Resource Summary Report

Generated by NIF on May 25, 2025

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-? 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.