

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 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: 20260912T195725+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 [PRECISE-TBI](#) .

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.

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.

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

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.

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

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.

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