

# Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 16, 2026

## NucPosSimulator

RRID:SCR\_004765

Type: Tool

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### Proper Citation

NucPosSimulator (RRID:SCR\_004765)

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### 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:** 20260912T195616+0000

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### Ratings and Alerts

No rating or validation information has been found for NucPosSimulator.

No alerts have been found for NucPosSimulator.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Zhang Z, et al. (2026) Bromodomain protein IBD1 bridges histone acetylation and H2A.Z deposition to fine-tune transcription. *Nucleic acids research*, 54(4).

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.