Resource Summary Report

Generated by NIF on Apr 26, 2025

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, data analysis software, simulation software, software resource, software application

Defining Citation: PMID:18194517

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

Funding:

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: 20250426T060741+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 37 mentions in open access literature.

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

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).

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.

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).

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.

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.

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.

Xiao M, et al. (2023) A high-quality chromosome-level Eutrema salsugineum genome, an extremophile plant model. BMC genomics, 24(1), 174.

Br?na T, et al. (2023) A chromosome-length genome assembly and annotation of blackberry (Rubus argutus, cv. "Hillquist"). G3 (Bethesda, Md.), 13(2).

Dong Z, et al. (2023) A chromosome-level genome assembly of Ostrea denselamellosa provides initial insights into its evolution. Genomics, 115(2), 110582.

Liu Q, et al. (2023) Genome-wide expansion and reorganization during grass evolution: from 30 Mb chromosomes in rice and Brachypodium to 550 Mb in Avena. BMC plant biology, 23(1), 627.

Zheng S, et al. (2023) Characterization of the male-specific region containing the candidate sex-determining gene in Amur catfish (Silurus asotus) using third-generation- and pool-sequencing data. International journal of biological macromolecules, 248, 125908.

Wang Z, et al. (2022) A chromosome-level reference genome of Ensete glaucum gives insight into diversity and chromosomal and repetitive sequence evolution in the Musaceae. GigaScience, 11.