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

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

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

Funding:

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: 20250418T055535+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 32 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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).

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).

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

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

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.

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

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.

Xu J, et al. (2023) Bedquiline Resistance Mutations: Correlations with Drug Exposures and Impact on the Proteome in M. tuberculosis. Antimicrobial agents and chemotherapy, 67(7), e0153222.

Zhang BL, et al. (2023) Comparative genomics reveals the hybrid origin of a macaque group. Science advances, 9(22), eadd3580.

Alathari S, et al. (2023) A Multiplexed, Tiled PCR Method for Rapid Whole-Genome Sequencing of Infectious Spleen and Kidney Necrosis Virus (ISKNV) in Tilapia. Viruses, 15(4).

Zadesenets KS, et al. (2023) Unraveling the Unusual Subgenomic Organization in the Neopolyploid Free-Living Flatworm Macrostomum lignano. Molecular biology and evolution, 40(12).

Xu MR, et al. (2023) Maternal dominance contributes to subgenome differentiation in allopolyploid fishes. Nature communications, 14(1), 8357.

Lai E, et al. (2022) A Method for Variant Agnostic Detection of SARS-CoV-2, Rapid Monitoring of Circulating Variants, and Early Detection of Emergent Variants Such as Omicron. Journal of clinical microbiology, 60(7), e0034222.

Li R, et al. (2022) Chromosome-level genome assembly of the Siberian chipmunk (Tamias sibiricus). Scientific data, 9(1), 783.