

Resource Summary Report

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GISTIC

RRID:SCR_000151

Type: Tool

Proper Citation

GISTIC (RRID:SCR_000151)

Resource Information

URL: <http://www.mmnt.net/db/0/0/ftp-genome.wi.mit.edu/distribution/GISTIC2.0>

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Description: Software to identify genes targeted by somatic copy-number alterations (SCNAs) that drive cancer growth. By separating SCNA profiles into underlying arm-level and focal alterations, they improve the estimation of background rates for each category.

Abbreviations: GISTIC

Synonyms: GISTIC2.0, GISTIC 2.0, GISTIC 2

Resource Type: software resource

Defining Citation: [PMID:21527027](#)

Keywords: somatic copy-number alteration, gene

Related Condition: Cancer

Availability: Free, Available for download, Freely available

Resource Name: GISTIC

Resource ID: SCR_000151

Alternate IDs: OMICS_02296

License URLs: <Ftp://ftp-genome.wi.mit.edu/distribution/GISTICv2/LICENSE.txt>

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260801T190110+0000

Ratings and Alerts

No rating or validation information has been found for GISTIC.

No alerts have been found for GISTIC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 58 mentions in open access literature.

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

Takahashi J, et al. (2026) Spatial Multiomic Analyses Reveal Carcinogenic Pathways in End-Stage Renal Disease. *Cancer discovery*, 16(3), 478.

Morrissey RL, et al. (2026) Elucidating cooperative genetic events in DCIS progression in mutant p53-driven breast cancer. *Proceedings of the National Academy of Sciences of the United States of America*, 123(2), e2526544123.

Chang HY, et al. (2026) Uniform Processing of Diverse Sequencing Data: A Cross-Population Comparison of Colon Cancer Genomic Landscapes from The Cancer Genome Atlas and a Chinese Cohort. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 35(5), 762.

Zhang J, et al. (2026) Biomimetic hydrogel for the construction of patient-derived bladder cancer organoids with aggressive growth. *iScience*, 29(2), 114786.

Avolio M, et al. (2026) The Molecular and Functional Landscape of Resistance to FOLFIRI Chemotherapy in Metastatic Colorectal Cancer. *Cancer discovery*, 16(2), 270.

Robinson E, et al. (2026) STK11 mutations and deletions define a distinct subtype of cervical adenocarcinoma. *medRxiv : the preprint server for health sciences*.

Culliford R, et al. (2026) Contrasting Features of Papillary and Chromophobe Renal Cell Carcinoma Revealed by Whole-Genome Sequencing. *Molecular cancer research : MCR*, 24(5), 327.

Pregnall AM, et al. (2026) Metastatic progression of pheochromocytoma and paraganglioma occurs via parallel evolution. *NPJ precision oncology*, 10(1).

Houl JH, et al. (2026) Role of the ETV5/p38 Signaling Axis in Aggressive Thyroid Cancer Cells. *Molecular cancer therapeutics*, 25(5), 844.

Siegel F, et al. (2026) Sevabertinib, a Reversible HER2 Inhibitor with Activity in Lung Cancer. *Cancer discovery*, 16(1), 81.

Yu K, et al. (2026) Phase II Trial of Ixazomib Combined with Gemcitabine and Doxorubicin in Patients with SMARCB1-Deficient Renal Medullary Carcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(10), 1946.

Ren W, et al. (2025) Whole-genome sequencing reveals three follicular lymphoma subtypes with distinct cell of origin and patient outcomes. *Cell reports. Medicine*, 6(8), 102278.

Ku AT, et al. (2025) Radiogenomic Profiling of Prostate Tumors prior to External Beam Radiotherapy Converges on a Transcriptomic Signature of TGF- β Activity Driving Tumor Recurrence. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(24), 5211.

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. *Clinical and translational medicine*, 15(1), e70094.

Lee M, et al. (2025) p16 Immunohistochemical Patterns in Triple-Negative Breast Cancer: Clinical and Genomic Similarities of the p16 Diffuse Pattern to pRB Deficiency. *Pathobiology : journal of immunopathology, molecular and cellular biology*, 92(2), 63.

Blomain ES, et al. (2025) Evolutionary Pressures Shape Undifferentiated Pleomorphic Sarcoma Development and Radiotherapy Response. *Cancer research*, 85(6), 1162.

Xu X, et al. (2025) Genomic Analyses Reveal the Evolving Characteristics of Intestinal Metaplasia and Gastric Cancer. *Cancer research*, 85(16), 3123.

Plitt G, et al. (2024) The Genomic Landscape of Benign and Malignant Thyroid Tumors from Individuals Carrying Germline PTEN Variants Is Distinct from Sporadic Thyroid Cancers. *Cancer research*, 84(21), 3657.

Krull JE, et al. (2024) Follicular lymphoma B cells exhibit heterogeneous transcriptional states with associated somatic alterations and tumor microenvironments. *Cell reports. Medicine*, 5(3), 101443.

Liu H, et al. (2024) Integrative molecular and spatial analysis reveals evolutionary dynamics and tumor-immune interplay of in situ and invasive acral melanoma. *Cancer cell*, 42(6), 1067.