

Resource Summary Report

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GenVisR

RRID:SCR_027559

Type: Tool

Proper Citation

GenVisR (RRID:SCR_027559)

Resource Information

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

Proper Citation: GenVisR (RRID:SCR_027559)

Description: Software R package for visualizing genomics data. Provides a user-friendly, flexible and comprehensive suite of tools for visualizing complex genomic data in three categories (small variants, copy number alterations and data quality) for multiple species of interest.

Resource Type: software toolkit, software resource

Defining Citation: [PMID:27288499](#)

Keywords: visualizing genomics data, genomics, genomics data, small variants, copy number alterations, data quality, multiple species,

Funding: NHGRI K99HG007940;
NCI K22CA188163

Availability: Free, Available for download, Freely available

Resource Name: GenVisR

Resource ID: SCR_027559

License: GNU GPL v3

Record Creation Time: 20251017T060948+0000

Record Last Update: 20260815T183303+0000

Ratings and Alerts

No rating or validation information has been found for GenVisR.

No alerts have been found for GenVisR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 42 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Seldomridge AN, et al. (2026) Clinicopathologic and Molecular Characteristics of High-Grade Appendiceal Mucinous Neoplasms. *Annals of surgical oncology*, 33(3), 2376.

Kerkhoff M, et al. (2026) New cell lines expanding the diversity of Ewing sarcoma models. *International journal of cancer*, 158(3), 642.

Fesiuk A, et al. (2025) Thyroid hormone receptor beta signaling is a targetable driver of prostate cancer growth. *Molecular cancer*, 24(1), 256.

Lei T, et al. (2025) Malignant phyllodes tumors with sarcomatous components: A histopathologic and molecular study. *Translational oncology*, 53, 102318.

Singh O, et al. (2025) Diffuse astrocytoma, AYA-type, frequently MAPK-altered: report of 45 patients. *Acta neuropathologica*, 149(1), 32.

Wang D, et al. (2025) Utilizing multi-omics analysis, a new signature has been identified and validated for predicting prognosis and response to immunotherapy in lung squamous cell carcinoma, which is based on tumor mutation burden. *Discover oncology*, 16(1), 539.

Wang X, et al. (2025) Common bean pan-genome reveals abundant variation patterns and relationships of stress response genes and pathways. *BMC genomics*, 26(1), 495.

Yang J, et al. (2025) Brain metastases lung adenocarcinoma patients with BRG1 loss have a grim prognosis, featuring unique morphological and methylation characteristics. *Clinical & experimental metastasis*, 42(3), 20.

Su Z, et al. (2024) Mutation patterns in colorectal cancer and their relationship with prognosis. *Heliyon*, 10(17), e36550.

Yang X, et al. (2024) Integrated multiomic analysis reveals disulfidptosis subtypes in glioblastoma: implications for immunotherapy, targeted therapy, and chemotherapy. *Frontiers in immunology*, 15, 1362543.

Qin G, et al. (2024) Mutation Patterns Predict Drug Sensitivity in Acute Myeloid Leukemia. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(12), 2659.

Zanabria D, et al. (2024) Socioeconomic disparities and the genomic landscape of gastric cancer. *Scientific reports*, 14(1), 15070.

Dottermusch M, et al. (2024) Pituitary neuroendocrine tumors with PIT1/SF1 co-expression show distinct clinicopathological and molecular features. *Acta neuropathologica*, 147(1), 16.

Wei G, et al. (2024) Comprehensive data mining reveals RTK/RAS signaling pathway as a promoter of prostate cancer lineage plasticity through transcription factors and CNV. *Scientific reports*, 14(1), 11688.

Zeng J, et al. (2023) A genetic mosaic mouse model illuminates the pre-malignant progression of basal-like breast cancer. *Disease models & mechanisms*, 16(11).

Zhang L, et al. (2023) Construction of a ferroptosis-based prognostic model for breast cancer helps to discriminate high/low risk groups and treatment priority. *Frontiers in immunology*, 14, 1264206.

Li L, et al. (2023) HYDIN mutation status as a potential predictor of immune checkpoint inhibitor efficacy in melanoma. *Aging*, 15(16), 7997.

Sun Y, et al. (2023) Pan-genome of *Citrullus* genus highlights the extent of presence/absence variation during domestication and selection. *BMC genomics*, 24(1), 332.

Andrews MC, et al. (2022) Multi-modal molecular programs regulate melanoma cell state. *Nature communications*, 13(1), 4000.

Gao Y, et al. (2021) Identification of Novel Metabolism-Associated Subtypes for Pancreatic Cancer to Establish an Eighteen-Gene Risk Prediction Model. *Frontiers in cell and developmental biology*, 9, 691161.