Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 18, 2025

NucPosSimulator

RRID:SCR_004765
Type: Tool

Proper Citation

NucPosSimulator (RRID:SCR_004765)

Resource Information

URL: http://bioinformatics.fh-stralsund.de/nucpos/

Proper Citation: NucPosSimulator (RRID:SCR_004765)

Description: A simulation tool to identify positions of nucleosomes from Next Generation Sequencing data.

Abbreviations: NucPosSimulator

Resource Type: software resource

Defining Citation: PMID:23846748

Funding: BMBF

Availability: Acknowledgement requested, Free, Public

Resource Name: NucPosSimulator

Resource ID: SCR_004765

Alternate IDs: OMICS_00512

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250410T065208+0000

Ratings and Alerts

No rating or validation information has been found for NucPosSimulator.

No alerts have been found for NucPosSimulator.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Duan L, et al. (2025) Methyl-dependent auto-regulation of the DNA N6-adenine methyltransferase AMT1 in the unicellular eukaryote Tetrahymena thermophila. Nucleic acids research, 53(3).

Wang Y, et al. (2019) A distinct class of eukaryotic MT-A70 methyltransferases maintain symmetric DNA N6-adenine methylation at the ApT dinucleotides as an epigenetic mark associated with transcription. Nucleic acids research, 47(22), 11771.

Wiese O, et al. (2019) Nucleosome positions alone can be used to predict domains in yeast chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 116(35), 17307.

Xiong J, et al. (2016) Dissecting relative contributions of cis- and trans-determinants to nucleosome distribution by comparing Tetrahymena macronuclear and micronuclear chromatin. Nucleic acids research, 44(21), 10091.