

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

long-read-tools

RRID:SCR_019116

Type: Tool

Proper Citation

long-read-tools (RRID:SCR_019116)

Resource Information

URL: <https://long-read-tools.org/>

Proper Citation: long-read-tools (RRID:SCR_019116)

Description: Interactive database of software tools for analysis of long read sequencing data. Catalogue of long-read sequencing data analysis tools. Catalogue of downstream analysis tools of real and synthetic long-read technologies.

Synonyms: Long-Read-Tools, long-read-tools.org

Resource Type: data or information resource, database, software repository, software resource

Defining Citation: [PMID:32033565](#)

Keywords: Software tools collection, long read sequencing data, long read sequencing, data analysis, data analysis tools, bio.tools

Availability: Free, Freely available

Resource Name: long-read-tools

Resource ID: SCR_019116

Alternate IDs: biotools:long-read-tools

Alternate URLs: https://github.com/shaniAmare/long_read_tools, <https://bio.tools/long-read-tools>

License: MIT

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260912T195910+0000

Ratings and Alerts

No rating or validation information has been found for long-read-tools.

No alerts have been found for long-read-tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Aliyev E, et al. (2026) A comprehensive assessment of tandem repeat genotyping methods for Nanopore long-read genomes. *bioRxiv : the preprint server for biology*.

Tafazoli A, et al. (2025) Leveraging long-read sequencing technologies for pharmacogenomic testing: applications, analytical strategies, challenges, and future perspectives. *Frontiers in genetics*, 16, 1435416.

Bhatia S, et al. (2025) Bioinformatics frameworks for single-cell long-read sequencing: unlocking isoform-level resolution. *Briefings in bioinformatics*, 26(6).

Szakállas N, et al. (2024) Can long-read sequencing tackle the barriers, which the next-generation could not? A review. *Pathology oncology research : POR*, 30, 1611676.

Deng CH, et al. (2023) Genotype and phenotype data standardization, utilization and integration in the big data era for agricultural sciences. *Database : the journal of biological databases and curation*, 2023.

Khan AS, et al. (2023) Report of the third conference on next-generation sequencing for adventitious virus detection in biologics for humans and animals. *Biologicals : journal of the International Association of Biological Standardization*, 83, 101696.

Brockley LJ, et al. (2023) Sequence-Based Platforms for Discovering Biomarkers in Liquid Biopsy of Non-Small-Cell Lung Cancer. *Cancers*, 15(8).

LoTempio J, et al. (2023) Benchmarking long-read genome sequence alignment tools for human genomics applications. *PeerJ*, 11, e16515.

White LK, et al. (2022) Modification mapping by nanopore sequencing. *Frontiers in genetics*, 13, 1037134.

Lüth T, et al. (2022) Benchmarking Low-Frequency Variant Calling With Long-Read Data on Mitochondrial DNA. *Frontiers in genetics*, 13, 887644.

Chen Z, et al. (2021) Application of third-generation sequencing in cancer research. *Medical review* (2021), 1(2), 150.

Amarasinghe SL, et al. (2021) long-read-tools.org: an interactive catalogue of analysis methods for long-read sequencing data. *GigaScience*, 10(2).

Jung H, et al. (2020) Twelve quick steps for genome assembly and annotation in the classroom. *PLoS computational biology*, 16(11), e1008325.

Kraft F, et al. (2020) Long-read sequencing to understand genome biology and cell function. *The international journal of biochemistry & cell biology*, 126, 105799.