

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

NSeq

RRID:SCR_010891

Type: Tool

Proper Citation

NSeq (RRID:SCR_010891)

Resource Information

URL: <https://github.com/songlab/NSeq>

Proper Citation: NSeq (RRID:SCR_010891)

Description: A multithreaded Java application for finding positioned nucleosomes from sequencing data.

Abbreviations: NSeq

Resource Type: software resource, software application

Resource Name: NSeq

Resource ID: SCR_010891

Alternate IDs: OMICS_00506

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260801T191102+0000

Ratings and Alerts

No rating or validation information has been found for NSeq.

No alerts have been found for NSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Chao KH, et al. (2025) Predicting dynamic expression patterns in budding yeast with a fungal DNA language model. *bioRxiv* : the preprint server for biology.

Anand R, et al. (2025) RNA-FrameFlow: Flow Matching for de novo 3D RNA Backbone Design. *ArXiv*.

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

Schwob G, et al. (2021) Exploring the Microdiversity Within Marine Bacterial Taxa: Toward an Integrated Biogeography in the Southern Ocean. *Frontiers in microbiology*, 12, 703792.

Martinez Boggio G, et al. (2021) Compositional analysis of ruminal bacteria from ewes selected for somatic cell score and milk persistency. *PloS one*, 16(7), e0254874.

Jose J, et al. (2021) Critically ill patients with diabetes and Middle East respiratory syndrome: a multi-center observational study. *BMC infectious diseases*, 21(1), 84.

Zheng K, et al. (2020) DBMDA: A Unified Embedding for Sequence-Based miRNA Similarity Measure with Applications to Predict and Validate miRNA-Disease Associations. *Molecular therapy. Nucleic acids*, 19, 602.

Svensson D, et al. (2019) doepipeline: a systematic approach to optimizing multi-level and multi-step data processing workflows. *BMC bioinformatics*, 20(1), 498.

Vonhof MJ, et al. (2015) Genetic approaches to the conservation of migratory bats: a study of the eastern red bat (*Lasiurus borealis*). *PeerJ*, 3, e983.

Byeon B, et al. (2013) NucVoter: A Voting Algorithm for Reliable Nucleosome Prediction Using Next-Generation Sequencing Data. *ISRN bioinformatics*, 2013, 174064.

Nellore A, et al. (2012) NSeq: a multithreaded Java application for finding positioned nucleosomes from sequencing data. *Frontiers in genetics*, 3, 320.