

Resource Summary Report

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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: NHGRI HG004069;
NHGRI HG004270;
NIDDK DK074967

Availability: Free, Available for download, Freely available

Resource Name: MACS

Resource ID: SCR_013291

Alternate IDs: OMICS_00446, biotools:macs

Alternate URLs: <https://bio.tools/macs>, <https://sources.debian.org/src/macs/>

License: Artistic License

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260729T044312+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 1325 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Nakamura M, et al. (2026) Chromatin-associated DEK proteins maintain H3K27me3 balance and coordinate developmental transitions in plants. *The New phytologist*, 249(2), 930.

Santos M, et al. (2026) Comprehensive Mapping of Functional Enhancers in Chinese Hamster Ovary Cells. *Biotechnology and bioengineering*, 123(1), 196.

Patel UA, et al. (2026) CRISPR Screen Identifies HDAC3 as a Novel Radiosensitizing Target in Small Cell Lung Cancer. *Molecular cancer therapeutics*, 25(1), 183.

Xu Y, et al. (2026) From degraded to deciphered: Applying ATAC-seq to forensic molecular diagnosis under degradation conditions. *Forensic science international*, 379, 112789.

Pereira-Martins DA, et al. (2026) ?Np73 isoform defines a TP53-mutant-like poor-risk subgroup of acute myeloid leukemia. *Cell reports. Medicine*, 102540.

Zhang Q, et al. (2025) Exploration of the mechanism of 5-Methylcytosine promoting the progression of hepatocellular carcinoma. *Translational oncology*, 52, 102257.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. *medRxiv : the preprint server for health sciences*.

Funasaki S, et al. (2025) Protocol for transcriptomic and epigenomic analyses of tip-like endothelial cells using scRNA-seq and ChIP-seq. *STAR protocols*, 6(1), 103326.

Villano DJ, et al. (2025) Widespread 3D genome reorganization precedes programmed DNA rearrangement in *Oxytricha trifallax*. *bioRxiv : the preprint server for biology*.

Bian L, et al. (2025) Single-cell eQTL mapping reveals cell-type-specific genes associated with the risk of gastric cancer. *Cell genomics*, 5(4), 100812.

Citu C, et al. (2025) Identification and catalog of viral transcriptional regulators in human diseases. *iScience*, 28(3), 112081.

Bafna A, et al. (2025) Zinc finger homeobox-3 (ZFHX3) orchestrates genome-wide daily gene expression in the suprachiasmatic nucleus. *eLife*, 14.

Liu J, et al. (2025) lncRNA-ZFAS1, an Emerging Gate-Keeper in DNA Damage-Dependent Transcriptional Regulation. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(31), e12385.

Zibetti C, et al. (2025) Molecular Determinants of the Human Retinal Pigment Epithelium Cell Fate and Potential Pharmacogenomic Targets for Precision Medicine. *International journal of molecular sciences*, 26(12).

Yao S, et al. (2025) Xist RNA binds select autosomal genes and depends on Repeat B to regulate their expression. *eLife*, 13.

Robert MG, et al. (2025) Uncovering biomarkers for chronic toxoplasmosis detection highlights alternative pathways shaping parasite dormancy. *EMBO molecular medicine*, 17(7), 1686.

Kim HB, et al. (2025) Estrogen Receptor Enhancers Sensitive to Low Doses of Hormone Specify Distinct Molecular and Biological Outcomes. *bioRxiv : the preprint server for biology*.

Engelhorn J, et al. (2025) Genetic variation at transcription factor binding sites largely explains phenotypic heritability in maize. *Nature genetics*, 57(9), 2313.

Lee S, et al. (2025) Combining Multiplexed CRISPR/Cas9-Nickase and PARP Inhibitors Efficiently and Precisely Targets Cancer Cells. *Cancer research*, 85(15), 2890.

Garzón-Partida AP, et al. (2025) Development of a Cohesive Predictive Model for Substance Use Disorder Rehabilitation Using Passive Digital Biomarkers, Psychological Assessments, and Automated Facial Emotion Recognition: Protocol for a Prospective Cohort Study. *JMIR research protocols*, 14, e71374.