

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## e-Driver

RRID:SCR\_002674

Type: Tool

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### Proper Citation

e-Driver (RRID:SCR\_002674)

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### Resource Information

**URL:** <https://github.com/eduardporta/e-Driver>

**Proper Citation:** e-Driver (RRID:SCR\_002674)

**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:** software resource, software application, standalone software

**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:** 20260801T191045+0000

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## Ratings and Alerts

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

No alerts have been found for e-Driver.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

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

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.