

Resource Summary Report

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

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 795 mentions in open access literature.

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

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

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

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

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).

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.

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.

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.

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

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.

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

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).

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).

Bao Y, et al. (2025) Discovery of endogenous retroviruses in the genome of the red panda (*Ailurus fulgens*). *Microbiology spectrum*, 13(8), e0002425.

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.

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

Jiang Z, et al. (2025) Chromosomal-level genome assembly of *Trichogramma japonicum* (Hymenoptera: Trichogrammatidae). *Scientific data*, 12(1), 1537.

Zhang X, et al. (2025) A telomere-to-telomere gap-free genome assembly of the protandrous hermaphrodite Asian seabass (*Lateolabrax japonicus*). *Scientific data*, 12(1), 1457.

Zhang L, et al. (2025) Achieving Chromosome-Level Genome Assembly of *Onychostoma macrolepis* with PacBio Sequencing and Hi-C Technologies. *Scientific data*, 12(1), 1410.