

Resource Summary Report

Generated by [Kravitz](#) on Sep 18, 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: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:28472504](#)

Keywords: analyze, mutagenic, factor, tumor, 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: 20260912T195841+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 [Kravitz](#) .

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 ϵ and δ 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.