

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>

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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, software application, data visualization software, software resource

Defining Citation: [PMID:27207943](#)

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

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

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

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.

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.