Resource Summary Report

Generated by NIF on Sep 5, 2026

SigProfilerAssignment

RRID:SCR_026899
Type: Tool

Proper Citation

SigProfilerAssignment (RRID:SCR_026899)

Resource Information

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

Proper Citation: SigProfilerAssignment (RRID:SCR_026899)

Description: Software tool for assignment of known mutational signatures to individual samples and individual somatic mutations.

Resource Type: software application, software resource, source code

Defining Citation: PMID:37502962

Keywords: assignment of known mutational signatures, individual samples, individual somatic mutations,

Funding: Cancer Research UK Grand Challenge Award ;
NCI R01CA269919;
NIEHS R01ES030993;
NIEHS R01ES032547;
Packard Fellowship for Science and Engineering

Availability: Free, Available for download, Freely available,

Resource Name: SigProfilerAssignment

Resource ID: SCR_026899

License: BSD-2-Clause license

Record Creation Time: 20250503T055712+0000

Record Last Update: 20260904T001033+0000

Ratings and Alerts

No rating or validation information has been found for SigProfilerAssignment.

No alerts have been found for SigProfilerAssignment.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Lee H, et al. (2026) Multimodal antigenic escape to GPRC5D-targeted T cell engagers in multiple myeloma. Nature medicine, 32(3), 964.

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.

Huffman BM, et al. (2026) A Phase II Trial of Niraparib in Patients with Advanced Pancreatic Cancer Harboring Pathogenic Variants in ATM, BRCA1, BRCA2, PALB2, and CHEK2. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1666.

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.

Chang HY, et al. (2026) Uniform Processing of Diverse Sequencing Data: A Cross-Population Comparison of Colon Cancer Genomic Landscapes from The Cancer Genome Atlas and a Chinese Cohort. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 35(5), 762.

Mitchell E, et al. (2025) The long-term effects of chemotherapy on normal blood cells. Nature genetics, 57(7), 1684.

Neville MDC, et al. (2025) Sperm sequencing reveals extensive positive selection in the male germline. Nature, 647(8089), 421.

Asada S, et al. (2025) Disruption of Microhomology-mediated End-joining in Ewing Sarcoma. bioRxiv : the preprint server for biology.

Micoli G, et al. (2025) Decoding the Genomic and Functional Landscape of Emerging Subtypes in Ovarian Cancer. Cancer discovery, 15(11), 2262.

Zhu G, et al. (2025) Defective Microhomology-Mediated End-joining in SMARCB1-Deficient Tumors. bioRxiv : the preprint server for biology.

Fielding D, et al. (2024) Evaluation of Endobronchial Ultrasound-Guided Transbronchial Needle Aspiration (EBUS-TBNA) Samples from Advanced Non-Small Cell Lung Cancer for Whole Genome, Whole Exome and Comprehensive Panel Sequencing. Cancers, 16(4).

Bonjoch L, et al. (2023) Unraveling the impact of a germline heterozygous POLD1 frameshift variant in serrated polyposis syndrome. Frontiers in molecular biosciences, 10, 1119900.