Resource Summary Report

Generated by dkNET on Sep 19, 2026

ABSOLUTE

RRID:SCR_005198
Type: Tool

Proper Citation

ABSOLUTE (RRID:SCR_005198)

Resource Information

URL: http://www.broadinstitute.org/cancer/cga/absolute

Proper Citation: ABSOLUTE (RRID:SCR_005198)

Description: Software to estimate purity / ploidy, and from that compute absolute copy-number and mutation multiplicities. When DNA is extracted from an admixed population of cancer and normal cells, the information on absolute copy number per cancer cell is lost in the mixing. The purpose of ABSOLUTE is to re-extract these data from the mixed DNA population. This process begins by generation of segmented copy number data, which is input to the ABSOLUTE algorithm together with pre-computed models of recurrent cancer karyotypes and, optionally, allelic fraction values for somatic point mutations. The output of ABSOLUTE then provides re-extracted information on the absolute cellular copy number of local DNA segments and, for point mutations, the number of mutated alleles.

Abbreviations: ABSOLUTE

Resource Type: software resource

Defining Citation: PMID:22544022

Related Condition: Cancer, Normal

Availability: Account required

Resource Name: ABSOLUTE

Resource ID: SCR_005198

Alternate IDs: OMICS_00217

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260912T195622+0000

Ratings and Alerts

No rating or validation information has been found for ABSOLUTE.

No alerts have been found for ABSOLUTE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 283 mentions in open access literature.

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

Song Y, et al. (2026) Evaluating and Optimizing Mass Spectrometry Proteomics Data to Deconvolve Cell-Type-Specific Protein Expression in Tumors. Journal of proteome research, 25(1), 471.

Cheng P, et al. (2026) PARP1 Suppression Drives ROS Resistance in Aneuploid Cancer Cells. bioRxiv : the preprint server for biology.

Cutler MC, et al. (2026) Chromosome 3p Deletion Leads to Extensive Genomic Alterations in Diverse Cancers and Confers Synthetic Lethality in Uveal Melanoma. Cancers, 18(4).

Li C, et al. (2026) Integrative dual ctDNA 5mC/5hmC methylomics and clonal reconstruction infer tumor transcription and resistance phenotypes in metastatic prostate cancer. Research square.

Wang Y, et al. (2026) A 15-layer multi-omics analysis of gastric cancer ecotypes provides therapeutic insights. Cell reports. Medicine, 7(5), 102756.

Heller EM, et al. (2026) Protein buffering of aneuploidy is driven by coordinated factors identified through machine learning. Molecular systems biology, 22(4), 563.

Callender T, et al. (2026) SynthCraft: An AI partner for synthetic data generation to support data access and augmentation in healthcare. PLOS digital health, 5(3), e0001290.

Saravi B, et al. (2026) Inverse relationship between neoantigen clonality and T-cell activity reveals distinct immune phenotypes in HNSCC. Journal of translational medicine, 24(1).

Shi Y, et al. (2026) Genomic, Clinical, and Spatial Predictors of Durable Response to BRAF/MEK Inhibition in BRAF-Mutant Melanoma. bioRxiv : the preprint server for biology.

Hu M, et al. (2026) A Phase II Trial of Perioperative Camrelizumab Plus Neoadjuvant Chemotherapy in Resectable Stage IIB-IIIB Lung Squamous Cell Carcinoma. MedComm, 7(7), e70793.

Li C, et al. (2026) Integrative molecular analyses of lineage identity and morphology in aggressive variant prostate cancer. NPJ precision oncology, 10(1).

Xia M, et al. (2026) Multi-Scale Environmental Gradients Govern Microbial Succession and Structure Functional Gene Divergence in Element Cycling Along a Desert Lakeshore. Microorganisms, 14(2).

Yim SY, et al. (2026) Identifying sorafenib benefit among patients with hepatocellular carcinoma: A transcriptomic and genomic approach. JHEP reports : innovation in hepatology, 8(4), 101742.

Li C, et al. (2026) Molecular decoupling of lineage identity and morphology in aggressive variant prostate cancer. medRxiv : the preprint server for health sciences.

Priebe O, et al. (2026) Haplotype-aware segmentation with HapASeg increases accuracy of detecting homolog-specific somatic copy number alterations. Genome biology, 27(1).

Lee DK, et al. (2026) Proteogenomic decoding of chemotherapy resistance in patients with triple-negative breast cancer. Genome biology, 27(1).

Chen Q, et al. (2026) Characteristics of chromosomal instability???related lncRNAs associated with progression and prognosis in breast cancer. Molecular medicine reports, 33(5).

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.

Almeida-Lima K, et al. (2025) Heterogeneous expression of immunotherapy response markers in non-small cell lung cancer with hyperactive NRF2 pathway: PD-L1 and beyond. Redox biology, 87, 103889.

Merzliakov S, et al. (2025) Widespread Epistasis between Cancer Driver Mutations and Allele-Specific Copy Number Variations. bioRxiv : the preprint server for biology.