Resource Summary Report

Generated by NIF on May 19, 2025

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

Funding:

Availability: BROAD INSTITUTE SINGLE USER LICENSE AGREEMENT FOR INTERNAL RESEARCH PURPOSES ONLY, Ftp://ftp-genome.wi.mit.edu/distribution/GISTICv2/LICENSE.txt

Resource Name: GISTIC

Resource ID: SCR_000151

Alternate IDs: OMICS_02296

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250519T203044+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 39 mentions in open access literature.

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

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.

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

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.

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.

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

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.

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.

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.

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

Dai Y, et al. (2023) Integrative Single-Cell and Bulk Transcriptomes Analyses Identify Intrinsic HNSCC Subtypes with Distinct Prognoses and Therapeutic Vulnerabilities. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(15), 2845.

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.

Bockmayr M, et al. (2022) Comprehensive profiling of myxopapillary ependymomas identifies a distinct molecular subtype with relapsing disease. Neuro-oncology, 24(10), 1689.

Trivieri N, et al. (2022) Growth factor independence underpins a paroxysmal, aggressive Wnt5aHigh/EphA2Low phenotype in glioblastoma stem cells, conducive to experimental combinatorial therapy. Journal of experimental & clinical cancer research : CR, 41(1), 139.

Xu X, et al. (2022) Gain of Chromosome 1q Perturbs a Competitive Endogenous RNA Network to Promote Melanoma Metastasis. Cancer research, 82(17), 3016.

Javellana M, et al. (2022) Neoadjuvant Chemotherapy Induces Genomic and Transcriptomic Changes in Ovarian Cancer. Cancer research, 82(1), 169.

Prasad K, et al. (2022) Whole-Genome Duplication Shapes the Aneuploidy Landscape of Human Cancers. Cancer research, 82(9), 1736.

Song X, et al. (2022) Genomic and Single-Cell Landscape Reveals Novel Drivers and Therapeutic Vulnerabilities of Transformed Cutaneous T-cell Lymphoma. Cancer discovery, 12(5), 1294.

Lafferty A, et al. (2021) Molecular Subtyping Combined with Biological Pathway Analyses to Study Regorafenib Response in Clinically Relevant Mouse Models of Colorectal Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 27(21), 5979.

Li C, et al. (2020) Integrated Omics of Metastatic Colorectal Cancer. Cancer cell, 38(5), 734.