

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

PBSIM

RRID:SCR_002512

Type: Tool

Proper Citation

PBSIM (RRID:SCR_002512)

Resource Information

URL: <http://code.google.com/p/pbsim/>

Proper Citation: PBSIM (RRID:SCR_002512)

Description: Software that simulates PacBio reads by using either a model-based or sampling-based simulation.

Synonyms: PacBio reads simulator

Resource Type: software resource, software application, simulation software

Defining Citation: [PMID:23129296](#), [DOI:10.1093/bioinformatics/bts649](#)

Keywords: pacbio simulation, model-based simulation, sampling-based simulation

Availability: Free, Available for download, Freely available

Resource Name: PBSIM

Resource ID: SCR_002512

Alternate IDs: OMICS_00253

Alternate URLs: <https://sources.debian.org/src/pbsim/>

License: GNU GPL v2

License URLs: <http://www.gnu.org/licenses/old-licenses/gpl-2.0.html>

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260801T190725+0000

Ratings and Alerts

No rating or validation information has been found for PBSIM.

No alerts have been found for PBSIM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Yu W, et al. (2024) Comprehensive assessment of 11 de novo HiFi assemblers on complex eukaryotic genomes and metagenomes. *Genome research*, 34(2), 326.

Zong P, et al. (2024) TSTA: thread and SIMD-based trapezoidal pairwise/multiple sequence-alignment method. *GigaByte (Hong Kong, China)*, 2024, gigabyte141.

Xie M, et al. (2022) gcaPDA: a haplotype-resolved diploid assembler. *BMC bioinformatics*, 23(1), 68.

Fukasawa Y, et al. (2020) LongQC: A Quality Control Tool for Third Generation Sequencing Long Read Data. *G3 (Bethesda, Md.)*, 10(4), 1193.

Fijarczyk A, et al. (2020) The Genome Sequence of the Jean-Talon Strain, an Archeological Beer Yeast from Québec, Reveals Traces of Adaptation to Specific Brewing Conditions. *G3 (Bethesda, Md.)*, 10(9), 3087.

Kosugi S, et al. (2019) Comprehensive evaluation of structural variation detection algorithms for whole genome sequencing. *Genome biology*, 20(1), 117.

Liu B, et al. (2019) deSALT: fast and accurate long transcriptomic read alignment with de Bruijn graph-based index. *Genome biology*, 20(1), 274.

Križanovic K, et al. (2018) Evaluation of tools for long read RNA-seq splice-aware alignment. *Bioinformatics (Oxford, England)*, 34(5), 748.

Zhao X, et al. (2017) A recurrence-based approach for validating structural variation using long-read sequencing technology. *GigaScience*, 6(8), 1.

Afshar PT, et al. (2017) COSINE: non-seeding method for mapping long noisy sequences. *Nucleic acids research*, 45(14), e132.

Gao S, et al. (2016) OPERA-LG: efficient and exact scaffolding of large, repeat-rich eukaryotic genomes with performance guarantees. *Genome biology*, 17, 102.