

Resource Summary Report

Generated by NIF on Apr 25, 2025

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.

Synonyms: LTR Finder

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

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

Record Last Update: 20250425T060055+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 677 mentions in open access literature.

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

Liang Y, et al. (2025) The giant genome of lily provides insights into the hybridization of cultivated lilies. *Nature communications*, 16(1), 45.

Liu Z, et al. (2025) Genome architecture of the allotetraploid wild grass *Aegilops ventricosa* reveals its evolutionary history and contributions to wheat improvement. *Plant communications*, 6(1), 101131.

Zhang D, et al. (2025) Chromosome level genome assembly of 'Wanfeng' almond (*Prunus dulcis*). *Scientific data*, 12(1), 179.

Liu R, et al. (2025) Chromosome-level reference genome and annotation of the Arctic fish *Anisarchus medius*. *Scientific data*, 12(1), 68.

Wang Y, et al. (2025) A high-quality chromosome-scale genome assembly of the Cherokee rose (*Rosa laevigata*). *Scientific data*, 12(1), 132.

Zou X, et al. (2025) Chromosome-level genome assembly of the pine wood nematode carrier *Arhopalus unicolor*. *Scientific data*, 12(1), 111.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

- Chen Y, et al. (2025) An improved chromosome-level genome assembly and annotation of Hong Kong catfish (*Clarias fuscus*). *Scientific data*, 12(1), 193.
- Li N, et al. (2025) Chromosome-scale genome assembly of three-spotted seahorse (*Hippocampus trimaculatus*) with a unique karyotype. *Scientific data*, 12(1), 49.
- Liu S, et al. (2025) Chromosome-level genome assembly and annotation of Japanese anchovy (*Engraulis japonicus*). *Scientific data*, 12(1), 134.
- Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (*Eleusine indica*). *Scientific data*, 12(1), 156.
- Yang Y, et al. (2025) Chromosome-level genome assembly of the sweet potato rot nematode *Ditylenchus destructor*. *Scientific data*, 12(1), 174.
- Li X, et al. (2025) Chromosome-level genome assembly and annotation of largemouth bronze gudgeon (*Coreius guichenoti*). *Scientific data*, 12(1), 76.
- Chen T, et al. (2024) Chromosome-level genome assembly and annotation of the tropical sea cucumber *Stichopus monotuberculatus*. *Scientific data*, 11(1), 1245.
- Zhang T, et al. (2024) A chromosome-level genome reveals genome evolution and molecular basis of anthraquinone biosynthesis in *Rheum palmatum*. *BMC plant biology*, 24(1), 261.
- Bai M, et al. (2024) The telomere-to-telomere (T2T) genome of *Peucedanum praeruptorum* Dunn provides insights into the genome evolution and coumarin biosynthesis. *GigaScience*, 13.
- Alami MM, et al. (2024) Chromosome-scale genome assembly of medicinal plant *Tinospora sagittata* (Oliv.) Gagnep. from the Menispermaceae family. *Scientific data*, 11(1), 610.
- Jiu S, et al. (2024) Haplotype-resolved genome assembly for tetraploid Chinese cherry (*Prunus pseudocerasus*) offers insights into fruit firmness. *Horticulture research*, 11(7), uhae142.
- Cao RB, et al. (2024) Karyotype and LTR-RTs analysis provide insights into oak genomic evolution. *BMC genomics*, 25(1), 328.
- Sun J, et al. (2024) The chromosome-scale genome and population genomics reveal the adaptative evolution of *Populus pruinosa* to desertification environment. *Horticulture research*, 11(3), uhae034.