Atac
RRID:SCR_015980
Type: Tool

Proper Citation
Atac (RRID:SCR_015980)

Resource Information

**URL:** [http://kmer.sourceforge.net](http://kmer.sourceforge.net)

**Proper Citation:** Atac (RRID:SCR_015980)

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

**Defining Citation:** DOI: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/

**Record Creation Time:** 20220129T080328+0000

**Record Last Update:** 20240702T054042+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 962 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Helminen L, et al. (2024) Chromatin accessibility and pioneer factor FOXA1 restrict glucocorticoid receptor action in prostate cancer. Nucleic acids research, 52(2), 625.


