Resource Summary Report

Generated by NIF on Aug 27, 2026

MutSig

RRID:SCR_010779
Type: Tool

Proper Citation

MutSig (RRID:SCR_010779)

Resource Information

URL: http://www.broadinstitute.org/cancer/cga/mutsig

Proper Citation: MutSig (RRID:SCR_010779)

Description: Software that analyzes lists of mutations discovered in DNA sequencing, to identify genes that were mutated more often than expected by chance given background mutation processes.

Abbreviations: MutSig

Synonyms: Mutation Significance

Resource Type: software resource

Defining Citation: PMID:23770567

Keywords: bio.tools

Resource Name: MutSig

Resource ID: SCR_010779

Alternate IDs: OMICS_00155, biotools:MutSig2CV

Alternate URLs: https://bio.tools/MutSig2CV

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260815T182411+0000

Ratings and Alerts

No rating or validation information has been found for MutSig.

No alerts have been found for MutSig.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 129 mentions in open access literature.

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

Feng EM, et al. (2025) Racial variation in the advanced prostate cancer genome. Prostate cancer and prostatic diseases, 28(4), 902.

Zou X, et al. (2025) Multi-omics and single-cell approaches reveal molecular subtypes and key cell interactions in hepatocellular carcinoma. Frontiers in pharmacology, 16, 1605162.

Jiao D, et al. (2025) Gastric cancer genomics study using reference human pangenomes. Life science alliance, 8(4).

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

Qin N, et al. (2025) Comprehensive Characterization of Somatic Mutation Timing Reveals the Evolutionary Trajectory of Lung Adenocarcinoma in Chinese Patients. Cancer research, 85(15), 2905.

Zhong C, et al. (2024) CRISPR screens reveal convergent targeting strategies against evolutionarily distinct chemoresistance in cancer. Nature communications, 15(1), 5502.

Zheng L, et al. (2024) Identification of molecular characteristics of hepatocellular carcinoma with microvascular invasion based on deep targeted sequencing. Cancer medicine, 13(7), e7043.

Lalagkas PN, et al. (2024) Shared etiology of Mendelian and complex disease supports drug discovery. BMC medical genomics, 17(1), 228.

Yu J, et al. (2024) A proteogenomic analysis of cervical cancer reveals therapeutic and biological insights. Nature communications, 15(1), 10114.

Khorani K, et al. (2024) Context-Dependent Regulation of Peripheral Nerve Abundance by the PI3K Pathway in the Tumor Microenvironment of Head and Neck Squamous Cell Carcinoma. Cells, 13(12).

Zhang H, et al. (2024) Proteogenomic analysis of air-pollution-associated lung cancer reveals prevention and therapeutic opportunities. eLife, 13.

Qi F, et al. (2024) A multidimensional recommendation framework for identifying biological targets to aid the diagnosis and treatment of liver metastasis in patients with colorectal cancer. Molecular cancer, 23(1), 239.

Li L, et al. (2023) Integrative proteogenomic characterization of early esophageal cancer. Nature communications, 14(1), 1666.

Zangene E, et al. (2023) SL-scan identifies synthetic lethal interactions in cancer using metabolic networks. Scientific reports, 13(1), 15763.

Spain L, et al. (2023) Late-Stage Metastatic Melanoma Emerges through a Diversity of Evolutionary Pathways. Cancer discovery, 13(6), 1364.

Song S, et al. (2023) Systematic analysis of Mendelian disease-associated gene variants reveals new classes of cancer-predisposing genes. Genome medicine, 15(1), 107.

Burkart S, et al. (2023) A Novel Subgroup of UCHL1-Related Cancers Is Associated with Genomic Instability and Sensitivity to DNA-Damaging Treatment. Cancers, 15(6).

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.

Abolhassani H, et al. (2022) Genetic and immunologic evaluation of children with inborn errors of immunity and severe or critical COVID-19. The Journal of allergy and clinical immunology, 150(5), 1059.

Zhang S, et al. (2022) Identification of seven-gene marker to predict the survival of patients with lung adenocarcinoma using integrated multi-omics data analysis. Journal of clinical laboratory analysis, 36(2), e24190.