

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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: 20260905T132425+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Warning: The URL does not work anymore but there might be an archived version here 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 [Kravitz](#) .

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.

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

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

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.

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.

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

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

Ardissone 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.