

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: software application, data processing software, data analysis software, simulation 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: 20260804T043706+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.

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.

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.

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.

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.

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

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.

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).

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).

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*.