Resource Summary Report

Generated by dkNET on Apr 29, 2025

Ginkgo

RRID:SCR_010931
Type: Tool

Proper Citation

Ginkgo (RRID:SCR_010931)

Resource Information

URL: http://pfgrc.jcvi.org/index.php/bioinformatics/ginkgo.html

Proper Citation: Ginkgo (RRID:SCR_010931)

Description: A spotted microarray data pre-processing platform featuring analysis functionalities for CGH and expression data.

Abbreviations: Ginkgo

Synonyms: Ginkgo: CGH and Expression Microarray Statistical Analysis and Normalization Platform

Resource Type: software resource

Funding:

Resource Name: Ginkgo

Resource ID: SCR_010931

Alternate IDs: OMICS_00725

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250420T014515+0000

Ratings and Alerts

No rating or validation information has been found for Ginkgo.

No alerts have been found for Ginkgo.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Mishra A, et al. (2025) Tumor cell-based liquid biopsy using high-throughput microfluidic enrichment of entire leukapheresis product. Nature communications, 16(1), 32.

Kalef-Ezra E, et al. (2024) Single-cell somatic copy number variants in brain using different amplification methods and reference genomes. Communications biology, 7(1), 1288.

Zhou Z, et al. (2024) Membrane Associated RNA-Containing Vesicles Regulate Cortical Astrocytic Microdomain Calcium Transients in Awake Ischemic Stroke Mice. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(46), e2404391.

Liu Y, et al. (2024) NestedBD: Bayesian inference of phylogenetic trees from single-cell copy number profiles under a birth-death model. Algorithms for molecular biology : AMB, 19(1), 18.

Sun C, et al. (2024) Mapping recurrent mosaic copy number variation in human neurons. Nature communications, 15(1), 4220.

Sun C, et al. (2023) Mapping the Complex Genetic Landscape of Human Neurons. bioRxiv : the preprint server for biology.

Kalef-Ezra E, et al. (2023) Single-cell somatic copy number variants in brain using different amplification methods and reference genomes. bioRxiv : the preprint server for biology.

Fan X, et al. (2022) Integrated single-cell multiomics analysis reveals novel candidate markers for prognosis in human pancreatic ductal adenocarcinoma. Cell discovery, 8(1), 13.

Almeida J, et al. (2022) Single-cell mtDNA heteroplasmy in colorectal cancer. Genomics, 114(2), 110315.

Baker NE, et al. (2022) Reducing the aneuploid cell burden - cell competition and the ribosome connection. Disease models & mechanisms, 15(11).

Erickson A, et al. (2022) Spatially resolved clonal copy number alterations in benign and malignant tissue. Nature, 608(7922), 360.

Lynch AR, et al. (2022) Quantifying chromosomal instability from intratumoral karyotype diversity using agent-based modeling and Bayesian inference. eLife, 11.

Alves JM, et al. (2022) Clonality and timing of relapsing colorectal cancer metastasis revealed through whole-genome single-cell sequencing. Cancer letters, 543, 215767.

Krol I, et al. (2021) Detection of clustered circulating tumour cells in early breast cancer. British journal of cancer, 125(1), 23.

Imai K, et al. (2021) In Silico Screening of a Bile Acid Micelle Disruption Peptide for Oral Consumptions from Edible Peptide Database. Foods (Basel, Switzerland), 10(10).

Jayakody H, et al. (2021) A generalised approach for high-throughput instance segmentation of stomata in microscope images. Plant methods, 17(1), 27.

Court CM, et al. (2020) Somatic copy number profiling from hepatocellular carcinoma circulating tumor cells. NPJ precision oncology, 4, 16.

Mallory XF, et al. (2020) Methods for copy number aberration detection from single-cell DNA-sequencing data. Genome biology, 21(1), 208.

Zhou X, et al. (2020) Comparison of Multiple Displacement Amplification (MDA) and Multiple Annealing and Looping-Based Amplification Cycles (MALBAC) in Limited DNA Sequencing Based on Tube and Droplet. Micromachines, 11(7).

Piqué DG, et al. (2019) Aneuvis: web-based exploration of numerical chromosomal variation in single cells. BMC bioinformatics, 20(1), 336.