

Resource Summary Report

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LTR_retriever

RRID:SCR_017623

Type: Tool

Proper Citation

LTR_retriever (RRID:SCR_017623)

Resource Information

URL: https://github.com/oushujun/LTR_retriever

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Description: Software package for identification of long terminal repeat retrotransposons (LTR-RTs). Removes false positives from initial software predictions. Achieves very high specificity, accuracy, and precision without significantly sacrificing sensitivity, hence significantly outperforming existing methods. Can construct LTR libraries directly from self-corrected PacBio reads prior to genome assembly.

Synonyms: Long Terminal Repeat retriver

Resource Type: data processing software, software resource, software application

Defining Citation: [PMID:29233850](#)

Keywords: Identification, long, terminal, repeat, retrotransponson, remove, false, positive, prediction, LTR, library, PacBio, read

Funding: NSF ;

United States Department of Agriculture National Institute of Food and Agriculture and AgBioResearch at Michigan State University

Availability: Free, Available for download, Freely available

Resource Name: LTR_retriever

Resource ID: SCR_017623

License: GNU General Public License v3.0

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260818T043613+0000

Ratings and Alerts

No rating or validation information has been found for LTR_retriever.

No alerts have been found for LTR_retriever.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 112 mentions in open access literature.

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

Aoyagi YB, et al. (2026) Chromosome-level genome assembly of the Gerbera (Gerbera hybrida) using HiFi long-read and Hi-C technologies. DNA research : an international journal for rapid publication of reports on genes and genomes, 33(1).

Luo Y, et al. (2026) A chromosome-level genome assembly and multi-omics analyses provide insights into the biosynthesis of piperlongumine in Piper sarmentosum. Communications biology, 9(1), 170.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, Carthamus tinctorius L. GigaScience, 15.

Huang Y, et al. (2026) The near-complete genome assembly of allotetraploid Pennisetum purpureum 'Purple' reveals the genetic and epigenetic landscape of centromeres. Horticulture research, 13(2), uhaf301.

Gao K, et al. (2026) Chromosome-level genome assembly and annotation of the schizothoracine fish Gymnodiptychus pachycheilus. Scientific data, 13(1).

Du J, et al. (2026) Chromosome-level genome assembly of the dwarf cattail Typha minima. Scientific data, 13(1), 231.

Zeng Z, et al. (2026) Three Near telomere-to-telomere Genomes for Gardenia jasminoides. Scientific data, 13(1).

Doré 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.

Jiu S, et al. (2026) Pangenome and resequencing analyses reveal flowering evolution and genetic control in Cerasus. Nature communications, 17(1).

Liu P, et al. (2026) Telomere-to-telomere genome of Stylosanthes guianensis uncovers symbiotic adaptation to phosphorus-deficient soils. Genome biology, 27(1).

Martin JA, et al. (2026) High-quality de novo genome assembly for the Galápagos endemic lava gull using Oxford Nanopore Technologies. *G3* (Bethesda, Md.), 16(3).

Li K, et al. (2026) Telomere-to-Telomere Genomes Reveal that Multiscale Evolution Shapes the Largest Metabolic Arsenal of Diaporthe Fungi. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(27), e13287.

Wang Y, et al. (2026) A chromosome level genome, as well as transcriptomes and metabolomes, insights into genome evolution and the biosynthesis of kaempferol and kaempferol derivatives in *Impatiens balsamina* (Balsaminaceae). *Frontiers in plant science*, 17, 1725789.

Li A, et al. (2025) Chromosomal-level genome assembly of an allotetraploid oyster. *Scientific data*, 12(1), 1492.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Lee JH, et al. (2025) Chromosome level de Novo hybrid assembly of Asian honeybee, *Apis cerana* Koreana. *Scientific reports*, 15(1), 26912.

Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. *GigaScience*, 14.

Wang T, et al. (2025) A high-quality chromosome-level reference genome of *Pulsatilla chinensis*. *Scientific data*, 13(1), 162.

Chen X, et al. (2025) High-quality genome assembly of the azooxanthellate coral *Tubastraea coccinea* (Lesson, 1829). *Scientific data*, 12(1), 507.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation. *GigaScience*, 14.