

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

ActiveDriver

RRID:SCR_008104

Type: Tool

Proper Citation

ActiveDriver (RRID:SCR_008104)

Resource Information

URL: <http://www.baderlab.org/Software/ActiveDriver>

Proper Citation: ActiveDriver (RRID:SCR_008104)

Description: A statistical method for interpreting variations in protein sequence (e.g. coding SNPs in the population, SNVs in cancer genomes) in the context of protein post-translational signaling modifications.

Abbreviations: ActiveDriver

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

Keywords: Protein sequence variation, variation interpretation, protein sequence, protein post-translational signaling modifications, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: ActiveDriver

Resource ID: SCR_008104

Alternate IDs: biotools:ActiveDriver, OMICS_00140

Alternate URLs: <http://reimandlab.org/software/activedriver/>, <https://cran.r-project.org/web/packages/ActiveDriver/ActiveDriver.pdf>, <https://bio.tools/ActiveDriver>

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260905T132618+0000

Ratings and Alerts

No rating or validation information has been found for ActiveDriver.

No alerts have been found for ActiveDriver.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Hu X, et al. (2026) Immune gene diversity and STING1 variants in shaping cancer immunity across different genetic ancestry populations. Cell reports, 45(2), 116882.

Zhu X, et al. (2026) Identification of cancer mini-drivers by deciphering selective landscape in the cancer genome. Briefings in bioinformatics, 27(1).

Farhi J, et al. (2025) Dynamic In Vivo Mapping of the Methylproteome Using a Chemoenzymatic Approach. Journal of the American Chemical Society, 147(9), 7214.

Rojas-Rodriguez F, et al. (2024) Assessing the validity of driver gene identification tools for targeted genome sequencing data. Bioinformatics advances, 4(1), vbae073.

Sipil?? LJ, et al. (2024) Genome-wide somatic mutation analysis of sinonasal adenocarcinoma with and without wood dust exposure. Genes and environment : the official journal of the Japanese Environmental Mutagen Society, 46(1), 12.

Lacoste J, et al. (2023) Pervasive mislocalization of pathogenic coding variants underlying human disorders. bioRxiv : the preprint server for biology.

Shi X, et al. (2022) Comprehensive evaluation of computational methods for predicting cancer driver genes. Briefings in bioinformatics, 23(2).

Jiang J, et al. (2022) Systematic illumination of druggable genes in cancer genomes. Cell reports, 38(8), 110400.

de Schaetzen van Brien L, et al. (2021) Network-Based Analysis to Identify Drivers of Metastatic Prostate Cancer Using GoNetic. Cancers, 13(21).

Chao JY, et al. (2021) Using bioinformatics approaches to investigate driver genes and identify BCL7A as a prognostic gene in colorectal cancer. Computational and structural biotechnology journal, 19, 3922.

Pham VVH, et al. (2021) Computational methods for cancer driver discovery: A survey. Theranostics, 11(11), 5553.

- Cascarina SM, et al. (2020) Natural and pathogenic protein sequence variation affecting prion-like domains within and across human proteomes. *BMC genomics*, 21(1), 23.
- Colaprico A, et al. (2020) Interpreting pathways to discover cancer driver genes with Moonlight. *Nature communications*, 11(1), 69.
- Han Y, et al. (2019) DriverML: a machine learning algorithm for identifying driver genes in cancer sequencing studies. *Nucleic acids research*, 47(8), e45.
- Hu Z, et al. (2019) Genomic characterization of genes encoding histone acetylation modulator proteins identifies therapeutic targets for cancer treatment. *Nature communications*, 10(1), 733.
- Buljan M, et al. (2018) Systematic characterization of pan-cancer mutation clusters. *Molecular systems biology*, 14(3), e7974.
- Zhang W, et al. (2018) Driver gene mutations based clustering of tumors: methods and applications. *Bioinformatics (Oxford, England)*, 34(13), i404.
- Cava C, et al. (2018) Integration of multiple networks and pathways identifies cancer driver genes in pan-cancer analysis. *BMC genomics*, 19(1), 25.
- Peterson LE, et al. (2017) Progression inference for somatic mutations in cancer. *Heliyon*, 3(4), e00277.
- Cho A, et al. (2016) MUFFINN: cancer gene discovery via network analysis of somatic mutation data. *Genome biology*, 17(1), 129.