

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

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

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: 20260728T043522+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 54 mentions in open access literature.

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

Kono T, et al. (2025) Protocol for characterizing craniopharyngioma subtypes and their microenvironments using single-cell RNA sequencing and immunohistochemistry. STAR protocols, 6(2), 103760.

Varadarajan K, et al. (2025) Efficacy of ATR Kinase Inhibitor Elimusertib Monotherapy or Combination in Tumors with DNA Damage Response Pathway and Other Genomic Alterations. Molecular cancer therapeutics, 24(9), 1402.

Msaouel P, et al. (2025) Identification of therapeutic targets for renal medullary carcinoma via integrated genomic and transcriptomic profiling. Cell reports. Medicine, 6(11), 102423.

Kushnarev V, et al. (2025) RNA sequencing and immunohistochemistry jointly improve tumor biomarker interpretation. Scientific reports, 15(1), 28264.

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.

Sousa-Squiavinato ACM, et al. (2025) Modelling Acral Melanoma in Admixed Brazilians Uncovers Genomic Drivers and Targetable Pathways. medRxiv : the preprint server for health sciences.

Buckley KH, et al. (2025) Gastric epithelium from BRCA1 and BRCA2 carriers harbors increased double-stranded DNA damage and augmented growth. bioRxiv : the preprint server for biology.

Stupichev D, et al. (2025) AI-driven multimodal algorithm predicts immunotherapy and targeted therapy outcomes in clear cell renal cell carcinoma. Cell reports. Medicine, 6(8), 102299.

Xie D, et al. (2025) Deciphering genomic evolution of metastatic organotropism with 535 paired primary lung cancers and metastases. Cell reports, 44(10), 116449.

Diamond B, et al. (2025) Mutagenic Impact and Evolutionary Influence of Chemoradiotherapy in Hematologic Malignancies. Blood cancer discovery, 6(5), 450.

Regan SB, et al. (2025) Megabase-scale loss of heterozygosity provoked by CRISPR-Cas9 DNA double-strand breaks. *Molecular cell*, 85(22), 4119.

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.

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.

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.

Ball M, et al. (2024) Leveraging Off-Target Reads in Panel Sequencing for Homologous Recombination Repair Deficiency Screening in Tumor. *The Journal of molecular diagnostics : JMD*, 26(6), 479.

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

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.