

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](https://pubmed.ncbi.nlm.nih.gov/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: 20260905T133008+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 [PRECISE-TBI](#) .

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.

Hao Q, et al. (2026) A pan-cancer single cell landscape reveals heterogeneity and functional diversity of double-negative T cells. *Molecular cancer*, 25(1), 24.

Schoof M, et al. (2026) Investigation of a global mouse methylome atlas reveals subtype-specific copy number alterations in pediatric cancer models. *Nature genetics*, 58(1), 143.

Chen L, et al. (2026) RNF39 promotes colorectal cancer progression by driving RINT1 degradation and suppressing ER stress-induced apoptosis. *Clinical and translational medicine*, 16(1), e70577.

Weidele K, et al. (2026) Micrometastasis-derived models enable drug testing for early-stage, high-risk melanoma patients. *EMBO molecular medicine*, 18(1), 297.

Chen Y, et al. (2026) The transcription factor CUX1 exerts opposing roles in human and mouse adipocyte differentiation. *Molecular metabolism*, 103, 102290.

Johansen Å, et al. (2026) Triazine-Trione Thermosets with High Processability for Scaffold Applications in Bone Tissue Engineering. *Advanced healthcare materials*, 15(7), e04163.

Roy N, et al. (2026) A Covalent Allosteric Molecular Glue Suppresses NRF2-Dependent Cancer Growth. *Cancer discovery*, 16(5), 953.

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. *Cancer discovery*, 16(3), 497.

Rahman AA, et al. (2026) Structural and functional gastrointestinal abnormalities in ACTA2 R179H mice modeling multisystemic smooth muscle dysfunction syndrome. *JCI*

insight, 11(4).

Follain G, et al. (2026) Fast label-free live imaging with FlowVision reveals key principles of cancer cell arrest on endothelial monolayers. *The EMBO journal*, 45(4), 1381.

Zavari A, et al. (2026) Molecular Epidemiology and Genetic Profile of Non-Typhoidal Salmonella Serovars Isolated From Poultry Production Chain in Khorasan Province, Iran: A Comprehensive Analysis of Prevalence, Virulence Genes, and Antibiotic Resistance. *Veterinary medicine and science*, 12(1), e70757.

Gao S, et al. (2026) A spatially resolved atlas of gastric cancer characterises a lymphocyte-aggregated region. *Nature communications*, 17(1).

Zhuo J, et al. (2026) Decrypting potential mechanisms linking ochratoxin A to hepatocellular carcinoma: an integrated approach combining toxicology, machine learning, molecular docking, and molecular dynamics simulation. *BMC pharmacology & toxicology*, 27(1).

de Menezes MN, et al. (2026) High efficiency CRISPR knock-in demonstrates that TCF1 is insufficient to reverse T cell exhaustion. *Nature communications*, 17(1).

López-Sampere Y, et al. (2026) NRF2 deficit prevents pathologic Tau seeding and spreading in an induced tauopathy mouse model. *Redox biology*, 91, 104068.

Das V, et al. (2026) Multi-omics data integration from patients with carotid stenosis illuminates key molecular signatures of atherosclerotic instability. *Genome medicine*, 18(1).

Pasanisi J, et al. (2026) Constitutional BRCA1 Methylation is associated with high level of tumoral BRCA1 methylation and homologous recombination deficiency in triple-negative breast cancer. *NPJ breast cancer*, 12(1).

Zhan Q, et al. (2026) Multi-Omics Analysis Reveals Sex-Specific Signatures for BCG Vaccine Efficacy. *European journal of immunology*, 56(2), e70144.