Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 30, 2024

MutSig

RRID:SCR_010779
Type: Tool

Proper Citation

MutSig (RRID:SCR_010779)

Resource Information

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

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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

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 115 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

Srivatsa S, et al. (2022) Discovery of synthetic lethal interactions from large-scale pan-cancer perturbation screens. Nature communications, 13(1), 7748.

Higgs EF, et al. (2022) Wilms tumor reveals DNA repair gene hyperexpression is linked to lack of tumor immune infiltration. Journal for immunotherapy of cancer, 10(6).

Hescheler DA, et al. (2022) Anaplastic thyroid cancer: genome-based search for new targeted therapy options. Endocrine connections, 11(4).

Petrov I, et al. (2022) Individualized discovery of rare cancer drivers in global network context. eLife, 11.

Li CH, et al. (2022) Age influences on the molecular presentation of tumours. Nature communications, 13(1), 208.

Wang Z, et al. (2021) Multi-omic analyses of hepatocellular carcinoma to determine immunological characteristics and key nodes in gene-expression network. Bioscience reports, 41(7).

Faden DL, et al. (2021) APOBEC Mutagenesis Is Concordant between Tumor and Viral Genomes in HPV-Positive Head and Neck Squamous Cell Carcinoma. Viruses, 13(8).

Mohsen H, et al. (2021) Network propagation-based prioritization of long tail genes in 17 cancer types. Genome biology, 22(1), 287.

Huo X, et al. (2021) Identification of a Six-Gene Signature for Predicting the Overall Survival of Cervical Cancer Patients. OncoTargets and therapy, 14, 809.

Lebovitz C, et al. (2021) Loss of Parkinson's susceptibility gene LRRK2 promotes carcinogen-induced lung tumorigenesis. Scientific reports, 11(1), 2097.

Chang D, et al. (2021) The landscape of driver mutations in cutaneous squamous cell carcinoma. NPJ genomic medicine, 6(1), 61.

Feng B, et al. (2021) Prognostic Gene Signature for Squamous Cell Carcinoma with a Higher Risk for Treatment Failure and Accelerated MEK-ERK Pathway Activity. Cancers, 13(20).

Xu D, et al. (2021) Development and clinical validation of a novel 9-gene prognostic model based on multi-omics in pancreatic adenocarcinoma. Pharmacological research, 164, 105370.