Resource Summary Report

Generated by RRID on May 22, 2025

MITE-Tracker

RRID:SCR_017030
Type: Tool

Proper Citation

MITE-Tracker (RRID:SCR_017030)

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: data analysis software, software resource, software application, data processing software, sequence analysis software

Defining Citation: DOI: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: 20250522T061113+0000

Ratings and Alerts

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

No alerts have been found for MITE-Tracker.

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.

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.