

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

nucleR

RRID:SCR_010895

Type: Tool

Proper Citation

nucleR (RRID:SCR_010895)

Resource Information

URL: <http://mmb.pcb.ub.es/nucleR/>

Proper Citation: nucleR (RRID:SCR_010895)

Description: A R/Bioconductor package for a flexible and fast recognition of nucleosome positioning from next generation sequencing and tiling arrays experiments. The software is integrated with standard high-throughput genomics R packages and allows for in situ visualization as well as to export results to common genome browser formats.

Abbreviations: nucleR

Resource Type: software resource

Defining Citation: [PMID:21653521](#)

Keywords: bio.tools

Resource Name: nucleR

Resource ID: SCR_010895

Alternate IDs: OMICS_00511, biotools:nucler

Alternate URLs: <https://bio.tools/nucler>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260905T132649+0000

Ratings and Alerts

No rating or validation information has been found for nucleR.

No alerts have been found for nucleR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Tallan A, et al. (2026) Comparative modes of chromatin engagement by PAX::FOXO1 fusions in rhabdomyosarcoma. *bioRxiv : the preprint server for biology*.

Vanhaeren T, et al. (2025) Enhancing R-loop prediction with high-throughput sequencing data. *NAR genomics and bioinformatics*, 7(2), lqaf077.

Milavetz B, et al. (2025) Dysregulation of histone methylation in SV40 chromosomes during replication results in aberrant transcription and chromatin structure. *Tumour virus research*, 20, 200326.

Genna V, et al. (2025) Systematic study of hybrid triplex topology and stability suggests a general triplex-mediated regulatory mechanism. *Nucleic acids research*, 53(5).

Sala A, et al. (2024) An integrated machine-learning model to predict nucleosome architecture. *Nucleic acids research*, 52(17), 10132.

Ma H, et al. (2023) Centromere Plasticity With Evolutionary Conservation and Divergence Uncovered by Wheat 10+ Genomes. *Molecular biology and evolution*, 40(8).

Brahma P, et al. (2023) Biased eviction of variant histone H3 nucleosomes triggers biofilm growth in *Candida albicans*. *mBio*, 14(5), e0206323.

Klein DC, et al. (2023) The esBAF and ISWI nucleosome remodeling complexes influence occupancy of overlapping dinucleosomes and fragile nucleosomes in murine embryonic stem cells. *BMC genomics*, 24(1), 201.

Schwartz U, et al. (2023) Changes in adenoviral chromatin organization precede early gene activation upon infection. *The EMBO journal*, 42(19), e114162.

Rutz A, et al. (2023) Automated Composition Assessment of Natural Extracts: Untargeted Mass Spectrometry-Based Metabolite Profiling Integrating Semiquantitative Detection. *Journal of agricultural and food chemistry*, 71(46), 18010.

Jaegle B, et al. (2023) Extensive sequence duplication in *Arabidopsis* revealed by pseudo-heterozygosity. *Genome biology*, 24(1), 44.

Parisis N, et al. (2023) Histone H3 serine-57 is a CHK1 substrate whose phosphorylation affects DNA repair. *Nature communications*, 14(1), 5104.

Huang Y, et al. (2022) NucleoMap: A computational tool for identifying nucleosomes in ultra-high resolution contact maps. *PLoS computational biology*, 18(7), e1010265.

Rowbotham K, et al. (2022) Early in an SV40 infection, histone modifications correlate with the presence or absence of RNAPII and direction of transcription. *Virology*, 573, 59.

Buitrago D, et al. (2021) Impact of DNA methylation on 3D genome structure. *Nature communications*, 12(1), 3243.

Martínez-García PM, et al. (2021) Genome-wide prediction of topoisomerase II β binding by architectural factors and chromatin accessibility. *PLoS computational biology*, 17(1), e1007814.

Rowbotham K, et al. (2020) Differential SP1 interactions in SV40 chromatin from virions and minichromosomes. *Virology*, 548, 124.

Hocher A, et al. (2019) The DNA-binding protein HTa from *Thermoplasma acidophilum* is an archaeal histone analog. *eLife*, 8.

Buitrago D, et al. (2019) Nucleosome Dynamics: a new tool for the dynamic analysis of nucleosome positioning. *Nucleic acids research*, 47(18), 9511.

Rojec M, et al. (2019) Chromatinization of *Escherichia coli* with archaeal histones. *eLife*, 8.