

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

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: 20260801T190245+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 [ASWG](#) .

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.