Resource Summary Report

Generated by SPARC SAWG on Jul 28, 2026

MutaGene

RRID:SCR_016574
Type: Tool

Proper Citation

MutaGene (RRID:SCR_016574)

Resource Information

URL: https://www.ncbi.nlm.nih.gov/projects/mutagene/

Proper Citation: MutaGene (RRID:SCR_016574)

Description: Software tool to explore and analyze mutagenic factors leading to tumors to decipher cancer genetic heterogeneity.

Resource Type: software application, software resource, data processing software, data analysis software

Defining Citation: PMID:28472504

Keywords: analyze, mutagenic, factor, turmor, decipher, cancer, genetic, heterogeneity

Funding: National Library of Medicine ;
NIH

Availability: Free, Available for download, Freely available

Resource Name: MutaGene

Resource ID: SCR_016574

Alternate URLs: https://ncbiinsights.ncbi.nlm.nih.gov/tag/mutagene/

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260728T043525+0000

Ratings and Alerts

No rating or validation information has been found for MutaGene.

No alerts have been found for MutaGene.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Espiritu D, et al. (2025) Cancer histone mutations impact protein binding and DNA repair with possible links to genomic instability. Nucleic acids research, 53(17).

Ostroverkhova D, et al. (2024) DNA polymerase ? and ? variants drive mutagenesis in polypurine tracts in human tumors. Cell reports, 43(1), 113655.

Landau J, et al. (2023) Shared Cancer Dataset Analysis Identifies and Predicts the Quantitative Effects of Pan-Cancer Somatic Driver Variants. Cancer research, 83(1), 74.

Rogozin IB, et al. (2021) DNA Methylation, Deamination, and Translesion Synthesis Combine to Generate Footprint Mutations in Cancer Driver Genes in B-Cell Derived Lymphomas and Other Cancers. Frontiers in genetics, 12, 671866.

Mei Y, et al. (2021) Gaining insights into relevance across cancers based on mutation features of TP53 gene. Biochemistry and biophysics reports, 28, 101165.

Fojo T, et al. (2020) Metastatic and recurrent adrenocortical cancer is not defined by its genomic landscape. BMC medical genomics, 13(1), 165.

Brown AL, et al. (2019) Finding driver mutations in cancer: Elucidating the role of background mutational processes. PLoS computational biology, 15(4), e1006981.

Stefanius K, et al. (2019) Human pancreatic cancer cell exosomes, but not human normal cell exosomes, act as an initiator in cell transformation. eLife, 8.

Zhang Z, et al. (2019) A survey and evaluation of Web-based tools/databases for variant analysis of TCGA data. Briefings in bioinformatics, 20(4), 1524.

Goncearenco A, et al. (2017) Exploring background mutational processes to decipher cancer genetic heterogeneity. Nucleic acids research, 45(W1), W514.