Resource Summary Report

Generated by NIF on Jul 30, 2026

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, software application, data analysis software, 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/

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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 33 mentions in open access literature.

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

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.

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

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

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.

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.

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.

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