# Resource Summary Report

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## LTRharvest

RRID:SCR_018970
Type: Tool

### Proper Citation

LTRharvest (RRID:SCR_018970)

### Resource Information

**URL:** http://genometools.org/

**Proper Citation:** LTRharvest (RRID:SCR_018970)

**Description:** Software tool for de novo detection of full length LTR retrotransposons in large sequence sets. Delivers high quality annotations based on known LTR transposon features like length, distance, and sequence motifs.

**Resource Type:** data processing software, software application, simulation software, data analysis software, software resource

**Defining Citation:** PMID:18194517

**Keywords:** De novo detection, full length LTR retrotransposons, retrotransposon, large sequence, annotation, sequence length, sequence distance, sequence motif

**Resource Name:** LTRharvest

**Resource ID:** SCR_018970

**Alternate URLs:** https://www.zbh.uni-hamburg.de/en/forschung/gi/software/ltrharvest.html

**License:** BSD-like open source licences

**Record Creation Time:** 20220129T080342+0000

**Record Last Update:** 20260806T054708+0000

### Ratings and Alerts

No rating or validation information has been found for LTRharvest.

No alerts have been found for LTRharvest.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 43 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET .


Gao C, et al. (2026) High-Quality Genome Assembly of Diplocarpon coronariae Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. Molecular ecology resources, 26(1), e70070.

Chen SY, et al. (2025) Chromosome-level reference genome assembly for the protected resource plant, Zenia insignis. Scientific data, 12(1), 459.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. GigaScience, 14.

Chen D, et al. (2025) Largest genome assembly in Brassicaceae: retrotransposon-driven genome expansion and karyotype evolution in Matthiola incana. Plant biotechnology journal, 23(9), 4109.

Zhang G, et al. (2025) Genomic and transcriptomic analyses of Heteropoda venatoria reveal the expansion of P450 family for starvation resistance in spiders. GigaScience, 14.

Liu SB, et al. (2025) High-quality genome assembly and annotation of Porodaedalea mongolica and Porodaedalea schrenkiana provide insights into potential industrial and medical application. G3 (Bethesda, Md.), 15(11).

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.

Brunharo CACG, et al. (2024) Chromosome-scale genome assembly of Poa trivialis and population genomics reveal widespread gene flow in a cool-season grass seed production system. Plant direct, 8(3), e575.

Lyu ZY, et al. (2024) The first high-altitude autotetraploid haplotype-resolved genome assembled (Rhododendron nivale subsp. boreale) provides new insights into mountaintop adaptation. GigaScience, 13.

Goodheart JA, et al. (2024) A chromosome-level genome for the nudibranch gastropod Berghia stephanieae helps parse clade-specific gene expression in novel and conserved phenotypes. BMC biology, 22(1), 9.

Albuja-Quintana M, et al. (2024) Genome report: First reference genome of Vaccinium floribundum Kunth, an emblematic Andean species. G3 (Bethesda, Md.), 14(8).

Jordan EN, et al. (2024) Integrated omics of Saccharomyces cerevisiae CENPK2-1C reveals pleiotropic drug resistance and lipidomic adaptations to cannabidiol. NPJ systems biology and applications, 10(1), 63.

Luciano-Rosario D, et al. (2024) The Near-Gapless Penicillium fuscoglaucum Genome Enables the Discovery of Lifestyle Features as an Emerging Post-Harvest Phytopathogen. Journal of fungi (Basel, Switzerland), 10(6).

Oliveira JIN, et al. (2024) Strain-specific evolution and host-specific regulation of transposable elements in the model plant symbiont Rhizophagus irregularis. G3 (Bethesda, Md.), 14(5).

Wolf M, et al. (2024) Near chromosome-level and highly repetitive genome assembly of the snake pipefish Entelurus aequoreus (Syngnathiformes: Syngnathidae). GigaByte (Hong Kong, China), 2024, gigabyte105.

Peng D, et al. (2024) The telomere-to-telomere (T2T) genome provides insights into the evolution of specialized centromere sequences in sandalwood. GigaScience, 13.

Deng J, et al. (2024) Chromosome-level genome assembly of the cottony cushion scale Icerya purchasi. Scientific data, 11(1), 639.

Wang Y, et al. (2024) Chromosome-scale genome, together with transcriptome and metabolome, provides insights into the evolution and anthocyanin biosynthesis of Rubus rosaefolius Sm. (Rosaceae). Horticulture research, 11(4), uhae064.

Bartholomew HP, et al. (2024) Omics-Based Comparison of Fungal Virulence Genes, Biosynthetic Gene Clusters, and Small Molecules in Penicillium expansum and Penicillium chrysogenum. Journal of fungi (Basel, Switzerland), 11(1).

Goodheart JA, et al. (2023) A chromosome-level genome for the nudibranch gastropod Berghia stephanieae helps parse clade-specific gene expression in novel and conserved phenotypes. bioRxiv : the preprint server for biology.