

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: data analysis software, data processing software, software application, software resource

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: 20260821T194007+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 1418 mentions in open access literature.

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

Lee HK, et al. (2026) STAT3 SH2 Domain Aspartic Acid 661 Mutations Activate Immune Gene Programs. Journal of cellular and molecular medicine, 30(1), e71015.

Li L, et al. (2026) Targeting G3BP1 Condensate Topology Promotes Stress Granule Assembly via m6A-IGF2BP1 for Ischemic Stroke Rescue. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(6), e14703.

Zhang H, et al. (2026) Allelic variation at a single locus distinguishes spring and winter faba beans. Nature genetics, 58(3), 655.

Zhou HQ, et al. (2026) Dynamic regulation of mRNA acetylation at synapses by spatial memory in mouse hippocampus. eLife, 14.

Tulloch AJ, et al. (2026) Massively parallel reporter assay for mapping gene-specific regulatory regions at single-nucleotide resolution. eLife, 14.

Obaji D, et al. (2026) TFIIIC regulates SMC complex binding and 3D DNA contacts between tRNA genes. bioRxiv : the preprint server for biology.

Reed KSM, et al. (2026) Genome reorganization and its functional impact during breast cancer progression. eLife, 14.

Malgulwar PB, et al. (2026) ATRX inactivation disrupts global chromatin state and topology to dysregulate neurodevelopmental pathways in glioma pathogenesis. Nucleic acids research, 54(12).

Kusumoto-Matsuo R, et al. (2026) Genome instability is increased during DNA replication in the presence of the CPD UV photoproduct in transcriptionally active genes. *iScience*, 29(7), 116322.

Thienger P, et al. (2026) A Double-Negative Prostate Cancer Subtype Is Vulnerable to SWI/SNF-Targeting Degradable Molecules. *Cancer research*, 86(7), 1570.

Selvam K, et al. (2026) Recruitment of BRD4 to the ASXL1 genomic targets depends on the extra-terminal domain of BRD4. *Nature communications*, 17(1).

Bergo V, et al. (2026) Lack of MDA5 delays hematopoietic aging by modulating inflammaging and proteostasis in mice. *Nature communications*, 17(1), 1645.

Hossain M, et al. (2026) ChromAcS: an automated and flexible GUI for end-to-end reproducible ATAC-seq analysis across multiple species. *BMC bioinformatics*, 27(1).

Aggrey-Fynn JE, et al. (2026) Epigenetic context defines the transcriptional activity of canonical and noncanonical NF- κ B signaling in pancreatic cancer. *Cell death discovery*, 12(1).

Citron F, et al. (2026) DPY30 Is an Epigenetic Decoupler Linking Replication Stress to Immunoediting in Pancreatic Cancer. *Cancer research*, 86(12), 2837.

Eyvazi S, et al. (2026) CLOCK is an Epigenetic Integrator of Circadian Rhythm and T Cell Immunity. *Research square*.

Fang X, et al. (2026) Protocol for identifying cell-type-specific genes associated with disease risk using single-cell eQTL data. *STAR protocols*, 7(2), 104545.

Haidar M, et al. (2026) Defining epitranscriptomic hallmarks at the host-parasite interface and their roles in virulence and disease progression in *Theileria annulata*-infected leukocytes. *Biomedical journal*, 49(1), 100828.

López-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. *Cancer discovery*, 16(2), 296.

Miyatake Y, et al. (2026) A single microRNA miR-195 rescues the arrested B cell development induced by EBF1 deficiency. *eLife*, 13.