

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 resource, software toolkit

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: 20260808T190536+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 53 mentions in open access literature.

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

Hendriksen JD, et al. (2026) Resolving clonal evolution and selection of extrachromosomal DNA at single-cell resolution. *Genome biology*, 27(1), 10.

Chong HB, et al. (2026) Human and viral whole genome sequencing identify HPV and APOBEC as oncogenic drivers in sinonasal squamous cell carcinoma. *medRxiv : the preprint server for health sciences*.

Culliford R, et al. (2026) Contrasting Features of Papillary and Chromophobe Renal Cell Carcinoma Revealed by Whole-Genome Sequencing. *Molecular cancer research : MCR*, 24(5), 327.

Tian X, et al. (2026) Proteogenomic characterization of cervical cancer identifies molecular subtypes predictive of clinical outcomes and subtype-specific targets. *The Journal of clinical investigation*, 136(7).

Moreno-Rodriguez T, et al. (2026) Convergent evolution of complex structural variants drives therapy resistance in metastatic prostate cancer. *Genome biology*, 27(1).

Kim R, et al. (2026) Whole-genome landscapes of 1,364 breast cancers. *Nature*, 649(8099), 1282.

Starble RM, et al. (2026) Epigenetic priming promotes tyrosine kinase inhibitor resistance and oncogene amplification. *Nature structural & molecular biology*, 33(1), 7.

Wong H, et al. (2026) An Analytic Framework Characterizes the Biological Processes That Shape Copy Number-Based Genome Instability Patterns in Breast Cancer. *Cancer research*, 86(13), 3344.

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.

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

Chowdhury B, et al. (2025) Reconstructing the three-dimensional architecture of extrachromosomal DNA with ec3D. *Nature communications*, 17(1), 894.

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

Jaworski JJ, et al. (2025) ecDNA replication is disorganized and vulnerable to replication stress. *Nucleic acids research*, 53(14).

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.

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.

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

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*.