

Resource Summary Report

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[ascat](#)

RRID:SCR_016868

Type: Tool

Proper Citation

ascat (RRID:SCR_016868)

Resource Information

URL: <https://github.com/Crick-CancerGenomics/ascat>

Proper Citation: ascat (RRID:SCR_016868)

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 processing software, data analysis 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

Ratings and Alerts

No rating or validation information has been found for ascacat.

No alerts have been found for ascacat.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 33 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#).

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.

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.

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.

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.

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.

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.

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.

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.

Burkert M, et al. (2024) Copy-number dosage regulates telomere maintenance and disease-associated pathways in neuroblastoma. *iScience*, 27(10), 110918.

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*.

Wang S, et al. (2024) Machine learning-based extrachromosomal DNA identification in large-scale cohorts reveals its clinical implications in cancer. *Nature communications*, 15(1), 1515.

Qin T, et al. (2024) Genomic profiling of a multi-lineage and multi-passage patient-derived xenograft biobank reflects heterogeneity of ovarian cancer. *Cell reports. Medicine*, 5(7), 101631.

Frontzek F, et al. (2023) Molecular profiling of EBV associated diffuse large B-cell lymphoma. *Leukemia*, 37(3), 670.

Senkowski W, et al. (2023) A platform for efficient establishment and drug-response profiling of high-grade serous ovarian cancer organoids. *Developmental cell*, 58(12), 1106.

Glodzik D, et al. (2023) Detection of Biallelic Loss of DNA Repair Genes in Formalin-Fixed, Paraffin-Embedded Tumor Samples Using a Novel Tumor-Only Sequencing Panel. *The Journal of molecular diagnostics : JMD*, 25(5), 295.

Olafsson S, et al. (2023) Effects of psoriasis and psoralen exposure on the somatic mutation landscape of the skin. *Nature genetics*, 55(11), 1892.