

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 application, software resource

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: 20260912T200106+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 [NIF](#) .

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.