MACS

RRID:SCR_013291
Type: Tool

Proper Citation

MACS (RRID:SCR_013291)

Resource Information

URL: 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.

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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
Alternate IDs: OMICS_00446

Abbreviations: MACS

Mentions Count: 455

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.


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


