

Resource Summary Report

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[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: 20260808T190700+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 [PRECISE-TBI](#) .

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.

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.

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

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.