

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 7, 2026

Atac

RRID:SCR_015980

Type: Tool

Proper Citation

Atac (RRID:SCR_015980)

Resource Information

URL: <http://kmer.sourceforge.net>

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Description: Alignment analysis software tool for comparative mapping between two genome assemblies or between two different genomes. It can cache intermediate results to speed a comparisons of multiple sequences.

Resource Type: sequence analysis software, software resource, image analysis software, alignment software, data analysis software, data processing software, software application

Defining Citation: [DOI:10.1093/bioinformatics/btr285](https://doi.org/10.1093/bioinformatics/btr285)

Keywords: software, tool, DNA, sequence, analysis, aligning, genome, compare, mapping, assembly, bio.tools

Availability: Free, Freely available, Available for download

Resource Name: Atac

Resource ID: SCR_015980

Alternate IDs: OMICS_29044, biotools:atac

Alternate URLs: <https://bio.tools/atac>, <https://sources.debian.org/src/atac/>

License: GNU General Public License version 2.0 (GPLv2)

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260807T042846+0000

Ratings and Alerts

No rating or validation information has been found for Atac.

No alerts have been found for Atac.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1826 mentions in open access literature.

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

Norouzi M, et al. (2026) DNA-PKcs promotes therapy resistance and metastatic recurrence in neuroblastoma. Cancer letters, 646, 218383.

Guo X, et al. (2026) VDLIN: A Deep Learning-Based Platform for Methylcobalamin-Inspired Immunomodulatory Compound Screening. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(7), e13775.

Hou Y, et al. (2026) The ChickenGTEx portal: a pan-tissue catalogue of regulatory variants shaping transcriptomic and phenotypic diversity. Nucleic acids research, 54(D1), D982.

Zhu L, et al. (2026) Temporal Transcriptional Regulation of Human Neuronal Differentiation via Forward Programming. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(6), e10641.

Santos M, et al. (2026) Comprehensive Mapping of Functional Enhancers in Chinese Hamster Ovary Cells. Biotechnology and bioengineering, 123(1), 196.

Weir K, et al. (2026) Heterochronic transcription factor expression drives cone-dominant retina development in 13-lined ground squirrels. eLife, 14.

Maziak N, et al. (2026) Three-dimensional genome reorganization foreshadows zygotic genome activation in Drosophila. Nature genetics, 58(3), 607.

Xu Z, et al. (2026) Mapping convergent regulators of melanoma drug resistance by PerturbFate. Nature, 654(8117), 261.

Zheng X, et al. (2026) In vivo multiomic Perturb-seq with enhanced nuclear gRNA capture. bioRxiv : the preprint server for biology.

Meng J, et al. (2026) Single-cell spatial map of cis-regulatory elements for disease-related genes in the macaque cortex. Nature communications, 17(1).

Du Z, et al. (2026) SMART: spatial multi-omic aggregation using graph neural networks and metric learning. Nature communications, 17(1).

- Malagoli G, et al. (2026) Geometry-aware graph attention networks to explain single-cell chromatin states and gene expression with SEAGALL. *Genome biology*, 27(1).
- Wang Z, et al. (2026) YAP-TEAD regulates the super-enhancer network to control early surface ectoderm commitment. *Nucleic acids research*, 54(1).
- Luo E, et al. (2026) A multi-modal diffusion model with dual-cross-attention for multi-omics data generation and translation. *Nature communications*, 17(1).
- Montero-Tena JA, et al. (2026) Machine learning and multi-omic analysis reveal contrasting recombination landscape of A and C subgenomes of winter oilseed rape. *The plant genome*, 19(1), e70209.
- Weissman S, et al. (2026) HIV-1 transcription dominates over host gene activity at the HIV-1 integration site. *mBio*, 17(1), e0275525.
- Karpova A, et al. (2026) Cellular senescence in human liver under normal aging and cancer. *Cell genomics*, 6(2), 101133.
- Brown TA, et al. (2026) Oxidized LDL Induces Pro-Inflammatory Transcriptomic and Epigenomic Responses in Human CD4+ T Cells. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 40(4), e71571.
- Gibson-Khademi A, et al. (2026) Developing a comprehensive database and search tool for single-cell ATAC-seq data. *Scientific reports*, 16(1), 2201.
- Deng C, et al. (2026) Bridging unpaired single-cell multimodal data for integrative analyses with SuperMap. *Proceedings of the National Academy of Sciences of the United States of America*, 123(6), e2505182123.