Resource Summary Report

Generated by NIF on May 15, 2025

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

Funding:

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

Record Last Update: 20250513T060406+0000

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 773 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Chen L, et al. (2025) Clinical significance and pro-oncogenic function of DBF4 in clear cell renal cell carcinoma. BMC urology, 25(1), 8.

Chen N, et al. (2025) KMO-driven metabolic reconfiguration and its impact on immune cell infiltration in nasopharyngeal carcinoma: a new avenue for immunotherapy. Cancer immunology, immunotherapy : CII, 74(3), 75.

Kasan M, et al. (2025) Genomic and phenotypic stability of fusion-driven pediatric sarcoma cell lines. Nature communications, 16(1), 380.

Charmant O, et al. (2025) The PIWI-interacting protein Gtsf1 controls the selective degradation of small RNAs in Paramecium. Nucleic acids research, 53(1).

Yue D, et al. (2025) Effects of cassava pellets and enzymes addition on growth performance, meat quality, serum biochemical indices and cecum microbiota of broilers. Poultry science, 104(1), 104480.

Ye L, et al. (2025) Multi?omics identification of a novel signature for serous ovarian carcinoma in the context of 3P medicine and based on twelve programmed cell death patterns: a multi-cohort machine learning study. Molecular medicine (Cambridge, Mass.), 31(1), 5.

van Gelderen TA, et al. (2025) Gonadal miRNomes and transcriptomes in infected fish reveal sexually dimorphic patterns of the immune response. Functional & integrative genomics, 25(1), 29.

Nie L, et al. (2025) Plastome data provides new insights into population differentiation and evolution of Ginkgo in the Sichuan Basin of China. BMC plant biology, 25(1), 48.

Biswas D, et al. (2025) Prospective validation of ORACLE, a clonal expression biomarker associated with survival of patients with lung adenocarcinoma. Nature cancer, 6(1), 86.

Yu T, et al. (2025) Identification and Immunological Characterization of Cuproptosis Related Genes in Preeclampsia Using Bioinformatics Analysis and Machine Learning. Journal of clinical hypertension (Greenwich, Conn.), 27(1), e14982.

Tenger-Trolander A, et al. (2025) Genomic Resources for the Scuttle Fly Megaselia abdita: A Model Organism for Comparative Developmental Studies in Flies. bioRxiv : the preprint server for biology.

Domínguez M, et al. (2025) Genomics Reveal Population Structure and Intergeneric Hybridization in an Endangered South American Bird: Implications for Management and Conservation. Ecology and evolution, 15(1), e70820.

Montagne JM, et al. (2025) CD137 agonism enhances anti-PD1 induced activation of expanded CD8+ T cell clones in a neoadjuvant pancreatic cancer clinical trial. iScience, 28(1), 111569.

Lee J, et al. (2025) A chromosome-level genome assembly of wild silkmoth, Bombyx mandarina. Scientific data, 12(1), 27.

Lin D, et al. (2025) Multiorgan proteomic analysis of infected animal models predict potential host factors for chikungunya virus. MedComm, 6(1), e70013.

Chen JW, et al. (2025) CDK14 regulates the development and repair of lung. Cell death discovery, 11(1), 12.

Tsukahara S, et al. (2025) Centrophilic retrotransposon integration via CENH3 chromatin in Arabidopsis. Nature, 637(8046), 744.

Kellett DO, et al. (2024) Transcriptional response of the heart to vagus nerve stimulation. Physiological genomics, 56(2), 167.

Kadam PS, et al. (2024) Single-Mitochondrion Sequencing Uncovers Distinct Mutational Patterns and Heteroplasmy Landscape in Mouse Astrocytes and Neurons. bioRxiv : the preprint server for biology.

Takahama M, et al. (2024) A pairwise cytokine code explains the organism-wide response to sepsis. Nature immunology, 25(2), 226.