment of Full-Scale Wastewater Treatment Plants Identifies Sentinel Antibiotic Resistance Gene Families for Monitoring Reclaimed Wastewater and Treated Sludge. *Environmental science & technology*, 60(6), 4632.

Swanepoel S, et al. (2026) A weighted gene co-expression network analysis characterises the common defence responses of Eucalyptus to diverse biotic challenges. *Scientific reports*, 16(1), 5387.

Gögenur M, et al. (2026) Preoperative positive ctDNA analysis is associated with the tumor microenvironment, and the risk of recurrence in non-metastatic colorectal cancer. *NPJ precision oncology*, 10(1).

Setti A, et al. (2026) The role of low-complexity repeats in RNA-RNA interactions and a deep learning framework for duplex prediction. *Nature communications*, 17(1), 1637.

Choi Y, et al. (2026) Combination of bacteriophage-probiotics alleviates intestinal barrier dysfunction by regulating gut microbiome in a chick model of multidrug-resistant *Salmonella* infection. *Journal of animal science and biotechnology*, 17(1), 14.

Ding N, et al. (2026) Transcriptome combined with single-cell data to construct a prognostic model for glycosylation-related genes in osteosarcoma. *Discover oncology*, 17(1).

Xue T, et al. (2026) Pan-genomic analysis and abiotic stress expression of eight TPS gene families in *Brassica napus*. *BMC plant biology*, 26(1).

Atkinson JR, et al. (2026) Alternatively activated neutrophils limit T cell-driven neuroinflammation. *Journal of neuroinflammation*, 23(1).

Nadernezhad A, et al. (2026) Bottom-Up Programming of Cell States in Cancer Organoids with Defined Synthetic Adhesion Cues. *Advanced materials* (Deerfield Beach, Fla.), 38(27), e17390.

Venkatesan S, et al. (2026) Cell type-agnostic transcriptomic signatures enable uniform comparisons of neural maturation. *PLoS biology*, 24(4), e3003757.

Piri R, et al. (2026) Host gene expression analysis in the detection of bacterial and viral etiology in children hospitalized with a suspected severe infection. *Communications medicine*, 6(1).

Stis AE, et al. (2026) Biosensor Cell Array Reveals Temporal GABA Secretion Dynamics from Pancreatic Islets. *bioRxiv : the preprint server for biology*.

Jang Y, et al. (2026) Innate immune sensing of dietary alcohol ignites inflammation to drive alcohol-related disease. *Science advances*, 12(15), eaea3979.

Xiang Y, et al. (2026) Construction of circadian clock signature for tumor microenvironment in predicting survival of esophageal squamous cell carcinoma. *Frontiers in immunology*, 17, 1738892.