

Resource Summary Report

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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, software application, software resource, sequence analysis software, data processing software

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: 20260801T190346+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 25 mentions in open access literature.

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

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*.

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

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

de Schaetzen van Brienen 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.

Waks Z, et al. (2016) Driver gene classification reveals a substantial overrepresentation of tumor suppressors among very large chromatin-regulating proteins. *Scientific reports*, 6, 38988.

Narayan S, et al. (2016) Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. *Genome medicine*, 8(1), 55.