

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

[atacr](#)

RRID:SCR_016286

Type: Tool

Proper Citation

atacr (RRID:SCR_016286)

Resource Information

URL: <https://github.com/TeamMacLean/atacr>

Proper Citation: atacr (RRID:SCR_016286)

Description: Software that analyzes count data from RNA-capture-seq and ATAC-capture-seq experiments. Using BioConductor RangedSummarizedExperiment objects, atacr implements a set of helper functions and quality control plots specific to the analysis of counts of reads in windows across genomes.

Resource Type: software resource, software application, data processing software

Keywords: normalization, bootstrap, bayes, factor, test, reference, design, seq, count, capture, data

Funding: Gatsby Charitable Foundation ;
Marie Curie 656243

Availability: Free, Available for download, Tutorial available

Resource Name: atacr

Resource ID: SCR_016286

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260804T043641+0000

Ratings and Alerts

No rating or validation information has been found for atacr.

No alerts have been found for atacr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Luo L, et al. (2022) Bibliometric review of ATAC-Seq and its application in gene expression. Briefings in bioinformatics, 23(3).

Shrestha RK, et al. (2018) A workflow for simplified analysis of ATAC-cap-seq data in R. GigaScience, 7(7).