**Atac**

RRID:SCR_015980  
Type: Tool

**Proper Citation**

Atac (RRID:SCR_015980)

**Resource Information**

**URL:** http://kmer.sourceforge.net

**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 comparison of multiple sequences.

**Resource Name:** Atac

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

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

**Keywords:** software, tool, DNA, sequence, analysis, aligning, genome, compare, mapping, assembly

**Resource ID:** SCR_015980

**Availability:** Free, Freely available, Available for download

**Website Status:** Last checked up

**Mentions Count:** 167

**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 167 mentions in open access literature.

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


Korchynska S, et al. (2020) Life-long impairment of glucose homeostasis upon prenatal exposure to psychostimulants. The EMBO journal, 39(1), e100882.


Weiterer SS, et al. (2020) Distinct IL-1?-responsive enhancers promote acute and coordinated changes in chromatin topology in a hierarchical manner. The EMBO journal, 39(1), e101533.


den Broeder MJ, et al. (2020) Inhibition of methyltransferase activity of enhancer of zeste 2 leads to enhanced lipid accumulation and altered chromatin status in zebrafish. Epigenetics & chromatin, 13(1), 5.


