

Resource Summary Report

Generated by [ASWG](#) on Aug 27, 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 [ASWG](#) .

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

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

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.

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.

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

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).

Yue H, et al. (2025) Enzyme Repertoires and Genomic Insights into *Lycium barbarum* Pectin Polysaccharide Biosynthesis. Genomics, proteomics & bioinformatics, 22(6).

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).

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).

- 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).
- Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.
- 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.
- 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).
- 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.
- Liang Y, et al. (2025) The giant genome of lily provides insights into the hybridization of cultivated lilies. *Nature communications*, 16(1), 45.
- Zheng S, et al. (2025) The origin, evolution, and translocation of sex chromosomes in *Silurus catfish* mediated by transposons. *BMC biology*, 23(1), 54.
- Bao Y, et al. (2025) Discovery of endogenous retroviruses in the genome of the red panda (*Ailurus fulgens*). *Microbiology spectrum*, 13(8), e0002425.
- Han LH, et al. (2025) Whole genome sequence of an edible mushroom *Strobilomyces alpinus* (Boletaceae). *G3 (Bethesda, Md.)*, 15(6).
- Cheng HY, et al. (2025) An annotated near-complete sequence assembly of the *Magnaporthe oryzae* 70-15 reference genome. *Scientific data*, 12(1), 758.