

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

[ntsm](#)

RRID:SCR_024994

Type: Tool

Proper Citation

ntsm (RRID:SCR_024994)

Resource Information

URL: <https://github.com/JustinChu/ntsm>

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Description: Software alignment free, ultra low coverage, sequencing technology agnostic, intraspecies sample comparison tool for sample swap detection. Used to count number of specific k-mers within sequence data. The counts can then be compare to other counts to determine to compute the probability that sample are of the same origin to discover incongruent samples or sample swaps.

Synonyms: ntsm: nucleotide sequence sample matcher

Resource Type: source code, software application, software resource

Defining Citation: [DOI:10.1101/2023.11.01.565041](https://doi.org/10.1101/2023.11.01.565041)

Keywords: intraspecies sample comparison, sample comparison, specific k-mers within sequence data count, sample swap detection,

Availability: Free, Available for download, Freely available,

Resource Name: ntsm

Resource ID: SCR_024994

License: MIT license

Record Creation Time: 20240209T050239+0000

Record Last Update: 20260815T042854+0000

Ratings and Alerts

No rating or validation information has been found for ntsm.

No alerts have been found for ntsm.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Xu Z, et al. (2025) PISAD: reference-free intraspecies sample anomalies detection tool based on k-mer counting. GigaScience, 14.

Chu J, et al. (2024) ntsm: an alignment-free, ultra-low-coverage, sequencing technology agnostic, intraspecies sample comparison tool for sample swap detection. GigaScience, 13.