Resource Summary Report

Generated by RRID on Aug 12, 2026

SigProfilerExtractor

RRID:SCR_023121
Type: Tool

Proper Citation

SigProfilerExtractor (RRID:SCR_023121)

Resource Information

URL: https://github.com/AlexandrovLab/SigProfilerExtractor/

Proper Citation: SigProfilerExtractor (RRID:SCR_023121)

Description: Software tool for de novo extraction of mutational signatures from data generated in matrix format. Identifies number of operative mutational signatures, their activities in each sample, and probability for each signature to cause specific mutation type in cancer sample.

Resource Type: data analysis software, data processing software, software resource, software application

Keywords: de novo extraction, mutational signatures, data generated in matrix format, operative mutational signatures identification, specific mutation type, cancer sample

Availability: Free, Available for download, Freely available

Resource Name: SigProfilerExtractor

Resource ID: SCR_023121

License: BSD 2-Clause "Simplified" License

Record Creation Time: 20230116T062750+0000

Record Last Update: 20260812T044424+0000

Ratings and Alerts

No rating or validation information has been found for SigProfilerExtractor.

No alerts have been found for SigProfilerExtractor.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 82 mentions in open access literature.

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

Zhu M, et al. (2026) Molecular insights into HER2/ERBB2 amplification and carcinogenesis in gallbladder cancer associated with pancreaticobiliary maljunction. Journal of gastroenterology, 61(2), 222.

Yaacov A, et al. (2026) Consensus Copy-Number Alteration Signatures from Clinical Panels Enable Pan-Cancer Risk Stratification and Therapy Response Association. International journal of molecular sciences, 27(4).

Robinson E, et al. (2026) STK11 mutations and deletions define a distinct subtype of cervical adenocarcinoma. medRxiv : the preprint server for health sciences.

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.

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. Cancer discovery, 16(3), 497.

Portasany-Rodríguez M, et al. (2026) PULPO: pipeline of understanding large-scale patterns of oncogenomic signatures. Bioinformatics (Oxford, England), 42(6).

Jiang J, et al. (2026) Single base focal hypermutation cooccurs with structural variation as an early event in advanced prostate tumourigenesis with ancestry specific independence: a multi-ancestral observational study. Genome medicine, 18(1).

Gurevich NQ, et al. (2026) Defining mutational signatures of lung cancer-associated carcinogens through in vitro exposure of human airway epithelial cells. bioRxiv : the preprint server for biology.

Barazas M, et al. (2026) A mutational scar-based genome-wide map of DNA double-strand break repair. Nature communications, 17(1).

Kawazu M, et al. (2026) Genomic and Transcriptomic Analysis of High-Grade Endometrial Carcinoma Reveals Biological Heterogeneity and Molecular Classification Challenges. Cancer research communications, 6(4), 961.

Kusumoto-Matsuo R, et al. (2026) Genome instability is increased during DNA replication in the presence of the CPD UV photoproduct in transcriptionally active genes. iScience, 29(7), 116322.

Dong YP, et al. (2026) Early replication fragile sites are associated with cancer-related CNVs and SNVs in human embryonic stem cells. Stem cell reports, 21(7), 102968.

Wong H, et al. (2026) An Analytic Framework Characterizes the Biological Processes That Shape Copy Number-Based Genome Instability Patterns in Breast Cancer. Cancer research, 86(13), 3344.

Gurjao C, et al. (2026) Germline Predisposition to Oncogenic Alkylating Damage in Colorectal Cancer. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 35(3), 420.

Hwang T, et al. (2025) Comprehensive whole-genome sequencing reveals origins of mutational signatures associated with aging, mismatch repair deficiency and temozolomide chemotherapy. Nucleic acids research, 53(1).

Kinnersley B, et al. (2025) Genomic landscape of diffuse glioma revealed by whole genome sequencing. Nature communications, 16(1), 4233.

Torrens L, et al. (2025) The complexity of tobacco smoke-induced mutagenesis in head and neck cancer. Nature genetics, 57(4), 884.

Lu B, et al. (2025) Cell-cycle dependent DNA repair and replication unifies patterns of chromosome instability. Nature communications, 16(1), 3033.

Bertoli R, et al. (2025) 5-Azacytidine and decitabine induce C > G transversions in both murine and human cells. Leukemia, 39(9), 2112.

Lecuyer G, et al. (2025) Recurrent spontaneous miscarriages from sperm after ABVD chemotherapy in a patient with Hodgkin's lymphoma: sperm DNA and methylation profiling. Asian journal of andrology, 27(5), 598.