

Resource Summary Report

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Oncodrive-fm

RRID:SCR_010781

Type: Tool

Proper Citation

Oncodrive-fm (RRID:SCR_010781)

Resource Information

URL: <http://bg.upf.edu/group/projects/oncodrive-fm.php>

Proper Citation: Oncodrive-fm (RRID:SCR_010781)

Description: An approach to uncover driver genes or gene modules.

Abbreviations: Oncodrive-fm

Resource Type: software resource

Keywords: bio.tools

Resource Name: Oncodrive-fm

Resource ID: SCR_010781

Alternate IDs: OMICS_00157, biotools:oncodrivefm

Alternate URLs: <https://bio.tools/oncodrivefm>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190416+0000

Ratings and Alerts

No rating or validation information has been found for Oncodrive-fm.

No alerts have been found for Oncodrive-fm.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Lundgren S, et al. (2024) Somatic mutations associate with clonal expansion of CD8+ T cells. *Science advances*, 10(23), eadj0787.

Yang Z, et al. (2024) Genomic characteristics and immune landscape of super multiple primary lung cancer. *EBioMedicine*, 101, 105019.

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

Johansson PA, et al. (2020) Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. *Nature communications*, 11(1), 2408.

Yang Z, et al. (2020) Integrated molecular characterization reveals potential therapeutic strategies for pulmonary sarcomatoid carcinoma. *Nature communications*, 11(1), 4878.

Xie L, et al. (2020) The Clinical Implications of Tumor Mutational Burden in Osteosarcoma. *Frontiers in oncology*, 10, 595527.

Shan W, et al. (2020) Systematic Characterization of Recurrent Genomic Alterations in Cyclin-Dependent Kinases Reveals Potential Therapeutic Strategies for Cancer Treatment. *Cell reports*, 32(2), 107884.

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.

Gotoh O, et al. (2019) Clinically relevant molecular subtypes and genomic alteration-independent differentiation in gynecologic carcinosarcoma. *Nature communications*, 10(1), 4965.

Dufva O, et al. (2018) Aggressive natural killer-cell leukemia mutational landscape and drug profiling highlight JAK-STAT signaling as therapeutic target. *Nature communications*, 9(1), 1567.

Lindqvist CM, et al. (2016) Deep targeted sequencing in pediatric acute lymphoblastic leukemia unveils distinct mutational patterns between genetic subtypes and novel relapse-associated genes. *Oncotarget*, 7(39), 64071.

Litchfield K, et al. (2015) Whole-exome sequencing reveals the mutational spectrum of testicular germ cell tumours. *Nature communications*, 6, 5973.

Labreche K, et al. (2015) TCF12 is mutated in anaplastic oligodendroglioma. *Nature communications*, 6, 7207.

Balbás-Martínez C, et al. (2013) Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. *Nature genetics*, 45(12), 1464.