

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org) on Apr 15, 2025

## libCSAM

RRID:SCR\_002766

Type: Tool

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### Proper Citation

libCSAM (RRID:SCR\_002766)

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### Resource Information

**URL:** <https://github.com/rcanovas/libCSAM>

**Proper Citation:** libCSAM (RRID:SCR\_002766)

**Description:** Contains several C++ codes for compress, decompress, and access each of the fields of any SAM format file.

**Resource Type:** software resource

**Defining Citation:** [PMID:24728856](https://pubmed.ncbi.nlm.nih.gov/24728856/)

**Keywords:** standalone software, c++, bio.tools

**Funding:**

**Resource Name:** libCSAM

**Resource ID:** SCR\_002766

**Alternate IDs:** OMICS\_03750, biotools:libcsam

**Alternate URLs:** <https://bio.tools/libcsam>

**Record Creation Time:** 20220129T080215+0000

**Record Last Update:** 20250410T064923+0000

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### Ratings and Alerts

No rating or validation information has been found for libCSAM.

No alerts have been found for libCSAM.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

Benoit G, et al. (2015) Reference-free compression of high throughput sequencing data with a probabilistic de Bruijn graph. BMC bioinformatics, 16, 288.