

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

BLASR

RRID:SCR_000764

Type: Tool

Proper Citation

BLASR (RRID:SCR_000764)

Resource Information

URL: <https://github.com/PacificBiosciences/blasr>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. C++ long-read aligner for PacBio reads., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: Basic Local Alignment with Successive Refinement, BLASR: The PacBio long read aligner

Resource Type: software resource

Defining Citation: [PMID:22988817](#), [DOI:10.1186/1471-2105-13-23](#)

Keywords: standalone software, c++, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: BLASR

Resource ID: SCR_000764

Alternate IDs: biotools:blasr, OMICS_05134

Alternate URLs: <https://bio.tools/blasr>, <https://sources.debian.org/src/blasr/>

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260725T190450+0000

Ratings and Alerts

No rating or validation information has been found for BLASR.

Warning: The URL does not work anymore but there might be an archived version here <https://github.com/BioinformaticsArchive/blasr>

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Park G, et al. (2025) NanoMnT: an STR analysis tool for Oxford Nanopore sequencing data driven by a comprehensive analysis of error profile in STR regions. *GigaScience*, 14.

Bernot JP, et al. (2022) Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle *Pollicipes pollicipes*. *GigaScience*, 11.

Wang X, et al. (2022) Chromosome-level genome and recombination map of the male buffalo. *GigaScience*, 12.

Wang K, et al. (2019) De novo genome assembly of the white-spotted flower chafer (*Protaetia brevitarsis*). *GigaScience*, 8(4).

Conte MA, et al. (2019) Chromosome-scale assemblies reveal the structural evolution of African cichlid genomes. *GigaScience*, 8(4).

Stroehlein AJ, et al. (2019) High-quality *Schistosoma haematobium* genome achieved by single-molecule and long-range sequencing. *GigaScience*, 8(9).

Xu CQ, et al. (2019) Genome sequence of *Malania oleifera*, a tree with great value for nervonic acid production. *GigaScience*, 8(2).

Arimoto A, et al. (2019) A draft nuclear-genome assembly of the acoel flatworm *Praesagittifera naikaiensis*. *GigaScience*, 8(4).

Prazsák I, et al. (2018) Full Genome Sequence of the Western Reserve Strain of Vaccinia Virus Determined by Third-Generation Sequencing. *Genome announcements*, 6(11).

Munhoz CF, et al. (2018) A gene-rich fraction analysis of the *Passiflora edulis* genome reveals highly conserved microsyntenic regions with two related Malpighiales species. *Scientific reports*, 8(1), 13024.

Yan B, et al. (2018) SMRT-Cappable-seq reveals complex operon variants in bacteria. *Nature communications*, 9(1), 3676.

Humble E, et al. (2018) RAD Sequencing and a Hybrid Antarctic Fur Seal Genome Assembly Reveal Rapidly Decaying Linkage Disequilibrium, Global Population Structure and Evidence for Inbreeding. *G3* (Bethesda, Md.), 8(8), 2709.

Jian J, et al. (2016) Association Between Progranulin and Gaucher Disease. *EBioMedicine*, 11, 127.

Ardisson S, et al. (2016) Cell Cycle Constraints and Environmental Control of Local DNA Hypomethylation in γ -Proteobacteria. *PLoS genetics*, 12(12), e1006499.

Dowell NL, et al. (2016) The Deep Origin and Recent Loss of Venom Toxin Genes in Rattlesnakes. *Current biology : CB*, 26(18), 2434.