

# Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

## LASTZ

RRID:SCR\_018556

Type: Tool

### Proper Citation

LASTZ (RRID:SCR\_018556)

### Resource Information

**URL:** [http://www.bx.psu.edu/miller\\_lab/dist/README.lastz-1.02.00/README.lastz-1.02.00a.html#install](http://www.bx.psu.edu/miller_lab/dist/README.lastz-1.02.00/README.lastz-1.02.00a.html#install)

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**Description:** Software package for sequence alignment. Pairwise aligner for aligning DNA sequences. Designed to handle sequences size of human chromosomes and from different species. Useful for sequences produced by NGS sequencing technologies.

**Resource Type:** alignment software, data processing software, image analysis software, software application, software resource, software toolkit

**Keywords:** Sequence, sequence alignment, pairwise aligner, DNA sequence alingning, human chromosome, Next Generation Sequencing technology data

**Availability:** Free, Available for download, Freely available

**Resource Name:** LASTZ

**Resource ID:** SCR\_018556

**Alternate URLs:** <http://www.bx.psu.edu/~rsharris/lastz/>, <https://github.com/lastz/lastz>

**License:** MIT License

**Record Creation Time:** 20220129T080340+0000

**Record Last Update:** 20260905T132838+0000

### Ratings and Alerts

No rating or validation information has been found for LASTZ.

No alerts have been found for LASTZ.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 54 mentions in open access literature.

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

Lan L, et al. (2026) Comparative Genomics Provide Insights Into Karyotype Evolution in Vespertilionid Bats (Vespertilionidae, Chiroptera). *Molecular ecology resources*, 26(3), e70129.

Dor?? G, et al. (2026) First draft genome of the decaploid species, *Ludwigia grandiflora* subsp. *hexapetala*, validated through gene expression. *GigaByte (Hong Kong, China)*, 2026, gigabyte176.

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.

Guo W, et al. (2025) Pygmy sperm whale multi-omics data reveal hypoxia adaptations in deep-diving cetaceans. *BMC biology*, 24(1), 20.

Ben-Rached F, et al. (2025) Leveraging genomic insights from the neglected malaria parasites *P. malariae* and *P. ovale* using selective whole genome amplification (SWGA) approach. *BMC genomics*, 26(1), 118.

Bai R, et al. (2025) Whole-Genome Characterization of *Inonotus hispidus* from *Ulmus macrocarpa* and Its Comparative Genomics with Strains from *Morus alba* and *Acer truncatum*. *Journal of fungi (Basel, Switzerland)*, 11(5).

Coulon PML, et al. (2025) Quorum sensing and DNA methylation play active roles in clinical *Burkholderia* phase variation. *Journal of bacteriology*, 207(3), e0053124.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte (Hong Kong, China)*, 2025, gigabyte155.

Liu YN, et al. (2025) Near complete assembly of *Drosophila melanogaster* Canton S strain genome. *Nature communications*, 17(1), 329.

Hauff L, et al. (2025) De Novo Genome Assembly for an Endangered Lemur Using Portable Nanopore Sequencing in Rural Madagascar. *Ecology and evolution*, 15(1), e70734.

Zhou Y, et al. (2025) Chromosome-level echidna genome illuminates evolution of multiple sex chromosome system in monotremes. *GigaScience*, 14.

Azam S, et al. (2025) Advancing the Indian cattle pangenome: characterizing non-reference sequences in *Bos indicus*. *Journal of animal science and biotechnology*, 16(1),

21.

Hartley GA, et al. (2025) Centromeric transposable elements and epigenetic status drive karyotypic variation in the eastern hoolock gibbon. *Cell genomics*, 5(4), 100808.

Dubocanin D, et al. (2025) Conservation of dichromatin organization along regional centromeres. *Cell genomics*, 5(4), 100819.

Li G, et al. (2024) Comparative analysis of chloroplast and mitochondrial genomes of sweet potato provides evidence of gene transfer. *Scientific reports*, 14(1), 4547.

Yang T, et al. (2024) A telomere-to-telomere gap-free reference genome assembly of avocado provides useful resources for identifying genes related to fatty acid biosynthesis and disease resistance. *Horticulture research*, 11(7), uhae119.

Iliopoulou E, et al. (2024) Extensive Loss and Gain of Conserved Noncoding Elements During Early Teleost Evolution. *Genome biology and evolution*, 16(4).

Zhang J, et al. (2024) Chromosome-Level Assembly and Comparative Genomic Analysis of *Suillus bovinus* Provides Insights into the Mechanism of Mycorrhizal Symbiosis. *Journal of fungi (Basel, Switzerland)*, 10(3).

Li Z, et al. (2024) Comparative analysis of the whole mitochondrial genomes of four species in sect. *Chrysanth* (*Camellia* L.), endemic taxa in China. *BMC plant biology*, 24(1), 955.

Wan JN, et al. (2024) The rise of baobab trees in Madagascar. *Nature*, 629(8014), 1091.