# Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

## 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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Abbreviations:** Ginkgo

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

**Resource Type:** software resource

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Ginkgo

**Resource ID:** SCR_010931

**Alternate IDs:** OMICS_00725

**Record Creation Time:** 20220129T080301+0000

**Record Last Update:** 20260725T190705+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 61 mentions in open access literature.

**Listed below are recent publications.** The full list is available at PRECISE-TBI .


Okonechnikov K, et al. (2025) Oncogene aberrations drive medulloblastoma progression, not initiation. Nature, 642(8069), 1062.

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

Kuipers J, et al. (2025) Single-cell copy number calling and event history reconstruction. Bioinformatics (Oxford, England), 41(3).

Kong Y, et al. (2025) Microglia-Derived Vitamin D Binding Protein Mediates Synaptic Damage and Induces Depression by Binding to the Neuronal Receptor Megalin. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(6), e2410273.

Chen Y, et al. (2025) A computational DNA methylation method to remove contaminated DNA from spent embryo culture medium for noninvasive preimplantation genetic testing. EBioMedicine, 114, 105669.

Zhao Y, et al. (2025) High-resolution detection of copy number alterations in single cells with HiScanner. Nature communications, 16(1), 5477.

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.

Feng Z, et al. (2024) An accurately supervised motion-aware deep network for non-contact pain assessment of trigeminal neuralgia mouse model. Journal of oral & facial pain and headache, 38(1), 77.

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.

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.

Sun C, et al. (2023) Mapping the Complex Genetic Landscape of Human Neurons. 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.

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

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

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.

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

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