Resource Summary Report

Generated by RRID on Aug 15, 2026

DPClust

RRID:SCR_027723
Type: Tool

Proper Citation

DPClust (RRID:SCR_027723)

Resource Information

URL: https://github.com/Wedge-lab/dpclust

Proper Citation: DPClust (RRID:SCR_027723)

Description: Software R package containing methods for sub-clonal reconstruction through SNVs and/or CNAs from whole genome or whole exome sequencing data.

Resource Type: software toolkit, source code, software resource

Keywords: Clonality, copy number variation, SNV, sub-clonal reconstruction, whole genome sequencing data, whole exome sequencing data,

Availability: Free, Available for download, Freely available

Resource Name: DPClust

Resource ID: SCR_027723

License: AGPL-3.0 license

Record Creation Time: 20251209T055452+0000

Record Last Update: 20260815T183309+0000

Ratings and Alerts

No rating or validation information has been found for DPClust.

No alerts have been found for DPClust.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Baker TM, et al. (2026) Genome-wide classification of tumor-derived reads from bulk long-read sequencing. bioRxiv : the preprint server for biology.

Leongamornlert D, et al. (2026) Genomic evolution and natural history of myeloproliferative neoplasms on therapy. Cancer discovery.

Wirth C, et al. (2025) Revealing the Drivers Underlying Distinct Evolutionary Trajectories in Lung Adenocarcinoma. bioRxiv : the preprint server for biology.

Salcedo A, et al. (2025) Crowd-sourced benchmarking of single-sample tumor subclonal reconstruction. Nature biotechnology, 43(4), 581.

He S, et al. (2025) Comprehensive assessment of computational methods for cancer immunoediting. Cell reports methods, 5(3), 101006.

Kinnersley B, et al. (2025) Genomic landscape of diffuse glioma revealed by whole genome sequencing. Nature communications, 16(1), 4233.

Maura F, et al. (2025) Plasma cell identity escape drives resistance to anti-BCMA T-cell-redirecting therapy in multiple myeloma. bioRxiv : the preprint server for biology.

Kuzmin E, et al. (2024) Evolution of chromosome-arm aberrations in breast cancer through genetic network rewiring. Cell reports, 43(4), 113988.

Cornish AJ, et al. (2024) The genomic landscape of 2,023 colorectal cancers. Nature, 633(8028), 127.

Dietzen M, et al. (2024) Replication timing alterations are associated with mutation acquisition during breast and lung cancer evolution. Nature communications, 15(1), 6039.

Baker TM, et al. (2024) The History of Chromosomal Instability in Genome-Doubled Tumors. Cancer discovery, 14(10), 1810.

N?? Leathlobhair M, et al. (2024) Genomic landscape of adult testicular germ cell tumours in the 100,000 Genomes Project. Nature communications, 15(1), 9247.

Senkin S, et al. (2024) Geographic variation of mutagenic exposures in kidney cancer genomes. Nature, 629(8013), 910.

Nurminen A, et al. (2023) Cancer origin tracing and timing in two high-risk prostate cancers using multisample whole genome analysis: prospects for personalized medicine. Genome medicine, 15(1), 82.

McClure MB, et al. (2023) Landscape of Genetic Alterations Underlying Hallmark Signature Changes in Cancer Reveals TP53 Aneuploidy-driven Metabolic Reprogramming. Cancer research communications, 3(2), 281.

Misund K, et al. (2022) Clonal evolution after treatment pressure in multiple myeloma: heterogenous genomic aberrations and transcriptomic convergence. Leukemia, 36(7), 1887.

Sousos N, et al. (2022) In utero origin of myelofibrosis presenting in adult monozygotic twins. Nature medicine, 28(6), 1207.

Dentro SC, et al. (2021) Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 184(8), 2239.

Studd JB, et al. (2021) Cancer drivers and clonal dynamics in acute lymphoblastic leukaemia subtypes. Blood cancer journal, 11(11), 177.

Rabbie R, et al. (2020) Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. Nature communications, 11(1), 4306.