

# Resource Summary Report

Generated by SPARC SAWG on Sep 15, 2026

## BCALM 2

RRID:SCR\_023975

Type: Tool

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### Proper Citation

BCALM 2 (RRID:SCR\_023975)

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### 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 application, software resource, 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:** 20260912T200113+0000

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### Ratings and Alerts

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

No alerts have been found for BCALM 2.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

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.