Resource Summary Report

Generated by RRID on Aug 2, 2026

CNAnorm

RRID:SCR_010816
Type: Tool

Proper Citation

CNAnorm (RRID:SCR_010816)

Resource Information

URL: http://www.precancer.leeds.ac.uk/software-and-datasets/cnanorm/

Proper Citation: CNAnorm (RRID:SCR_010816)

Description: A Bioconductor package to estimate Copy Number Aberrations (CNA) in cancer samples.

Abbreviations: CNAnorm

Resource Type: software resource

Resource Name: CNAnorm

Resource ID: SCR_010816

Alternate IDs: OMICS_00336

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190416+0000

Ratings and Alerts

No rating or validation information has been found for CNAnorm.

No alerts have been found for CNAnorm.

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 .

Min Z, et al. (2024) Paromomycin targets HDAC1-mediated SUMOylation and IGF1R translocation in glioblastoma. Frontiers in pharmacology, 15, 1490878.

Hecht V, et al. (2023) Analyzing histone ChIP-seq data with a bin-based probability of being signal. PLoS computational biology, 19(10), e1011568.

Symer DE, et al. (2022) Diverse tumorigenic consequences of human papillomavirus integration in primary oropharyngeal cancers. Genome research, 32(1), 55.

Kashofer K, et al. (2022) Driver gene mutations in micro-invasive cervical squamous cancers have no prognostic significance. Gynecologic oncology, 165(1), 121.

Dharanipragada P, et al. (2018) iCopyDAV: Integrated platform for copy number variations-Detection, annotation and visualization. PloS one, 13(4), e0195334.

Chu Y, et al. (2018) Modeling and correct the GC bias of tumor and normal WGS data for SCNA based tumor subclonal population inferring. BMC bioinformatics, 19(Suppl 5), 112.

Luo Z, et al. (2018) Accurity: accurate tumor purity and ploidy inference from tumor-normal WGS data by jointly modelling somatic copy number alterations and heterozygous germline single-nucleotide-variants. Bioinformatics (Oxford, England), 34(12), 2004.

Lohberger B, et al. (2017) Establishment of a novel cellular model for myxofibrosarcoma heterogeneity. Scientific reports, 7, 44700.

Weil T, et al. (2017) Adaptive Mistranslation Accelerates the Evolution of Fluconazole Resistance and Induces Major Genomic and Gene Expression Alterations in Candida albicans. mSphere, 2(4).

Wood HM, et al. (2017) The genomic road to invasion-examining the similarities and differences in the genomes of associated oral pre-cancer and cancer samples. Genome medicine, 9(1), 53.

Zhang Z, et al. (2015) SAAS-CNV: A Joint Segmentation Approach on Aggregated and Allele Specific Signals for the Identification of Somatic Copy Number Alterations with Next-Generation Sequencing Data. PLoS computational biology, 11(11), e1004618.

Quenel-Tueux N, et al. (2015) Clinical and genomic analysis of a randomised phase II study evaluating anastrozole and fulvestrant in postmenopausal patients treated for large operable or locally advanced hormone-receptor-positive breast cancer. British journal of cancer, 113(4), 585.

De Faveri LE, et al. (2015) Polycomb Repressor Complex 1 Member, BMI1 Contributes to Urothelial Tumorigenesis through p16-Independent Mechanisms. Translational oncology, 8(5), 387.

Akagi K, et al. (2014) Genome-wide analysis of HPV integration in human cancers reveals recurrent, focal genomic instability. Genome research, 24(2), 185.

Belvedere O, et al. (2012) A computational index derived from whole-genome copy number analysis is a novel tool for prognosis in early stage lung squamous cell carcinoma. Genomics, 99(1), 18.