

# Resource Summary Report

Generated by [dkNET](#) on Sep 19, 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:** 20260912T195948+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 [dkNET](#) .

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).