

Resource Summary Report

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

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: 20260821T194031+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 [dkNET](#).

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.