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 retrotranspsons.

Synonyms: LTR Finder

Resource Type: analysis service resource, service resource, data access protocol, production service resource, web service, software 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: 20250402T061233+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 FDI Lab - SciCrunch.org.

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.

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

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

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

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.

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

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.

Li X, et al. (2025) Chromosome-level genome assembly and annotation of largemouth bronze gudgeon (Coreius guichenoti). Scientific data, 12(1), 76.

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.

Zhang H, et al. (2024) The haplotype-resolved genome assembly of autotetraploid rhubarb Rheum officinale provides insights into its genome evolution and massive accumulation of anthraquinones. Plant communications, 5(1), 100677.

Xiong Z, et al. (2024) Chromosome-level genome assembly of navel orange cv. Gannanzao (Citrus sinensis Osbeck cv. Gannanzao). G3 (Bethesda, Md.), 14(2).

Lee DJ, et al. (2024) Selection of Catechin Biosynthesis-Related Genes and Functional Analysis from Chromosome-Level Genome Assembly in C. sinensis L. Variety 'Sangmok'. International journal of molecular sciences, 25(7).

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.

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.

Li X, et al. (2024) Large-scale gene expression alterations introduced by structural variation drive morphotype diversification in Brassica oleracea. Nature genetics, 56(3), 517.

Shao L, et al. (2024) High-quality genomes of Bombax ceiba and Ceiba pentandra provide insights into the evolution of Malvaceae species and differences in their natural fiber development. Plant communications, 5(5), 100832.