

# Resource Summary Report

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## LTR\_FINDER\_parallel

RRID:SCR\_018969

Type: Tool

### Proper Citation

LTR\_FINDER\_parallel (RRID:SCR\_018969)

### Resource Information

**URL:** [https://github.com/oushujun/LTR\\_FINDER\\_parallel](https://github.com/oushujun/LTR_FINDER_parallel)

**Proper Citation:** LTR\_FINDER\_parallel (RRID:SCR\_018969)

**Description:** Software tool for parallelization of LTR\_FINDER enabling rapid identification of long terminal repeat retrotransposons.

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

**Defining Citation:** [PMID:31857828](#)

**Keywords:** Parallelization, rapid identification, retrotransposons identification, repetitive sequences, large genomes, long terminal repeat, retrotransposon, parallel operation, bio.tools

**Funding:** NSF IOS 1740874;  
United States Department of Agriculture National Institute of Food ;  
Agriculture and AgBioResearch at Michigan State University

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

**Resource Name:** LTR\_FINDER\_parallel

**Resource ID:** SCR\_018969

**Alternate IDs:** biotools:LTR\_FINDER\_parallel

**Alternate URLs:** [https://bio.tools/LTR\\_FINDER\\_parallel](https://bio.tools/LTR_FINDER_parallel)

**License:** MIT License

**Record Creation Time:** 20220129T080342+0000

**Record Last Update:** 20250517T060408+0000

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## Ratings and Alerts

No rating or validation information has been found for LTR\_FINDER\_parallel.

No alerts have been found for LTR\_FINDER\_parallel.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Li H, et al. (2024) Chromosome-scale assembly and annotation of the wild wheat relative *Aegilops comosa*. *Scientific data*, 11(1), 1454.

Gao T, et al. (2024) An improved chromosome-level genome assembly and annotation of *Echeneis naucrates*. *Scientific data*, 11(1), 452.

Feng L, et al. (2024) A reference-grade genome of the xerophyte *Ammopiptanthus mongolicus* sheds light on its evolution history in legumes and drought-tolerance mechanisms. *Plant communications*, 5(7), 100891.

Phillips AL, et al. (2022) The first long-read nuclear genome assembly of *Oryza australiensis*, a wild rice from northern Australia. *Scientific reports*, 12(1), 10823.

Niu S, et al. (2022) The Chinese pine genome and methylome unveil key features of conifer evolution. *Cell*, 185(1), 204.

Zhang Y, et al. (2021) The genome of the naturally evolved obesity-prone Ossabaw miniature pig. *iScience*, 24(9), 103081.

Qin P, et al. (2021) Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. *Cell*, 184(13), 3542.

Pham GM, et al. (2020) Construction of a chromosome-scale long-read reference genome assembly for potato. *GigaScience*, 9(9).