

Resource Summary Report

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PILER

RRID:SCR_017333

Type: Tool

Proper Citation

PILER (RRID:SCR_017333)

Resource Information

URL: <https://www.drive5.com/piler/>

Proper Citation: PILER (RRID:SCR_017333)

Description: Software tool for analyzing repetitive DNA found in genome sequences. Software package for identification and classification of genomic repeats. Used for identifying patterns of local alignments induced by certain classes of repeats.

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

Defining Citation: [PMID:15961452](#)

Keywords: analysis, repetitive, DNA, genome, sequence, classification, alignment

Availability: Free, Available for download, Freely available

Resource Name: PILER

Resource ID: SCR_017333

Alternate URLs: <https://omictools.com/piler-tool>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260729T044433+0000

Ratings and Alerts

No rating or validation information has been found for PILER.

No alerts have been found for PILER.

Data and Source Information

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Li Z, et al. (2024) Intraspecific diploidization of a halophyte root fungus drives heterosis. *Nature communications*, 15(1), 5872.

Shang H, et al. (2024) Genome assembly of *Stephania longa* provides insight into cepharanthine biosynthesis. *Frontiers in plant science*, 15, 1414636.

Chen G, et al. (2023) The Jasmine (*Jasminum sambac*) Genome Provides Insight into the Biosynthesis of Flower Fragrances and Jasmonates. *Genomics, proteomics & bioinformatics*, 21(1), 127.

Yan H, et al. (2023) Pangenomic analysis identifies structural variation associated with heat tolerance in pearl millet. *Nature genetics*, 55(3), 507.

Lu X, et al. (2022) A high-quality assembled genome and its comparative analysis decode the adaptive molecular mechanism of the number one Chinese cotton variety CRI-12. *GigaScience*, 11.

Yin Y, et al. (2021) The chromosome-scale genome of *Magnolia officinalis* provides insight into the evolutionary position of magnoliids. *iScience*, 24(9), 102997.

Zhao T, et al. (2021) A chromosome-level reference genome of the hazelnut, *Corylus heterophylla* Fisch. *GigaScience*, 10(4).

Guo XM, et al. (2021) Chromosomal-level assembly of the *Leptodermis oblonga* (Rubiaceae) genome and its phylogenetic implications. *Genomics*, 113(5), 3072.

Suo Y, et al. (2020) A high-quality chromosomal genome assembly of *Diospyros oleifera* Cheng. *GigaScience*, 9(1).

Yu J, et al. (2020) Draft genome of the aquatic moss *Fontinalis antipyretica* (Fontinalaceae, Bryophyta). *GigaByte* (Hong Kong, China), 2020, gigabyte8.

Wang L, et al. (2019) A draft genome assembly of halophyte *Suaeda aralocaspica*, a plant that performs C4 photosynthesis within individual cells. *GigaScience*, 8(9).

Ou C, et al. (2019) A de novo genome assembly of the dwarfing pear rootstock Zhongai 1. *Scientific data*, 6(1), 281.

Korb J, et al. (2015) A genomic comparison of two termites with different social complexity. *Frontiers in genetics*, 6, 9.

Gao C, et al. (2014) Oil accumulation mechanisms of the oleaginous microalga *Chlorella protothecoides* revealed through its genome, transcriptomes, and proteomes. *BMC genomics*, 15(1), 582.