Resource Summary Report

Generated by ASWG on Aug 2, 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: 20260801T190350+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 ASWG .

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.