

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org) on Mar 28, 2025

## MACS

RRID:SCR\_013291

Type: Tool

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### Proper Citation

MACS (RRID:SCR\_013291)

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### Resource Information

**URL:** <https://github.com/macs3-project/MACS>

**Proper Citation:** MACS (RRID:SCR\_013291)

**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 resource, software application, data processing software, data analysis software

**Defining Citation:** [PMID:18798982](https://pubmed.ncbi.nlm.nih.gov/18798982/), [DOI:10.1186/gb-2008-9-9-r137](https://doi.org/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:** 20250328T060801+0000

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## Ratings and Alerts

No rating or validation information has been found for MACS.

No alerts have been found for MACS.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1184 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

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.

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

Han H, et al. (2025) NSUN5 Facilitates Hepatocellular Carcinoma Progression by Increasing SMAD3 Expression. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2404083.

Wang N, et al. (2025) Loss of Kmt2c or Kmt2d primes urothelium for tumorigenesis and redistributes KMT2A-menin to bivalent promoters. Nature genetics, 57(1), 165.

Guo C, et al. (2025) LEDGF/p75 promotes transcriptional pausing through preventing SPT5 phosphorylation. *Science advances*, 11(3), eadr2131.

Ahn M, et al. (2025) Beta cell-specific PAK1 enrichment ameliorates diet-induced glucose intolerance in mice by promoting insulin biogenesis and minimising beta cell apoptosis. *Diabetologia*, 68(1), 152.

Carlson NA, et al. (2025) A Comprehensive Assessment of the Marginal Abatement Costs of CO<sub>2</sub> of Co-Optima Multi-Mode Vehicles. *Energy & fuels : an American Chemical Society journal*, 39(1), 444.

Zhang T, et al. (2025) An epigenetic pathway regulates MHC-II expression and function in B cell lymphoma models. *The Journal of clinical investigation*, 135(2).

Adlakha A, et al. (2025) Interferon-gamma rescues dendritic cell calcineurin-dependent responses to *Aspergillus fumigatus* via Stat3 to Stat1 switching. *iScience*, 28(2), 111535.

Magnitov MD, et al. (2025) ZNF143 is a transcriptional regulator of nuclear-encoded mitochondrial genes that acts independently of looping and CTCF. *Molecular cell*, 85(1), 24.

Chen PB, et al. (2024) Complementation testing identifies genes mediating effects at quantitative trait loci underlying fear-related behavior. *Cell genomics*, 4(5), 100545.

Raffalli MC, et al. (2024) Population-specific responses to pollution exposure suggest local adaptation of invasive red swamp crayfish *Procambarus clarkii* along the Mediterranean French coastline. *Environmental science and pollution research international*, 31(29), 42314.

Gawriyski L, et al. (2024) Interaction network of human early embryonic transcription factors. *EMBO reports*, 25(3), 1589.

Bassani S, et al. (2024) Variant-specific pathophysiological mechanisms of AFF3 differently influence transcriptome profiles. *medRxiv : the preprint server for health sciences*.

Kuehn HS, et al. (2024) Disease-associated AIOLOS variants lead to immune deficiency/dysregulation by haploinsufficiency and redefine AIOLOS functional domains. *The Journal of clinical investigation*, 134(3).

Tay T, et al. (2024) Degradation of IKZF1 prevents epigenetic progression of T cell exhaustion in an antigen-specific assay. *Cell reports. Medicine*, 5(11), 101804.

Loi P, et al. (2024) Epigenetic and Oncogenic Inhibitors Cooperatively Drive Differentiation and Kill KRAS-Mutant Colorectal Cancers. *Cancer discovery*, 14(12), 2430.

Cheng S, et al. (2024) Review and Evaluate the Bioinformatics Analysis Strategies of ATAC-seq and CUT&Tag Data. *Genomics, proteomics & bioinformatics*, 22(3).

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