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: production service resource, analysis service resource, software application, data analysis service, service resource, data processing software, software 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 Agency:** 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:** 20240702T053446+0000

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**Ratings and Alerts**

No rating or validation information has been found for LAST.

No alerts have been found for LAST.

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**Data and Source Information**

**Source:** [SciCrunch Registry](https://scicrunch.org)

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**Usage and Citation Metrics**

We found 348 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](https://fdi.org).


Wu Y, et al. (2023) The genome sequence and demographic history of Przewalskia tangutica (Solanaceae), an endangered alpine plant on the Qinghai-Tibet Plateau. DNA research : an international journal for rapid publication of reports on genes and genomes, 30(2).


Winn AN, et al. (2023) Estimated Savings After Stopping Tyrosine Kinase Inhibitor Treatment Among Patients With Chronic Myeloid Leukemia. JAMA network open, 6(12), e2347950.


Ohori S, et al. (2023) Biallelic structural variations within FGF12 detected by long-read sequencing in epilepsy. Life science alliance, 6(8).


