

Resource Summary Report

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

[m6anet](#)

RRID:SCR_025234

Type: Tool

Proper Citation

m6anet (RRID:SCR_025234)

Resource Information

URL: <https://github.com/GoekeLab/m6anet>

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Description: Software Python tool for detection of m6A from direct RNA-Seq data. Leverages multiple instance learning framework to detect m6a modifications from Nanopore Direct RNA Sequencing data.

Resource Type: data processing software, software application, data analysis software, source code, software resource

Defining Citation: [PMID:36357692](#)

Keywords: Nanopore Direct RNA Sequencing data, detection of m6A, RNA-Seq data,

Availability: Free, Available for download, Freely available

Resource Name: m6anet

Resource ID: SCR_025234

License: MIT license

Record Creation Time: 20240409T053245+0000

Record Last Update: 20260815T042911+0000

Ratings and Alerts

No rating or validation information has been found for m6anet.

No alerts have been found for m6anet.

Data and Source Information

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Wang F, et al. (2026) Stoichiometry-preserving and stochasticity-aware identification of m6A from direct RNA sequencing. *Briefings in bioinformatics*, 27(2).

Cheng G, et al. (2026) Raw signal segmentation for estimating RNA modification from Nanopore direct RNA sequencing data. *eLife*, 14.

Liu C, et al. (2025) Decoding the m6A epitranscriptomic landscape for biotechnological applications using a direct RNA sequencing approach. *Nature communications*, 16(1), 798.

Roy P, et al. (2025) A tale of two parasites: a glimpse into the RNA methylome of patient-derived *Plasmodium falciparum* and *Plasmodium vivax* isolates. *Malaria journal*, 24(1), 139.

Spangenberg J, et al. (2025) The RMaP challenge of predicting RNA modifications by nanopore sequencing. *Communications chemistry*, 8(1), 115.

Guo W, et al. (2025) Single-molecule m6A detection empowered by endogenous labeling unveils complexities across RNA isoforms. *Molecular cell*, 85(6), 1233.

Cao S, et al. (2024) Gapless genome assembly and epigenetic profiles reveal gene regulation of whole-genome triplication in lettuce. *GigaScience*, 13.