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 analysis software, software application, data processing software, software resource

Defining Citation: PMID:20837533

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

Funding:

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 22 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

Lee H, et al. (2023) Mechanisms of antigen escape from BCMA- or GPRC5D-targeted immunotherapies in multiple myeloma. Nature medicine, 29(9), 2295.

Olafsson S, et al. (2023) Effects of psoriasis and psoralen exposure on the somatic mutation

landscape of the skin. Nature genetics, 55(11), 1892.

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.

Díaz de Ståhl T, et al. (2023) The Swedish childhood tumor biobank: systematic collection and molecular characterization of all pediatric CNS and other solid tumors in Sweden. Journal of translational medicine, 21(1), 342.

Montero-Conde C, et al. (2022) Comprehensive molecular analysis of immortalization hallmarks in thyroid cancer reveals new prognostic markers. Clinical and translational medicine, 12(8), e1001.

Chen K, et al. (2022) Spatiotemporal genomic analysis reveals distinct molecular features in recurrent stage I non-small cell lung cancers. Cell reports, 40(2), 111047.

Litchfield K, et al. (2021) Meta-analysis of tumor- and T cell-intrinsic mechanisms of sensitization to checkpoint inhibition. Cell, 184(3), 596.

Robinson PS, et al. (2021) Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature genetics, 53(10), 1434.

Oben B, et al. (2021) Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. Nature communications, 12(1), 1861.

Litchfield K, et al. (2020) Representative Sequencing: Unbiased Sampling of Solid Tumor Tissue. Cell reports, 31(5), 107550.

Garcia M, et al. (2020) Sarek: A portable workflow for whole-genome sequencing analysis of germline and somatic variants. F1000Research, 9, 63.

Steele CD, et al. (2019) Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. Cancer cell, 35(3), 441.

Inman GJ, et al. (2018) The genomic landscape of cutaneous SCC reveals drivers and a novel azathioprine associated mutational signature. Nature communications, 9(1), 3667.

Espiritu SMG, et al. (2018) The Evolutionary Landscape of Localized Prostate Cancers Drives Clinical Aggression. Cell, 173(4), 1003.