

Resource Summary Report

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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

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

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: 20260729T044446+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 39 mentions in open access literature.

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

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

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).

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

Haufl 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.

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

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.

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.

Chen Z, et al. (2024) Chromosomal-level genome assembly of *Hylurgus ligniperda*: insights into host adaptation and environmental tolerance. *BMC genomics*, 25(1), 792.

Newman T, et al. (2024) *PRKACB* is a novel imprinted gene in marsupials. *Epigenetics & chromatin*, 17(1), 29.

Zhang Y, et al. (2024) A trade-off in evolution: the adaptive landscape of spiders without venom glands. *GigaScience*, 13.

Huang X, et al. (2024) The genome of African manatee *Trichechus senegalensis* reveals secondary adaptation to the aquatic environment. *iScience*, 27(7), 110394.

Tian R, et al. (2024) Sirenian genomes illuminate the evolution of fully aquatic species within the mammalian superorder afrotheria. *Nature communications*, 15(1), 5568.

Byerly PA, et al. (2024) Haplotype-resolved genome and population genomics of the threatened garden dormouse in Europe. *Genome research*, 34(11), 2094.