Resource Summary Report

Generated by dkNET on May 20, 2025

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

Funding:

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: 20250519T203630+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 24 mentions in open access literature.

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

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

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.

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).

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

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.

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.

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

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? 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.

Choi K, et al. (2016) Recombination Rate Heterogeneity within Arabidopsis Disease Resistance Genes. PLoS genetics, 12(7), e1006179.

Hildebrand EM, et al. (2016) Regulation of Budding Yeast CENP-A levels Prevents Misincorporation at Promoter Nucleosomes and Transcriptional Defects. PLoS genetics, 12(3), e1005930.

Deniz Ö, et al. (2016) Nucleosome architecture throughout the cell cycle. Scientific reports, 6, 19729.

Liu J, et al. (2015) DNA sequence templates adjacent nucleosome and ORC sites at gene amplification origins in Drosophila. Nucleic acids research, 43(18), 8746.