

Resource Summary Report

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EDTA

RRID:SCR_022063

Type: Tool

Proper Citation

EDTA (RRID:SCR_022063)

Resource Information

URL: <https://github.com/oushujun/EDTA>

Proper Citation: EDTA (RRID:SCR_022063)

Description: Software package to filter out false discoveries in raw TE candidates and generate high quality non redundant TE library for whole genome TE annotations. Produces filtered non redundant TE library for annotation of structurally intact and fragmented elements.

Synonyms: Extensive de novo TE Annotator

Resource Type: software resource, software toolkit

Defining Citation: [PMID:31843001](#)

Keywords: automated whole-genome de-novo, TE annotation, TE library

Funding: NSF Plant Genome Research Program ;
USDA National Institute of Food and Agriculture ;
State of Iowa ;
Canada First Research Excellence Fund Ontario

Availability: Free, Available for download, Freely available

Resource Name: EDTA

Resource ID: SCR_022063

License: GNU General Public License v3.0

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260808T190532+0000

Ratings and Alerts

No rating or validation information has been found for EDTA.

No alerts have been found for EDTA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 80 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Yu H, et al. (2026) Chromosome-level genome assembly of the Leopard Wrasse *Macropharyngodon Meleagris*. *Scientific data*, 13(1).

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

Chen H, et al. (2026) A telomere-to-telomere genome assembly of *Nymphaea minima* provides details into the developmental transcriptome atlas and adaptive regulatory mechanisms. *Horticulture research*, 13(6), uhag085.

Chen Q, et al. (2026) Chromosome-level genome assembly and annotation of the critically endangered Siberian crane (*Leucogeranus leucogeranus*). *Scientific data*, 13(1).

Bentz PC, et al. (2026) Two independent origins of XY sex chromosomes in *Asparagus*. *Molecular biology and evolution*, 43(2).

Yang L, et al. (2026) Two Indel Variations in the Regulated Carotenoid Pigment Gene Hold the Key to the Interspecies Flower Colour Differentiation in *Liriodendron* Plants. *Plant biotechnology journal*, 24(4), 2260.

Fiesinger A, et al. (2026) The genome of the reef-building coral *Porites harrisoni* from the southern Persian/Arabian Gulf. *GigaByte (Hong Kong, China)*, 2026, gigabyte174.

Yue Y, et al. (2026) Genome assemblies of the liverwort *Blasia pusilla* uncover a well-defined pseudoautosomal region on homomorphic UV sex chromosomes. *Genome biology*, 27(1).

Chen D, et al. (2026) Insights into karyotype evolution and flower color variation from the genome assembly of wallflower (*Erysimum cheiri*). *Plant physiology*, 200(4).

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.

Kirzinger MW, et al. (2026) Haploid Mutation Mapping Identifies a Homoeologous Non-Reciprocal Translocation Linked to Reduced Fibre and Enhanced Protein in Brassica

napus. Plant biotechnology journal, 24(5), 3219.

Gu C, et al. (2026) A chromosomal haplotype-resolved genome assembly of *Cuphea hookeriana*. Scientific data, 13(1).

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort *Apopellia endiviifolia* (Jungermanniopsida, Marchantiophyta). GigaScience, 15.

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.

Costa MFS, et al. (2026) EDTA-GUI: a plant-optimized graphical implementation of the EDTA pipeline enabling lineage-level classification and analysis. BMC genomics, 27(1).

Yi L, et al. (2026) Comparative genomics across *Linum* illuminates the evolutionary basis of flax domestication, genome diversification, and seed oil biosynthesis. Frontiers in genetics, 17, 1835945.

Zhang RG, et al. (2025) Convergent Patterns of Karyotype Evolution Underlying Karyotype Uniformity in Conifers. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(7), e2411098.

Movilli A, et al. (2025) Long-read detection of transposable element mobilization in the soma of hypomethylated *Arabidopsis thaliana* individuals. Genome biology, 26(1), 231.

Bec B, et al. (2025) Phylogenomics Untangles the Metabolic Potential of *Picochlorum tauri*, a New Picoalgal Species Causing a Winter Bloom in the Mediterranean Thau Lagoon. Environmental microbiology, 27(9), e70174.

Robbins MD, et al. (2025) Haplotype-resolved genome assembly of 'Manhattan' perennial ryegrass (*Lolium perenne* L.) and characterization of drought responsive late embryogenesis abundant genes. BMC genomics, 26(1), 1125.