

Resource Summary Report

Generated by ASWG on Aug 21, 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

Proper Citation: LASTZ (RRID:SCR_018556)

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: software application, data processing software, software toolkit, image analysis software, alignment software, software resource

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: 20260821T043040+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 [ASWG](#) .

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.

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).

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.

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

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

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

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.

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

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

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.

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).

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.

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

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.