

Resource Summary Report

Generated by [RRID](#) on Aug 7, 2026

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: LAST

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

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: 20260807T042631+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 403 mentions in open access literature.

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

Sekar YS, et al. (2026) Genomic adaptability and virulence of Bacillus anthracis: a machine learning-based pan-genome and comparative analysis. BMC genomics, 27(1), 141.

Ma HY, et al. (2026) A pangenome insight into the genome divergence and flower color diversity among Rhododendron species. BMC genomics, 27(1), 101.

Li H, et al. (2026) Comparative genome analysis provides a foundation for defining salvinatorin A biosynthesis in Salvia divinorum. Nature communications, 17(1).

Antipov D, et al. (2026) Automatic Generation of Model Sequences for Complex Regions in Assembly Graphs. bioRxiv : the preprint server for biology.

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 DHHs in Saccharinae. Scientific reports, 15(1), 2290.

- Dong C, et al. (2025) Subcellular Enrichment Patterns of New Genes in *Drosophila* Evolution. *Molecular biology and evolution*, 42(2).
- Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.
- Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.
- Mohammadi KM, et al. (2025) The Prevalence and Associated Factors of Domestic Violence Against Pregnant Women During the COVID-19 Pandemic: A Systematic Review and Meta-Analysis. *Brain and behavior*, 15(3), e70345.
- 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.
- Fang ?? Y, et al. (2025) Duckweed Evolution: from Land back to Water. *Genomics, proteomics & bioinformatics*, 23(4).
- 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.
- Polinski JM, et al. (2025) Chromosome-level reference genome for the Jonah crab, *Cancer borealis*. *G3 (Bethesda, Md.)*, 15(1).
- 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.
- Rimbara E, et al. (2024) Characterization of three novel *Helicobacter* species infecting stomachs of dogs and cats: *Helicobacter gastrocanis* sp. nov., *Helicobacter gastrofelis* sp. nov., and *Helicobacter felistomachi* sp. nov. *Frontiers in microbiology*, 15, 1459401.
- 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.
- Chen W, et al. (2024) Two telomere-to-telomere gapless genomes reveal insights into *Capsicum* evolution and capsaicinoid biosynthesis. *Nature communications*, 15(1), 4295.