MACS
RRID:SCR_013291
Type: Tool

Proper Citation

MACS (RRID:SCR_013291)

Resource Information

URL: https://github.com/macs3-project/MACS

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Description: Software Python package for identifying transcript factor binding sites. Used to evaluate significance of enriched ChIP regions. Improves spatial resolution of binding sites through combining information of both sequencing tag position and orientation. Can be used for ChIP-Seq data alone, or with control sample with increase of specificity.

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

References: PMID:18798982

Keywords: identify, transcript, factor, binding, site, model, based, analysis, CHIP Seq, short, read, sequencer, protein, DNA, bio.tools

Parent Organization: Dana-Farber Cancer Institute

Funding Agency: NHGRI, NIDDK

Availability: Free, Available for download, Freely available

Website Status: Last checked up

Abbreviations: MACS

Resource Name: MACS
Resource ID: SCR_013291

Alternate IDs: OMICS_00446, OMICS_00446, biotools:macs

Alternate URLs: https://bio.tools/macs

Ratings and Alerts

No rating or validation information has been found for MACS.

No alerts have been found for MACS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 558 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](https://fdi-scicrunch.org).


Sze CC, et al. (2020) Coordinated regulation of cellular identity-associated H3K4me3 breadth by the COMPASS family. Science advances, 6(26), eaaz4764.


