Resource Summary Report

Generated by NIF on Apr 26, 2025

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

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

Funding:

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: 20250426T060023+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 24 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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

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

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.

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.

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.