# Resource Summary Report

Generated by NIF on Aug 23, 2026

## ascat

RRID:SCR_016868
Type: Tool

### Proper Citation

ascat (RRID:SCR_016868)

### Resource Information

**URL:** https://github.com/Crick-CancerGenomics/ascat

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**Description:** Software R package to infer tumor purity, ploidy and allele-specific copy number profiles. It is platform and species independent, and works for both Illumina and Affymetrix SNP arrays, as well as for massively parallel sequencing data.

**Abbreviations:** ASCAT

**Synonyms:** ASCAT 3.0, ASCAT 2.0, ASCAT 4.0, ASCAT 1.0, Allele-Specific Copy Number Analysis of Tumors, Allele Specific Copy Number Analysis of Tumors

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

**Defining Citation:** PMID:20837533

**Keywords:** allele, specific, copy, number, analysis, tumor, purity, ploidy, sequencing, data, bio.tools

**Availability:** Free, Available for download, Freely available

**Resource Name:** ascat

**Resource ID:** SCR_016868

**Alternate IDs:** BioTools:ascat, biotools:ascat

**Alternate URLs:** https://github.com/VanLoo-lab/ascat, https://www.crick.ac.uk/research/labs/peter-van-loo/software, https://bio.tools/ascat, https://sources.debian.org/src/r-other-ascat/

**Record Creation Time:** 20220129T080332+0000

**Record Last Update:** 20260821T194111+0000

## Ratings and Alerts

No rating or validation information has been found for ascat.

No alerts have been found for ascat.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 42 mentions in open access literature.

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


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

Pradhan B, et al. (2026) Dynamic and Ongoing De Novo L1 Retrotransposition Contributes to Genome Plasticity and Intrapatient Heterogeneity in Ovarian Cancer. Cancer research, 86(4), 1073.

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

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.

Foidart P, et al. (2026) Whole-genome doubling drives immune evasion by silencing antigen presentation. Cancer cell, 44(7), 1418.

Li S, et al. (2026) PRECISE: A Prognostic Thyrocyte-Derived Gene Signature for Papillary Thyroid Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(13), 2667.

George SL, et al. (2025) Stratified Medicine Pediatrics: Cell-Free DNA and Serial Tumor Sequencing Identifies Subtype-Specific Cancer Evolution and Epigenetic States. Cancer discovery, 15(4), 717.

Patte C, et al. (2025) Comprehensive molecular portrait reveals genetic diversity and distinct molecular subtypes of small intestinal neuroendocrine tumors. Nature communications, 16(1), 2197.

Cheek D, et al. (2025) Age distinguishes selection from causation in cancer genomes. bioRxiv : the preprint server for biology.

Li H, et al. (2025) Assessment of CDKN2A homozygous and heterozygous deletions in gliomas across multiple detection platforms. BMC cancer, 25(1), 1007.

Treger TD, et al. (2025) Predisposition Footprints in the Somatic Genome of Wilms Tumors. Cancer discovery, 15(2), 286.

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. Cancer research communications, 5(10), 1910.

Abbasi A, et al. (2025) HRProfiler Detects Homologous Recombination Deficiency in Breast and Ovarian Cancers Using Whole-Genome and Whole-Exome Sequencing Data. Cancer research, 85(13), 2504.

Brzozowska N, et al. (2025) Selection for somatic escape variants in SERPINA1 in the liver of patients with alpha-1 antitrypsin deficiency. Nature genetics, 57(4), 875.

Gao J, et al. (2025) Comprehensive genomic and transcriptomic analyses reveal prognostic stratification for esophageal squamous cell carcinoma. Signal transduction and targeted therapy, 10(1), 223.

Arenillas C, et al. (2025) Convergent Genetic Adaptation in Human Tumors Developed Under Systemic Hypoxia and in Populations Living at High Altitudes. Cancer discovery, 15(5), 1037.

Papadimitriou M, et al. (2025) Timing Genomic Antigen Loss in Multiple Myeloma Treated with T Cell-Redirecting Immunotherapies. Blood cancer discovery, 6(6), 572.

Xie D, et al. (2025) Deciphering genomic evolution of metastatic organotropism with 535 paired primary lung cancers and metastases. Cell reports, 44(10), 116449.

Diamond B, et al. (2025) Mutagenic Impact and Evolutionary Influence of Chemoradiotherapy in Hematologic Malignancies. Blood cancer discovery, 6(5), 450.

Abbasi A, et al. (2024) Detecting HRD in whole-genome and whole-exome sequenced breast and ovarian cancers. medRxiv : the preprint server for health sciences.