

Resource Summary Report

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AmpliconArchitect

RRID:SCR_023150

Type: Tool

Proper Citation

AmpliconArchitect (RRID:SCR_023150)

Resource Information

URL: <https://github.com/virajbdeshpande/AmpliconArchitect>

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Description: Software package designed to call circular DNA from short read WGS data.Used to identify one or more connected genomic regions which have simultaneous copy number amplification and elucidates architecture of amplicon.Used to reconstruct structure of focally amplified regions using whole genome sequencing and validate it extensively on multiple simulated and real datasets, across wide range of coverage and copy numbers.

Resource Type: software toolkit, software resource

Defining Citation: [DOI:10.1038/s41467-018-08200-y](https://doi.org/10.1038/s41467-018-08200-y)

Keywords: call circular DNA, short read WGS data, connected genomic regions identification, simultaneous copy number amplification, amplicon

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Resource Name: AmpliconArchitect

Resource ID: SCR_023150

Record Creation Time: 20230118T050205+0000

Record Last Update: 20260803T040840+0000

Ratings and Alerts

No rating or validation information has been found for AmpliconArchitect.

No alerts have been found for AmpliconArchitect.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 42 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Mout L, et al. (2025) Genetic and Epigenetic Reprogramming of Transposable Elements Drives ecDNA-Mediated Metastatic Prostate Cancer. bioRxiv : the preprint server for biology.

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

Yost KE, et al. (2025) Three-dimensional genome landscape of primary human cancers. Nature genetics, 57(5), 1189.

Noorani I, et al. (2025) Extrachromosomal DNA-Driven Oncogene Spatial Heterogeneity and Evolution in Glioblastoma. Cancer discovery, 15(10), 2078.

Zeng Y, et al. (2025) Mapping the chromothripsis landscape in urothelial carcinoma unravels great intratumoral and intertumoral heterogeneity. iScience, 28(1), 111510.

Raeisi Dehkordi S, et al. (2025) Breakage fusion bridge cycles drive high oncogene number with moderate intratumoural heterogeneity. Nature communications, 16(1), 1497.

Starble RM, et al. (2025) Epigenetic priming promotes acquisition of tyrosine kinase inhibitor resistance and oncogene amplification in human lung cancer. bioRxiv : the preprint server for biology.

Fiorini E, et al. (2025) MYC ecDNA promotes intratumour heterogeneity and plasticity in PDAC. Nature, 640(8059), 811.

Li G, et al. (2025) Methylation aberrations and genomic instability synergistically drive the evolution of intrahepatic cholangiocarcinoma. Epigenomics, 17(10), 661.

Nakagawa T, et al. (2025) Inhibition of human-HPV hybrid ecDNA enhancers reduces oncogene expression and tumor growth in oropharyngeal cancer. Nature communications, 16(1), 2964.

Han P, et al. (2025) Extrachromosomal circular miRNA-gene amplifications contribute to the renal cancer phenotype. Cell reports, 44(12), 116660.

Smirnov P, et al. (2024) Multi-omic and single-cell profiling of chromothriptic medulloblastoma reveals genomic and transcriptomic consequences of genome instability. Nature communications, 15(1), 10183.

Yuan XQ, et al. (2024) Decoding the genomic enigma: Approaches to studying extrachromosomal circular DNA. *Heliyon*, 10(17), e36659.

Wang S, et al. (2024) Machine learning-based extrachromosomal DNA identification in large-scale cohorts reveals its clinical implications in cancer. *Nature communications*, 15(1), 1515.

Wu N, et al. (2024) Innovative insights into extrachromosomal circular DNAs in gynecologic tumors and reproduction. *Protein & cell*, 15(1), 6.

Zhao SG, et al. (2024) Integrated analyses highlight interactions between the three-dimensional genome and DNA, RNA and epigenomic alterations in metastatic prostate cancer. *Nature genetics*, 56(8), 1689.

Zhou L, et al. (2024) Characterization, biogenesis model, and current bioinformatics of human extrachromosomal circular DNA. *Frontiers in genetics*, 15, 1385150.

Nguyen DD, et al. (2024) The interplay of mutagenesis and ecDNA shapes urothelial cancer evolution. *Nature*, 635(8037), 219.

Bailey C, et al. (2024) Origins and impact of extrachromosomal DNA. *Nature*, 635(8037), 193.

Lv W, et al. (2024) Extrachromosomal circular DNA orchestrates genome heterogeneity in urothelial bladder carcinoma. *Theranostics*, 14(13), 5102.