

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/>

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

Defining Citation: [PMID:25319062](#)

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

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

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: 20260905T132812+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 59 mentions in open access literature.

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

Tirtei E, et al. (2026) Mapping Genomic Heterogeneity in Pediatric and Adolescent-Young Adult Sarcomas: Insights from the Italian SAR-GEN2016 and SAR-GEN_ITA Prospective Multicenter Trials. *Cancer research communications*, 6(4), 857.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Bassiouni R, et al. (2026) Integrated Single-Cell Whole-Genome Sequencing and Spatial Transcriptomics Reveal Intratumoral Heterogeneity in Ovarian Cancer. *Cancer research communications*, 6(5), 1020.

Pregnall AM, et al. (2026) Metastatic progression of pheochromocytoma and paraganglioma occurs via parallel evolution. *NPJ precision oncology*, 10(1).

Yu K, et al. (2026) Phase II Trial of Ixazomib Combined with Gemcitabine and Doxorubicin in Patients with SMARCB1-Deficient Renal Medullary Carcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(10), 1946.

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.

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.

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.

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*.

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*.

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.

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.