

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

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

Defining Citation: [PMID:31857828](#)

Keywords: Parallelization, rapid identification, retrotransposons identification, repetitive sequences, large genomes, long terminal repeat, retrotrnsposon, 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

License: MIT License

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260801T190621+0000

Ratings and Alerts

No rating or validation information has been found for LTR_FINDER_parallel.

No alerts have been found for LTR_FINDER_parallel.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Wang P, et al. (2025) A chromosome-level genome assembly and annotation of the *Pseudorasbora elongata* (Cypriniformes: Cyprinidae). *Scientific data*, 12(1), 554.

Ren L, et al. (2025) Genomes reveal pervasive distant hybridization in nature among cyprinid fishes. *GigaScience*, 14.

Shuang H, et al. (2025) A High-quality chromosome-level genome assembly of *Swertia przewalskii* Pissjauk. *Scientific data*, 12(1), 2026.

Robbins MD, et al. (2025) Haplotype-resolved genome assembly of 'Manhattan' perennial ryegrass (*Lolium perenne* L.) and characterization of drought responsive late embryogenesis abundant genes. *BMC genomics*, 26(1), 1125.

Ding Y, et al. (2025) High-quality assembly of the chromosomal genome for *Flemingia macrophylla* reveals genomic structural characteristics. *BMC genomics*, 26(1), 535.

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.

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

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.

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

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

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.

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).