

Resource Summary Report

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Sequenza

RRID:SCR_016662

Type: Tool

Proper Citation

Sequenza (RRID:SCR_016662)

Resource Information

URL: <http://www.cbs.dtu.dk/biotools/sequenza/>

Proper Citation: Sequenza (RRID:SCR_016662)

Description: Software package for copy number estimation from tumor genome sequencing data. Tools to analyze genomic sequencing data from paired normal-tumor samples, including cellularity and ploidy estimation; mutation and copy number (allele-specific and total copy number) detection, quantification and visualization.

Resource Type: software application, data visualization software, data analysis software, data processing software, software resource

Defining Citation: [PMID:25319062](#)

Keywords: estimate, copy, number, tumor, genome, sequencing, data, cellularity, ploidy, alteration, cancer, mutation, detection, quantification, visualization

Funding: European Commission 7th Framework Programme ;
Danish Council for Independent Research ;
Breast Cancer Research Foundation

Availability: Free, Available for download, Freely available

Resource Name: Sequenza

Resource ID: SCR_016662

Alternate URLs: <https://cran.r-project.org/web/packages/sequenza/>

License: GPL 3

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250525T031452+0000

Ratings and Alerts

No rating or validation information has been found for Sequenza.

No alerts have been found for Sequenza.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 43 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#).

Chen YC, et al. (2025) Multiomics Analysis Reveals Molecular Changes during Early Progression of Precancerous Lesions to Lung Adenocarcinoma in Never-Smokers. *Cancer research*, 85(3), 602.

Lee HHY, et al. (2024) Inhibition of Aberrantly Overexpressed Polo-like Kinase 4 Is a Potential Effective Treatment for DNA Damage Repair-Deficient Uterine Leiomyosarcoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(17), 3904.

Boruah N, et al. (2024) Distinct genomic and immunologic tumor evolution in germline TP53-driven breast cancers. *bioRxiv : the preprint server for biology*.

Gardi N, et al. (2024) Natural History of Germline BRCA1 Mutated and BRCA Wild-type Triple-negative Breast Cancer. *Cancer research communications*, 4(2), 404.

Kacar Z, et al. (2024) Characterization of tumor evolution by functional clonality and phylogenetics in hepatocellular carcinoma. *Communications biology*, 7(1), 383.

Zhang C, et al. (2024) Neoadjuvant sintilimab plus chemotherapy in EGFR-mutant NSCLC: Phase 2 trial interim results (NEOTIDE/CTONG2104). *Cell reports. Medicine*, 5(7), 101615.

Nguyen DD, et al. (2024) The interplay of mutagenesis and ecDNA shapes urothelial cancer evolution. *Nature*, 635(8037), 219.

Liu H, et al. (2024) Integrative molecular and spatial analysis reveals evolutionary dynamics and tumor-immune interplay of in situ and invasive acral melanoma. *Cancer cell*, 42(6), 1067.

Sun Y, et al. (2024) Integrated multi-omics profiling to dissect the spatiotemporal evolution of metastatic hepatocellular carcinoma. *Cancer cell*, 42(1), 135.

Kashani E, et al. (2023) Integrated longitudinal analysis of adult grade 4 diffuse gliomas with long-term relapse interval revealed upregulation of TGF- β signaling in recurrent tumors. *Neuro-oncology*, 25(4), 662.

Wineland D, et al. (2023) Biallelic BRCA Loss and Homologous Recombination Deficiency in Nonbreast/Ovarian Tumors in Germline BRCA1/2 Carriers. *JCO precision oncology*, 7, e2300036.

Farin HF, et al. (2023) Colorectal Cancer Organoid-Stroma Biobank Allows Subtype-Specific Assessment of Individualized Therapy Responses. *Cancer discovery*, 13(10), 2192.

Parikh AY, et al. (2023) Using patient-derived tumor organoids from common epithelial cancers to analyze personalized T-cell responses to neoantigens. *Cancer immunology, immunotherapy : CII*, 72(10), 3149.

O'Brien VP, et al. (2023) *Helicobacter pylori* Chronic Infection Selects for Effective Colonizers of Metaplastic Glands. *mBio*, 14(1), e0311622.

Chow RD, et al. (2023) Distinct Mechanisms of Mismatch-Repair Deficiency Delineate Two Modes of Response to Anti-PD-1 Immunotherapy in Endometrial Carcinoma. *Cancer discovery*, 13(2), 312.

Andrews MC, et al. (2022) Multi-modal molecular programs regulate melanoma cell state. *Nature communications*, 13(1), 4000.

Abdelfattah N, et al. (2022) Single-cell analysis of human glioma and immune cells identifies S100A4 as an immunotherapy target. *Nature communications*, 13(1), 767.

Heide T, et al. (2022) The co-evolution of the genome and epigenome in colorectal cancer. *Nature*, 611(7937), 733.

Karlow JA, et al. (2022) Developmental Pathways Are Epigenetically Reprogrammed during Lung Cancer Brain Metastasis. *Cancer research*, 82(15), 2692.

Nguyen PHD, et al. (2021) Intratumoural immune heterogeneity as a hallmark of tumour evolution and progression in hepatocellular carcinoma. *Nature communications*, 12(1), 227.