

Resource Summary Report

Generated by [NIF](#) on Aug 18, 2026

[DrGaP](#)

RRID:SCR_008670

Type: Tool

Proper Citation

DrGaP (RRID:SCR_008670)

Resource Information

URL: <http://code.google.com/p/drgap/>

Proper Citation: DrGaP (RRID:SCR_008670)

Description: Designed to identify Driver Genes and Pathways in cancer genome sequencing studies.

Abbreviations: DrGaP

Resource Type: software resource

Related Condition: Cancer

Resource Name: DrGaP

Resource ID: SCR_008670

Alternate IDs: OMICS_00149

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260815T182350+0000

Ratings and Alerts

No rating or validation information has been found for DrGaP.

No alerts have been found for DrGaP.

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 [NIF](#) .

Guerrini-Rousseau L, et al. (2024) Glioma oncogenesis in the Constitutional mismatch repair deficiency (CMMRD) syndrome. *Neuro-oncology advances*, 6(1), vdae120.

Cheng X, et al. (2023) WMDS.net: a network control framework for identifying key players in transcriptome programs. *Bioinformatics (Oxford, England)*, 39(2).

Fan Z, et al. (2020) Comprehensive characterization of driver genes in diffuse large B cell lymphoma. *Oncology letters*, 20(1), 382.

Zhu CY, et al. (2019) C3: Consensus Cancer Driver Gene Caller. *Genomics, proteomics & bioinformatics*, 17(3), 311.

Han Y, et al. (2019) DriverML: a machine learning algorithm for identifying driver genes in cancer sequencing studies. *Nucleic acids research*, 47(8), e45.

Zhao X, et al. (2019) Integrative analysis of cancer driver genes in prostate adenocarcinoma. *Molecular medicine reports*, 19(4), 2707.

Pan Q, et al. (2017) Genomic variants in mouse model induced by azoxymethane and dextran sodium sulfate improperly mimic human colorectal cancer. *Scientific reports*, 7(1), 25.

Merlevede J, et al. (2016) Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. *Nature communications*, 7, 10767.

Tian R, et al. (2015) Computational methods and resources for the interpretation of genomic variants in cancer. *BMC genomics*, 16 Suppl 8(Suppl 8), S7.

Magi A, et al. (2015) Characterization and identification of hidden rare variants in the human genome. *BMC genomics*, 16(1), 340.