Resource Summary Report

Generated by NIF on Sep 17, 2026

SomaticSignatures

RRID:SCR_025620
Type: Tool

Proper Citation

SomaticSignatures (RRID:SCR_025620)

Resource Information

URL: https://bioconductor.org/packages/release/bioc/html/SomaticSignatures.html

Proper Citation: SomaticSignatures (RRID:SCR_025620)

Description: Software R package for identifying mutational signatures of single nucleotide variants (SNVs) from high-throughput experiments.

Resource Type: software resource, software toolkit, source code

Defining Citation: PMID:26163694

Keywords: R, identifying mutational signatures, single nucleotide variants, high-throughput experiments,

Funding: NSF

Availability: Free, Available for download, Freely available,

Resource Name: SomaticSignatures

Resource ID: SCR_025620

Alternate URLs: https://github.com/juliangehring/SomaticSignatures

License: MIT license

Record Creation Time: 20240815T053252+0000

Record Last Update: 20260912T200448+0000

Ratings and Alerts

No rating or validation information has been found for SomaticSignatures.

No alerts have been found for SomaticSignatures.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Shi Y, et al. (2026) Genomic, Clinical, and Spatial Predictors of Durable Response to BRAF/MEK Inhibition in BRAF-Mutant Melanoma. bioRxiv : the preprint server for biology.

Zhang C, et al. (2022) Comprehensive Genomic Characterization of Tumor Microenvironment and Relevant Signature in Clear Cell Renal Cell Carcinoma. Frontiers in oncology, 12, 749119.

Tian Y, et al. (2022) The Significance of Tumor Microenvironment Score for Breast Cancer Patients. BioMed research international, 2022, 5673810.

Lu J, et al. (2021) Whole-exome sequencing of alpha-fetoprotein producing gastric carcinoma reveals genomic profile and therapeutic targets. Nature communications, 12(1), 3946.

Skowron MA, et al. (2019) Distinctive mutational spectrum and karyotype disruption in long-term cisplatin-treated urothelial carcinoma cell lines. Scientific reports, 9(1), 14476.

Volinia S, et al. (2017) The ubiquitous 'cancer mutational signature' 5 occurs specifically in cancers with deleted FHIT alleles. Oncotarget, 8(60), 102199.

Nagahashi M, et al. (2016) Genomic landscape of colorectal cancer in Japan: clinical implications of comprehensive genomic sequencing for precision medicine. Genome medicine, 8(1), 136.