

Resource Summary Report

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ATACseqMappingPipeline

RRID:SCR_017558

Type: Tool

Proper Citation

ATACseqMappingPipeline (RRID:SCR_017558)

Resource Information

URL: <https://github.com/lufuhao/ATACseqMappingPipeline>

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Description: Software tool as pipeline to map ATAC-seq data to large genome, for example, for wheat. It splits large genome files into parts and do mapping and then finally merge them.

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

Keywords: Map, ATAC-seq, data, genome, large, merge

Availability: Free, Freely available

Resource Name: ATACseqMappingPipeline

Resource ID: SCR_017558

License: GNU General Public License v3.0

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260905T133053+0000

Ratings and Alerts

No rating or validation information has been found for ATACseqMappingPipeline.

No alerts have been found for ATACseqMappingPipeline.

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 [NIF](#) .

Wang X, et al. (2022) Mapping open chromatin by ATAC-seq in bread wheat. *Frontiers in plant science*, 13, 1074873.

Lu FH, et al. (2020) Reduced chromatin accessibility underlies gene expression differences in homologous chromosome arms of diploid *Aegilops tauschii* and hexaploid wheat. *GigaScience*, 9(6).