Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

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

Proper Citation: GISTIC (RRID:SCR_000151)

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: 20260725T190436+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 48 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

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.

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

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

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.

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.

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

Umeda M, et al. (2024) A new genomic framework to categorize pediatric acute myeloid leukemia. Nature genetics, 56(2), 281.

Pinton A, et al. (2024) PHF6-altered T-ALL Harbor Epigenetic Repressive Switch at Bivalent Promoters and Respond to 5-Azacitidine and Venetoclax. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(1), 94.

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.

Kazandjian D, et al. (2024) Genomic Profiling to Contextualize the Results of Intervention for Smoldering Multiple Myeloma. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(19), 4482.

Chojnacka M, et al. (2024) Impact of Rare Structural Variant Events in Newly Diagnosed Multiple Myeloma. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(3), 575.

Sun Y, et al. (2024) Integrated multi-omics profiling to dissect the spatiotemporal evolution of metastatic hepatocellular carcinoma. Cancer cell, 42(1), 135.

Modi A, et al. (2023) Integrative Genomic Analyses Identify LncRNA Regulatory Networks across Pediatric Leukemias and Solid Tumors. Cancer research, 83(20), 3462.

Xing X, et al. (2023) Integrated omics landscape of hepatocellular carcinoma suggests proteomic subtypes for precision therapy. Cell reports. Medicine, 4(12), 101315.

Jin B, et al. (2023) Immune checkpoint inhibitor-related molecular markers predict prognosis in extrahepatic cholangiocarcinoma. Cancer medicine, 12(20), 20470.

Striker SS, et al. (2023) Systematic integration of protein-affecting mutations, gene fusions, and copy number alterations into a comprehensive somatic mutational profile. Cell reports methods, 3(4), 100442.

Zhang R, et al. (2023) Urinary Tumor DNA MRD Analysis to Identify Responders to Neoadjuvant Immunotherapy in Muscle-invasive Bladder Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(20), 4040.