

Resource Summary Report

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

Skera

RRID:SCR_025482

Type: Tool

Proper Citation

Skera (RRID:SCR_025482)

Resource Information

URL: <https://skera.how>

Proper Citation: Skera (RRID:SCR_025482)

Description: Software Pacbio analysis tool. Deconcat PacBio reads.

Resource Type: data processing software, software application, data analysis software, software resource, source code

Keywords: Deconcat PacBio reads, PacBio, PacBio reads, Pacbio analysis,

Availability: Free, Available for download, Freely available,

Resource Name: Skera

Resource ID: SCR_025482

Alternate URLs: <https://github.com/PacificBiosciences/skera?tab=readme-ov-file>

License: BSD-3-Clause-Clear license

Record Creation Time: 20240716T053232+0000

Record Last Update: 20260815T042901+0000

Ratings and Alerts

No rating or validation information has been found for Skera.

No alerts have been found for Skera.

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](#) .

Sison SL, et al. (2026) Single-cell and isoform-specific translational profiling of the mouse brain. *Nature*, 652(8111), 965.

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

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*.

Wedemeyer MA, et al. (2024) Defining the transcriptome of PIK3CA-altered cells in a human capillary malformation using single cell long-read sequencing. *Scientific reports*, 14(1), 25440.