

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

Cellsnp-lite

RRID:SCR_025515

Type: Tool

Proper Citation

Cellsnp-lite (RRID:SCR_025515)

Resource Information

URL: <https://github.com/single-cell-genetics/cellsnp-lite>

Proper Citation: Cellsnp-lite (RRID:SCR_025515)

Description: Software C/C++ tool for efficient genotyping bi-allelic SNPs on single cells. You can use cellsnp-lite after read alignment to obtain the snp x cell pileup UMI or read count matrices for each alleles of given or detected SNPs.

Resource Type: software application, software resource, source code

Defining Citation: [PMID:33963851](#)

Keywords: C, C++, genotyping bi-allelic SNPs on single cells, after read alignment,

Funding: University of Hong Kong

Availability: Free, Available for download, Freely available,

Resource Name: Cellsnp-lite

Resource ID: SCR_025515

License: Apache-2.0 license

Record Creation Time: 20240720T053301+0000

Record Last Update: 20260815T042938+0000

Ratings and Alerts

No rating or validation information has been found for Cellsnp-lite.

No alerts have been found for Cellsnp-lite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

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

Jacobs BM, et al. (2025) Single-cell analysis of cerebrospinal fluid reveals common features of neuroinflammation. *Cell reports. Medicine*, 6(1), 101733.

Marot-Lassauzaie V, et al. (2024) Identifying cancer cells from calling single-nucleotide variants in scRNA-seq data. *Bioinformatics (Oxford, England)*, 40(9).

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*.