Resource Summary Report

Generated by NIF on Apr 17, 2025

LAST

RRID:SCR_006119
Type: Tool

Proper Citation

LAST (RRID:SCR_006119)

Resource Information

URL: http://last.cbrc.jp/

Proper Citation: LAST (RRID:SCR_006119)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Software tool for aligning sequences, similar to BLAST 2 sequences that colour-codes the alignments by reliability. Another useful feature of LAST is that it can compare huge (vertebrate-genome-sized) datasets. Unfortunately, this only applies to the downloadable version of LAST, not the web service. The web service can just about handle bacterial genomes, but it will take a few minutes and the output will be large. LAST can: * Handle big sequence data, e.g: ** Compare two vertebrate genomes ** Align billions of DNA reads to a genome * Indicate the reliability of each aligned column. * Use sequence quality data properly. * Compare DNA to proteins, with frameshifts. * Compare PSSMs to sequences * Calculate the likelihood of chance similarities between random sequences. LAST cannot (yet): * Do spliced alignment.

Abbreviations: LAST

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

Defining Citation: PMID:21209072, PMID:20144198, PMID:20110255, DOI:10.1093/nar/gkq010

Keywords: sequence alignment, align, vertebrate, genome, sequence, alignment, bio.tools

Funding: National Genome Research Network ;
INTEuropean Union Systems Institute ;
Japanese Ministry of Education Culture Sports Science and Technology MEXT

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: LAST

Resource ID: SCR_006119

Alternate IDs: nlx_151594, biotools:last, OMICS_15813

Alternate URLs: https://bio.tools/last, https://sources.debian.org/src/last-align/

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250416T063430+0000

Ratings and Alerts

No rating or validation information has been found for LAST.

No alerts have been found for LAST.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 392 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Frankenberg SR, et al. (2025) Unearthing the secrets of Australia's most enigmatic and cryptic mammal, the marsupial mole. Science advances, 11(1), eado4140.

Gaston JM, et al. (2025) X-Mapper: fast and accurate sequence alignment via gapped x-mers. Genome biology, 26(1), 15.

Wen H, et al. (2025) Evolutionary analysis of the DHHCs in Saccharinae. Scientific reports, 15(1), 2290.

Jin F, et al. (2025) Does use of anal cytology as a triage test improve the performance of high-risk human papillomavirus screening in gay and bisexual men for anal cancer prevention? International journal of cancer, 156(3), 575.

Polinski JM, et al. (2025) Chromosome-level reference genome for the Jonah crab, Cancer borealis. G3 (Bethesda, Md.), 15(1).

Mahfouz AM, et al. (2025) Genetic determinants of silver nanoparticle resistance and the impact of gamma irradiation on nanoparticle stability. BMC microbiology, 25(1), 18.

Li A, et al. (2024) Chromosome-Level Genome Assembly for the Chinese Serow (Capricornis milneedwardsii) Provides Insights Into Its Taxonomic Status and Evolution. Ecology and evolution, 14(10), e70400.

Zhang W, et al. (2024) Chromosome-level genome assembly of the medicinal insect Blaps rhynchopetera using Nanopore and Hi-C technologies. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(6).

Plessy C, et al. (2024) Extreme genome scrambling in marine planktonic Oikopleura dioica cryptic species. Genome research, 34(3), 426.

Liao B, et al. (2024) Dysfunction of duplicated pair rice histone acetyltransferases causes segregation distortion and an interspecific reproductive barrier. Nature communications, 15(1), 996.

Chen W, et al. (2024) Two telomere-to-telomere gapless genomes reveal insights into Capsicum evolution and capsaicinoid biosynthesis. Nature communications, 15(1), 4295.

Sylvester T, et al. (2024) A reference quality genome assembly for the jewel scarab Chrysina gloriosa. G3 (Bethesda, Md.), 14(6).

Sun N, et al. (2024) Chromosome-level genome provides insight into the evolution and conservation of the threatened goral (Naemorhedus goral). BMC genomics, 25(1), 92.

Hu M, et al. (2024) A chromosome-level genome of the striated frogfish (Antennarius striatus). Scientific data, 11(1), 654.

Fang Y, et al. (2024) Pan-genome and phylogenomic analyses highlight Hevea species delineation and rubber trait evolution. Nature communications, 15(1), 7232.

Zhou B, et al. (2024) Evolutionary patterns and functional effects of 3D chromatin structures in butterflies with extensive genome rearrangements. Nature communications, 15(1), 6303.

Yang H, et al. (2024) High-quality assembly of the T2T genome for Isodon rubescens f. lushanensis reveals genomic structure variations between 2 typical forms of Isodon rubescens. GigaScience, 13.

Li W, et al. (2024) Effects of dietary rosemary ultrafine powder supplementation on aged hen health and productivity: a randomized controlled trial. Poultry science, 103(11), 104133.

Resta F, et al. (2024) Simulation-based training in ultrasound-guided regional anaesthesia for emergency physicians: insights from an Italian pre/post intervention study. BMC medical education, 24(1), 1510.

Zhou W, et al. (2024) A chromosome-level genome assembly of anesthetic drug-producing Anisodus acutangulus provides insights into its evolution and the biosynthesis of tropane alkaloids. Plant communications, 5(1), 100680.