

Resource Summary Report

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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: source code, software application, software resource

Defining Citation: [PMID:37502962](#)

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

Funding: Cancer Research UK Grand Challenge Award ;
NIEHS R01ES030993;
NIEHS R01ES032547;
NCI R01CA269919;
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: 20260815T183255+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 [dkNET](#) .

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.