

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

LTR_Finder

RRID:SCR_015247

Type: Tool

Proper Citation

LTR_Finder (RRID:SCR_015247)

Resource Information

URL: http://tlife.fudan.edu.cn/ltr_finder/

Proper Citation: LTR_Finder (RRID:SCR_015247)

Description: Web software capable of scanning large-scale sequences for full-length LTR retrotransposons., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: LTR Finder

Resource Type: analysis service resource, data access protocol, production service resource, service resource, software resource, web service

Defining Citation: [PMID:17485477](#)

Keywords: Long Terminal Repeat retrotransposons, Long Terminal Repeat, retrotransposon prediction, genome sequences, LTR prediction, LTR structure prediction, DNA sequence, biotools

Funding: Fudan University ;
Shanghai ;
China

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: LTR_Finder

Resource ID: SCR_015247

Alternate IDs: SCR_020944, biotools:ltr_finder

Alternate URLs: https://bio.tools/ltr_finder

Record Creation Time: 20220129T080324+0000

Ratings and Alerts

No rating or validation information has been found for LTR_Finder.

No alerts have been found for LTR_Finder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 807 mentions in open access literature.

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

Ju X, et al. (2026) De novo chromosome-level genome assembly and annotation of the Muscovy duck (*Cairina moschata*). Poultry science, 105(7), 106973.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. GigaScience, 15.

Ma Q, et al. (2026) The pan-genome provides insights into evolutionary dynamics and fatty acid metabolism in Aceraceae family. Genome biology, 27(1).

Ouyang Y, et al. (2026) Chromosome-scale Genome Assembly of the Critically Endangered Blue-crowned Laughingthrush (*Pterorhinus courtoisi*, Leiothrichidae). Scientific data, 13(1).

Dor?? G, et al. (2026) First draft genome of the decaploid species, *Ludwigia grandiflora* subsp. *hexapetala*, validated through gene expression. GigaByte (Hong Kong, China), 2026, gigabyte176.

Jian J, et al. (2026) The genome of *Pleurosigma* provides insights into the evolutionary adaptations of pelagic diatoms. DNA research : an international journal for rapid publication of reports on genes and genomes, 33(1).

Chen C, et al. (2025) Revealing Genomic Traits and Evolutionary Insights of *Oryza officinalis* from Southern China Through Genome Assembly and Transcriptome Analysis. Rice (New York, N.Y.), 18(1), 15.

Cheng HY, et al. (2025) An annotated near-complete sequence assembly of the *Magnaporthe oryzae* 70-15 reference genome. Scientific data, 12(1), 758.

Zhu XL, et al. (2025) Potential risk of dipterocarps in the marginal Asian rainforests: low population size and high genomic erosion. BMC biology, 23(1), 161.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Yang J, et al. (2025) Genomic Analysis of *Penicillium griseofulvum* CF3 Reveals Potential for Plant Growth Promotion and Disease Resistance. *Journal of fungi (Basel, Switzerland)*, 11(2).

Zheng S, et al. (2025) The origin, evolution, and translocation of sex chromosomes in *Silurus catfish* mediated by transposons. *BMC biology*, 23(1), 54.

Wu C, et al. (2025) The Three-Dimensional Structure of the Genome of the Dark Septate Endophyte *Exophiala tremulae* and Its Symbiosis Effect on Alpine Meadow Plant Growth. *Journal of fungi (Basel, Switzerland)*, 11(4).

Han LH, et al. (2025) Whole genome sequence of an edible mushroom *Strobilomyces alpinus* (Boletaceae). *G3 (Bethesda, Md.)*, 15(6).

Shu J, et al. (2025) The chromosome-level genome assembly of Broad-Leaf Fern (*Dipteris shenzhenensis*). *Scientific data*, 12(1), 475.

Feng K, et al. (2025) Telomere-to-telomere genome assembly reveals insights into the adaptive evolution of herbivore-defense mediated by volatile terpenoids in *Oenanthe javanica*. *Plant biotechnology journal*, 23(6), 2346.

Castellanos-Labarcena J, et al. (2025) Single specimen genome assembly of *Culicoides stellifer* shows evidence of a non-retroviral endogenous viral element. *BMC genomics*, 26(1), 247.

Garg V, et al. (2025) An Australian chickpea pan-genome provides insights into genome organization and offers opportunities for enhancing drought adaptation for crop improvement. *Plant biotechnology journal*, 23(9), 3967.

Zilov D, et al. (2025) Genome structure and molecular phylogeny of the only Eurasian *Boechera* species, *Boechera falcata* (Brassicaceae). *G3 (Bethesda, Md.)*, 15(7).

Hartmann FE, et al. (2025) An Inversion Polymorphism Under Balancing Selection, Involving Giant Mobile Elements, in an Invasive Fungal Pathogen. *Molecular biology and evolution*, 42(2).