

Resource Summary Report

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[circlize](#)

RRID:SCR_002141

Type: Tool

Proper Citation

circlize (RRID:SCR_002141)

Resource Information

URL: <http://cran.r-project.org/web/packages/circlize/>

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Description: Software package that implements and enhances circular visualization in R. Due to natural born feature of R to draw statistical graphics, this package can provide more general and flexible way to visualize huge information in circular style.

Synonyms: circlize: Circular Visualization in R

Resource Type: software resource, software application, standalone software

Defining Citation: [PMID:24930139](#)

Keywords: circular visualization, draw statistical graphics, circular style graphics, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: circlize

Resource ID: SCR_002141

Alternate IDs: OMICS_04658, biotools:circlize

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

License: GNU General Public License, v2, v3

Record Creation Time: 20220129T080211+0000

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Ratings and Alerts

No rating or validation information has been found for circlize.

No alerts have been found for circlize.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1073 mentions in open access literature.

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

Safari M, et al. (2026) Combined HDAC and eIF4A inhibition: A novel epigenetic therapy for pancreatic ductal adenocarcinoma. Drug resistance updates : reviews and commentaries in antimicrobial and anticancer chemotherapy, 84, 101312.

Luo H, et al. (2026) EasyAmplicon 2: Expanding PacBio and Nanopore Long Amplicon Sequencing Analysis Pipeline for Microbiome. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(1), e12447.

Makhmut A, et al. (2026) Spatial proteomics of ovarian cancer precursors delineates early disease changes and drug targets. Molecular systems biology, 22(1), 7.

Mbano IM, et al. (2026) Single-cell and spatial profiling highlights TB-induced myofibroblasts as drivers of lung pathology. The Journal of experimental medicine, 223(3).

Lawson LP, et al. (2026) Whole-genome sequence of the African Common Reed Frog (*Hyperolius viridiflavus viridiflavus*) from Ethiopia. G3 (Bethesda, Md.), 16(1).

Tingvall-Gustafsson J, et al. (2025) Chromatin interaction-based annotation of regulatory elements reveals dynamic promoter-enhancer interactions in lymphocyte development. iScience, 28(7), 112855.

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1 charts the structural landscape of human early endosome complexes. Nature, 643(8070), 252.

Paloviita P, et al. (2025) Integrated transcriptomic analysis reveals metabolic remodeling and gene expression networks related to human 8-cell-stage embryo-like cells. Cell reports, 45(1), 116748.

Liu X, et al. (2025) SpatialDeX Is a Reference-Free Method for Cell-Type Deconvolution of Spatial Transcriptomics Data in Solid Tumors. Cancer research, 85(1), 171.

Lall D, et al. (2025) An organ-chip model of sporadic ALS using iPSC-derived spinal cord motor neurons and an integrated blood-brain-like barrier. Cell stem cell, 32(7), 1139.

Bensberg M, et al. (2025) Exposing the DNA methylation-responsive compartment of the leukaemic genome in T-ALL cell lines support its potential as a novel therapeutic target in

T-ALL. *Clinical epigenetics*, 17(1), 114.

Mout L, et al. (2025) Genetic and Epigenetic Reprogramming of Transposable Elements Drives ecDNA-Mediated Metastatic Prostate Cancer. *bioRxiv : the preprint server for biology*.

Zamuner FT, et al. (2025) Epigenetic profiling reveals key super-enhancer networks driving oncogenesis in HPV-positive HNSCC. *iScience*, 28(11), 113911.

Qian W, et al. (2025) Single-cell transcriptomic and m6A methylation analyses reveal platelet-mediated immune regulatory mechanisms in sepsis. *Frontiers in immunology*, 16, 1607732.

Ruiz-Ruano FJ, et al. (2025) Programmed DNA elimination drives rapid genomic innovation in two thirds of all bird species. *bioRxiv : the preprint server for biology*.

Gopaulchan D, et al. (2025) A defined microbial community reproduces attributes of fine flavour chocolate fermentation. *Nature microbiology*, 10(9), 2130.

Isaza-Correa JM, et al. (2025) Childhood resolution of early abnormal miRNA following neonatal encephalopathy. *Scientific reports*, 15(1), 30489.

Peng R, et al. (2025) The causal effects between low back pain and cerebrospinal fluid metabolites: a two-sample Mendelian randomization study. *Hereditas*, 162(1), 18.

Duran-Roma??a R, et al. (2025) Native Fold Delay and its implications for co-translational chaperone binding and protein aggregation. *Nature communications*, 16(1), 1673.

Ziegler FMR, et al. (2025) A full genome assembly reveals drought stress effects on gene expression and metabolite profiles in blackcurrant (*Ribes nigrum* L.). *Horticulture research*, 12(2), uhae313.