**MACS**

**RRID:** SCR_013291  
**Type:** Tool

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**Proper Citation**

MACS (RRID:SCR_013291)

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**Resource Information**

**URL:** [http://liulab.dfci.harvard.edu/MACS/](http://liulab.dfci.harvard.edu/MACS/)

**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 Name:** MACS

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

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

**Resource ID:** SCR_013291

**Parent Organization:** Dana-Farber Cancer Institute

**Funding Agency:** NHGRI, NIDDK

**References:** PMID:18798982

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

**Website Status:** Last checked up
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 455 mentions in open access literature.

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


Kentepozidou E, et al. (2020) Clustered CTCF binding is an evolutionary mechanism to maintain topologically associating domains. Genome biology, 21(1), 5.


