

Resource Summary Report

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Pyclone

RRID:SCR_016873

Type: Tool

Proper Citation

Pyclone (RRID:SCR_016873)

Resource Information

URL: <https://github.com/arothon85/pyclone>

Proper Citation: Pyclone (RRID:SCR_016873)

Description: Software tool to infer the prevalence of point mutations in heterogeneous cancer samples. Probabilistic model for inferring clonal population structure from deep NGS sequencing.

Synonyms: PyClone

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

Defining Citation: [PMID:24633410](#)

Keywords: infer, prevalence, point, mutation, heterogeneous, cancer, probabilistic, population, NGS, sequencing, data, analysis

Availability: Available for download, Free for academic, nonprofit use

Resource Name: Pyclone

Resource ID: SCR_016873

Alternate URLs: <https://bitbucket.org/arothon85/pyclone/wiki/Home>

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260903T235355+0000

Ratings and Alerts

No rating or validation information has been found for Pyclone.

No alerts have been found for Pyclone.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Hu M, et al. (2026) A Phase II Trial of Perioperative Camrelizumab Plus Neoadjuvant Chemotherapy in Resectable Stage IIB-IIIB Lung Squamous Cell Carcinoma. MedComm, 7(7), e70793.

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.

Liao R, et al. (2026) Integrative multi-omics profiling reveals distinct evolutionary and immunogenic features of brain oligometastasis in lung adenocarcinoma. Genome medicine, 18(1).

Cioppi F, et al. (2026) In-depth Genetic and Molecular Characterization of Unilateral Coexisting Adrenal Cortical Adenoma and Carcinoma in the Context of MEN1 Syndrome. Endocrine pathology, 37(1).

Willoughby D, et al. (2025) Exome sequencing shows same pattern of clonal tumor mutational burden, intratumor heterogeneity and clonal neoantigen between autologous tumor and Vigil product. Scientific reports, 15(1), 8637.

Lv D, et al. (2025) Exploration of the clonal evolution and construction of the tumor clonal evolution rate as a prognostic indicator in metastatic breast cancer. BMC medicine, 23(1), 122.

Miceikaite I, et al. (2025) Deep genome sequencing reveals extensive genetic heterogeneity in early human placentas. Nature communications, 16(1), 7873.

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. Cancer discovery, 15(8), 1630.

Leko V, et al. (2025) Utilization of primary tumor samples for cancer neoantigen discovery. Journal for immunotherapy of cancer, 13(1).

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.

Bobin C, et al. (2024) Sequential Analysis of cfDNA Reveals Clonal Evolution in Patients with Neuroblastoma Receiving ALK-Targeted Therapy. Clinical cancer research : an

official journal of the American Association for Cancer Research, 30(15), 3316.

Deng Y, et al. (2024) Multicellular ecotypes shape progression of lung adenocarcinoma from ground-glass opacity toward advanced stages. *Cell reports. Medicine*, 5(4), 101489.

Sveen A, et al. (2024) Evolutionary mode and timing of dissemination of high-grade serous carcinomas. *JCI insight*, 9(3).

Fridland S, et al. (2024) Differential impact of intratumor heterogeneity (ITH) on survival outcomes in early-stage lung squamous and adenocarcinoma based on tumor mutational burden (TMB). *Translational lung cancer research*, 13(7), 1481.

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.

Fitzpatrick A, et al. (2023) Genomic profiling and pre-clinical modelling of breast cancer leptomeningeal metastasis reveals acquisition of a lobular-like phenotype. *Nature communications*, 14(1), 7408.

Spain L, et al. (2023) Late-Stage Metastatic Melanoma Emerges through a Diversity of Evolutionary Pathways. *Cancer discovery*, 13(6), 1364.

Chen G, et al. (2023) The clonal heterogeneity of colon cancer with liver metastases. *Journal of gastroenterology*, 58(7), 642.

Huang J, et al. (2023) Analysis of genomic and immune intratumor heterogeneity in linitis plastica via multiregional exome and T-cell receptor sequencing. *Molecular oncology*, 17(8), 1531.