**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.

**Abbreviations:** MACS

**Synonyms:** MACS - Model-based Analysis for ChIP-Seq, Model-based Analysis for ChIP-Seq, MACS2

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

**Defining Citation:** PMID:18798982, DOI:10.1186/gb-2008-9-9-r137

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

**Funding Agency:** NHGRI, NHGRI, NIDDK

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

**Resource Name:** MACS

**Resource ID:** SCR_013291
Alternate IDs: OMICS_00446, biotools:macs


Record Creation Time: 20220129T080315+0000

Record Last Update: 20240616T053722+0000

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 1083 mentions in open access literature.

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


Zheng R, et al. (2024) Remodeling of the endothelial cell transcriptional program via paracrine and DNA-binding activities of MPO. iScience, 27(2), 108898.


Zhao H, et al. (2024) Pluripotency state transition of embryonic stem cells requires the turnover of histone chaperone FACT on chromatin. iScience, 27(1), 108537.


