Resource Summary Report

Generated by RRID on Sep 17, 2026

alleleCount

RRID:SCR_023961
Type: Tool

Proper Citation

alleleCount (RRID:SCR_023961)

Resource Information

URL: https://github.com/cancerit/alleleCount

Proper Citation: alleleCount (RRID:SCR_023961)

Description: Software package to prevent code duplication. Support code for NGS copy number algorithms. Generates count of coverage of each allele ACGT at that location given any filter settings.

Synonyms: allelecount

Resource Type: software resource, source code

Keywords: NGS copy number, allele ACGT coverage,

Availability: Free, Available for download, Freely available

Resource Name: alleleCount

Resource ID: SCR_023961

Alternate URLs: https://sources.debian.org/src/allelecount/, http://cancerit.github.io/alleleCount/

License: GNU Affero General Public License

Record Creation Time: 20230824T050210+0000

Record Last Update: 20260912T200427+0000

Ratings and Alerts

No rating or validation information has been found for alleleCount.

No alerts have been found for alleleCount.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Mäntylä S, et al. (2026) Genomic analysis of PLNTY-like tumor progression into epithelioid glioblastoma: a case report. Acta neuropathologica communications, 14(1), 35.

Gori K, et al. (2025) Horizontal transfer of nuclear DNA in transmissible cancer. Proceedings of the National Academy of Sciences of the United States of America, 122(18), e2424634122.

Gómez-López S, et al. (2025) Aberrant basal cell clonal dynamics shape early lung carcinogenesis. Science (New York, N.Y.), 388(6752), eads9145.

Ferreira I, et al. (2025) The molecular cartography of malignant and benign sebaceous tumours. Nature communications, 17(1), 14.

Körber V, et al. (2025) Detecting and quantifying clonal selection in somatic stem cells. Nature genetics, 57(7), 1718.

Kyung SM, et al. (2025) Delineating molecular mechanisms on the acquisition of in vitro-adapted colistin-resistant Klebsiella pneumoniae by transcriptomic analysis. Microbiology spectrum, 13(12), e0342824.

Stammnitz MR, et al. (2024) No evidence that a transmissible cancer has shifted from emergence to endemism in Tasmanian devils. Royal Society open science, 11(4), 231875.

Schott CR, et al. (2024) Osteosarcoma PDX-Derived Cell Line Models for Preclinical Drug Evaluation Demonstrate Metastasis Inhibition by Dinaciclib through a Genome-Targeted Approach. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(4), 849.

Pourebrahim R, et al. (2024) Age-specific induction of mutant p53 drives clonal hematopoiesis and acute myeloid leukemia in adult mice. Cell reports. Medicine, 5(5), 101558.

Ji S, et al. (2024) Accelerated somatic mutation calling for whole-genome and whole-exome sequencing data from heterogenous tumor samples. Genome research, 34(4), 633.

Spencer Chapman M, et al. (2023) Clonal selection of hematopoietic stem cells after gene therapy for sickle cell disease. Nature medicine, 29(12), 3175.

Krali O, et al. (2023) Multimodal classification of molecular subtypes in pediatric acute lymphoblastic leukemia. NPJ precision oncology, 7(1), 131.

Incze E, et al. (2023) Potential Association of Cytochrome P450 Copy Number Alteration in Tumour with Chemotherapy Resistance in Lung Adenocarcinoma Patients. International journal of molecular sciences, 24(17).

Trinh MK, et al. (2022) Precise identification of cancer cells from allelic imbalances in single cell transcriptomes. Communications biology, 5(1), 884.

Neves JB, et al. (2022) Defining the origin, evolution, and immune composition of SDH-deficient renal cell carcinoma. iScience, 25(11), 105389.