Resource Summary Report

Generated by dkNET on Aug 6, 2026

e-Driver

RRID:SCR_002674
Type: Tool

Proper Citation

e-Driver (RRID:SCR_002674)

Resource Information

URL: https://github.com/eduardporta/e-Driver

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Description: Software tool to identify cancer driver genes based on linear annotations of biological regions such as protein domains.Uses information on three-dimensional structures of mutated proteins to identify specific structural features. Then algorithm analyzes whether these features are enriched in cancer somatic mutations and are candidate driver genes.

Resource Type: standalone software, software application, software resource

Defining Citation: PMID:25064568

Keywords: Identify cancer driver genes, candidate driver genes, perl, protein, mutated proteins, cancer somatic mutations, bio.tools

Related Condition: Cancer

Availability: Free, Available for download, Freely available

Resource Name: e-Driver

Resource ID: SCR_002674

Alternate IDs: biotools:e-Driver, OMICS_05288

Alternate URLs: https://bio.tools/e-Driver

License: Apache License, v2

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260807T042541+0000

Ratings and Alerts

No rating or validation information has been found for e-Driver.

No alerts have been found for e-Driver.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Colaprico A, et al. (2020) Interpreting pathways to discover cancer driver genes with Moonlight. Nature communications, 11(1), 69.

Bailey MH, et al. (2018) Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 173(2), 371.

Cava C, et al. (2018) Integration of multiple networks and pathways identifies cancer driver genes in pan-cancer analysis. BMC genomics, 19(1), 25.

Mészáros B, et al. (2016) Systematic analysis of somatic mutations driving cancer: uncovering functional protein regions in disease development. Biology direct, 11, 23.

Chen T, et al. (2016) Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. BMC genomics, 17 Suppl 2(Suppl 2), 394.