

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

BCALM 2

RRID:SCR_023975

Type: Tool

Proper Citation

BCALM 2 (RRID:SCR_023975)

Resource Information

URL: <https://github.com/GATB/bcalm>

Proper Citation: BCALM 2 (RRID:SCR_023975)

Description: Software tool for constructing compacted de Bruijn graph from sequencing data.Parallel algorithm that distributes the input based on minimizer hashing technique, allowing for good balance of memory usage throughout its execution.

Synonyms: bcalm

Resource Type: software resource, software application, source code

Defining Citation: [PMID:27307618](#)

Keywords: constructing compacted de Bruijn graph, sequencing data,

Availability: Free, Available for download, Freely available

Resource Name: BCALM 2

Resource ID: SCR_023975

Alternate IDs: OMICS_12164

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

License: MIT License

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260731T043153+0000

Ratings and Alerts

No rating or validation information has been found for BCALM 2.

No alerts have been found for BCALM 2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Levallois V, et al. (2024) The backpack quotient filter: A dynamic and space-efficient data structure for querying k-mers with abundance. iScience, 27(12), 111435.

Bessière C, et al. (2024) Transipedia.org: k-mer-based exploration of large RNA sequencing datasets and application to cancer data. Genome biology, 25(1), 266.

Faltejsková K, et al. (2023) PAPERFly: Partial Assembly-based Peak Finder for ab initio binding site reconstruction. BMC bioinformatics, 24(1), 487.