

Resource Summary Report

Generated by [NIF](#) on Sep 8, 2026

MITE-Hunter

RRID:SCR_020946

Type: Tool

Proper Citation

MITE-Hunter (RRID:SCR_020946)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3001096/>

Proper Citation: MITE-Hunter (RRID:SCR_020946)

Description: Software pipeline to identify MITEs as well as other small Class 2 non autonomous Transposable Elements from genomic DNA data sets. Used for discovering miniature inverted repeat transposable elements from genomic sequences. Can search large genomic data sets including whole genome sequences.

Synonyms: Miniature Inverted repeat Transposable Elements Hunter

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

Defining Citation: [PMID:20880995](#)

Keywords: Class 2 non-autonomous transposable element, genes non-coding regions, genome evolution, coding sequence, genomic DNA data sets,

Funding: NSF 0607123

Availability: Free, Available for download, Freely available

Resource Name: MITE-Hunter

Resource ID: SCR_020946

Alternate URLs: <https://github.com/jburnette/MITE-Hunter>

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260905T132931+0000

Ratings and Alerts

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

No alerts have been found for MITE-Hunter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Loreto ELS, et al. (2024) The good, the bad and the ugly of transposable elements annotation tools. *Genetics and molecular biology*, 46(3 Suppl 1), e20230138.

Cao J, et al. (2024) Chromosome-level genome assembly and characterization of the *Calophaca sinica* genome. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 31(3).

De Silva NP, et al. (2022) Genome assembly of an Australian native grass species reveals a recent whole-genome duplication and biased gene retention of genes involved in stress response. *GigaScience*, 12.

Cui J, et al. (2022) Chromosome-level reference genome of tetraploid *Isoetes sinensis* provides insights into evolution and adaption of lycophytes. *GigaScience*, 12.

Qiao G, et al. (2022) Genetic Basis of Dorper Sheep (*Ovis aries*) Revealed by Long-Read De Novo Genome Assembly. *Frontiers in genetics*, 13, 846449.

Zhao T, et al. (2021) A chromosome-level reference genome of the hazelnut, *Corylus heterophylla* Fisch. *GigaScience*, 10(4).