

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

[pbmm2](#)

RRID:SCR_025549

Type: Tool

Proper Citation

pbmm2 (RRID:SCR_025549)

Resource Information

URL: <https://github.com/PacificBiosciences/pbmm2?tab=readme-ov-file>

Proper Citation: pbmm2 (RRID:SCR_025549)

Description: Software application as minimap2 frontend for PacBio native data formats. SMRT C++ wrapper for minimap2's C API.

Resource Type: source code, software resource

Keywords: minimap2, PacBio, native data formats, SMRT C++ wrapper, minimap2 C API,

Availability: Free, Available for download, Freely available,

Resource Name: pbmm2

Resource ID: SCR_025549

License: BSD-3-Clause-Clear license

Record Creation Time: 20240730T053256+0000

Record Last Update: 20260810T040917+0000

Ratings and Alerts

No rating or validation information has been found for pbmm2.

No alerts have been found for pbmm2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (*Leuciscidae: Phoxinus phoxinus*) provide evidence of haplotype diversity. *GigaScience*, 14.

Conn T, et al. (2025) Genome assembly and annotation of *Acropora pulchra* from Mo'orea French Polynesia. *GigaByte (Hong Kong, China)*, 2025, gigabyte153.

Mochales-Riaño G, et al. (2025) Chromosome-level reference genome for the medically important Arabian horned viper (*Cerastes gasperettii*). *GigaScience*, 14.

Rathinam M, et al. (2025) A chromosome-scale reference genome assembly of pigeonpea wild relative *Cajanus platycarpus* highlights the evolutionary decline of defence genes in *Cajanus cajan*. *Journal of experimental botany*, 76(20), 6166.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. *bioRxiv : the preprint server for biology*.