

Resource Summary Report

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OncodriveFML

RRID:SCR_027731

Type: Tool

Proper Citation

OncodriveFML (RRID:SCR_027731)

Resource Information

URL: <https://bitbucket.org/bbglab/oncodrivefml/src/master>

Proper Citation: OncodriveFML (RRID:SCR_027731)

Description: Software tool that estimates accumulated functional impact bias of somatic mutations in any genomic region of interest based on local simulation of the mutational process affecting it.

Resource Type: software application, software resource

Keywords: Cancer Genes, SNV, indel, estimate accumulated functional impact bias, somatic mutations in any genomic region,

Availability: Free, Freely available

Resource Name: OncodriveFML

Resource ID: SCR_027731

Record Creation Time: 20251209T055452+0000

Record Last Update: 20260810T040930+0000

Ratings and Alerts

No rating or validation information has been found for OncodriveFML.

No alerts have been found for OncodriveFML.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Culliford R, et al. (2026) Contrasting Features of Papillary and Chromophobe Renal Cell Carcinoma Revealed by Whole-Genome Sequencing. *Molecular cancer research : MCR*, 24(5), 327.

Rao Z, et al. (2025) POCALI: Prediction and Insight on CAncer LncRNAs by Integrating Multi-Omics Data with Machine Learning. *Small methods*, 9(7), e2401987.

Ewing A, et al. (2025) Divergent trajectories to structural diversity impact patient survival in high grade serous ovarian cancer. *Nature communications*, 16(1), 5586.

Wong K, et al. (2025) Wnt/ β -catenin activation by mutually exclusive FBXW11 and CTNNB1 hotspot mutations drives salivary basal cell adenoma. *Nature communications*, 16(1), 4657.

Ferreira I, et al. (2025) The molecular cartography of malignant and benign sebaceous tumours. *Nature communications*, 17(1), 14.

Newell F, et al. (2022) Comparative Genomics Provides Etiologic and Biological Insight into Melanoma Subtypes. *Cancer discovery*, 12(12), 2856.

Mosquera Orgueira A, et al. (2021) Detection of new drivers of frequent B-cell lymphoid neoplasms using an integrated analysis of whole genomes. *PloS one*, 16(5), e0248886.

Ülgen E, et al. (2021) driveR: a novel method for prioritizing cancer driver genes using somatic genomics data. *BMC bioinformatics*, 22(1), 263.

Mosquera Orgueira A, et al. (2020) Novel Mutation Hotspots within Non-Coding Regulatory Regions of the Chronic Lymphocytic Leukemia Genome. *Scientific reports*, 10(1), 2407.

Fennell LJ, et al. (2020) APC Mutation Marks an Aggressive Subtype of BRAF Mutant Colorectal Cancers. *Cancers*, 12(5).

Nguyen QH, et al. (2020) Improving existing analysis pipeline to identify and analyze cancer driver genes using multi-omics data. *Scientific reports*, 10(1), 20521.