

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## MITE-Tracker

RRID:SCR\_017030

Type: Tool

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### Proper Citation

MITE-Tracker (RRID:SCR\_017030)

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### Resource Information

**URL:** <https://github.com/INTABiotechMJ/MITE-Tracker>

**Proper Citation:** MITE-Tracker (RRID:SCR\_017030)

**Description:** Open source software tool for identifying miniature inverted repeat transposable elements in large genomes. Used to process large scale genomes, to find and classify MITEs using an efficient alignment strategy to retrieve nearby inverted repeat sequences.

**Abbreviations:** MITE Tracker

**Synonyms:** MITE Tracker, Miniature Inverted repeats Transposable Elements Tracker

**Resource Type:** sequence analysis software, data analysis software, software resource, software application, data processing software

**Defining Citation:** [DOI:10.1186/s12859-018-2376-y](https://doi.org/10.1186/s12859-018-2376-y)

**Keywords:** genomic, sequence, discover, miniature, inverted, repeat, transposable, element, clustering, cdhit

**Funding:** National Institute of Agricultural Technology ;  
National Council for Science and Technology ;  
Argentina

**Availability:** Free, Available for download, Freely available

**Resource Name:** MITE-Tracker

**Resource ID:** SCR\_017030

**Alternate IDs:** OMICS\_32242

**License:** GNU GPL

**Record Creation Time:** 20220129T080333+0000

**Record Last Update:** 20260728T043529+0000

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## Ratings and Alerts

No rating or validation information has been found for MITE-Tracker.

No alerts have been found for MITE-Tracker.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

Zhang G, et al. (2025) Genomic and transcriptomic analyses of Heteropoda venatoria reveal the expansion of P450 family for starvation resistance in spiders. GigaScience, 14.

Riehl K, et al. (2022) TransposonUltimate: software for transposon classification, annotation and detection. Nucleic acids research, 50(11), e64.

Brückner A, et al. (2021) Evolutionary assembly of cooperating cell types in an animal chemical defense system. Cell, 184(25), 6138.