Resource Summary Report

Generated by NIF on Apr 26, 2025

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

Funding:

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: 20250420T014509+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 NIF.

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

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

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.