

Resource Summary Report

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Deeptools

RRID:SCR_016366

Type: Tool

Proper Citation

Deeptools (RRID:SCR_016366)

Resource Information

URL: <https://deeptools.readthedocs.io/en/develop/>

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Description: Python based tools to process, visualize and analyse high-throughput sequencing data, such as ChIP-seq, RNA-seq or MNase-seq. Implemented within Galaxy framework. Used to perform complete bioinformatic workflows ranging from quality controls and normalizations of aligned reads to integrative analyses, including clustering and visualization approaches.

Resource Type: data processing software, data analysis software, software resource, software application, data visualization software, software toolkit

Defining Citation: [PMID:27079975](#)

Keywords: process, visualize, analysis, sequencing, data, ChIP-seq, RNA-seq, MNase-seq, quality, control, normalization, aligned, read, clustering, bioinformatic

Funding: German Research Foundation SFB 992;
German Epigenome Programme DEEP 01KU1216G

Availability: Free, Available for download, Freely available

Resource Name: Deeptools

Resource ID: SCR_016366

Alternate URLs: <http://deeptools.ie-freiburg.mpg.de/>

License: Public

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260805T044352+0000

Ratings and Alerts

No rating or validation information has been found for Deeptools.

No alerts have been found for Deeptools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2418 mentions in open access literature.

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

Mauksch C, et al. (2026) FACT depletion demonstrates a role for nucleosome organization in TAD formation. *Molecular systems biology*, 22(1), 119.

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

Sankar V, et al. (2026) Genetic elements promote retention of extrachromosomal DNA in cancer cells. *Nature*, 649(8095), 152.

Mao L, et al. (2026) Super-enhancer-driven core transcription factor FOXP1 delays endothelial cell senescence via phase separation-mediated SESN3 activation. *Theranostics*, 16(3), 1386.

Lu P, et al. (2026) Bromodomain-containing protein 4 knockdown promotes neuronal ferroptosis in a mouse model of subarachnoid hemorrhage. *Neural regeneration research*, 21(2), 715.

Arai M, et al. (2026) Oral antigen exposure under costimulation blockade induces Treg cells to establish immune tolerance. *The Journal of experimental medicine*, 223(3).

De Luca DG, et al. (2026) Phylogenomic analysis and genetic mechanisms of antifungal resistance in clinical isolates of *Candida glabrata* (*Nakaseomyces glabratus*) from across Canada, 2013-2020. *Microbiology spectrum*, 14(1), e0180325.

Wang Z, et al. (2026) Multidimensional mapping of stimulation-responsive regulatory elements and candidate causal variants in T cell activation. *Science advances*, 12(1), eady2539.

Li JJ, et al. (2026) NSD2 targeting reverses plasticity and drug resistance in prostate cancer. *Nature*, 649(8095), 216.

Zhang G, et al. (2026) Spatial Reorganization of Chromatin Architecture Shapes the Expression Phenotype of Therapy-Induced Senescent Cells. *Aging cell*, 25(1), e70366.

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.

De Bolòs A, et al. (2025) The SOX11:SMARCA4 complex is a driver of oncogenic transcriptional programs in mantle cell lymphoma. *Blood cancer journal*, 15(1), 127.

Yao Y, et al. (2025) Akkermansia muciniphila-Derived N-Acetylspermidine Modulates the Localization of Intestinal α 1,2-Fucosylated Proteins to Maintain Gut Homeostasis. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(38), e06576.

Uranishi K, et al. (2025) MGA directly recruits SETDB1/ATF7IP for histone H3K9me3 mark on meiosis-related genes in mouse embryonic stem cells. *iScience*, 28(8), 113059.

Xiang D, et al. (2025) HLF transactivates TFEB to promote gallbladder cancer stem cells' self-renewal and determines tumor response to distinct therapies. *Science advances*, 11(32), eadv6723.

Xue L, et al. (2025) A Novel Nuclear Protein Complex Controlling the Expression of Developmentally Regulated Genes in *Toxoplasma Gondii*. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(7), e2412000.

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.

Wang C, et al. (2025) Viral oncogene EBNA1P regulates YY1 DNA binding and alters host 3D genome organization. *EMBO reports*, 26(3), 810.

Zhang S, et al. (2025) Dynamics and regulatory roles of RNA m6A methylation in unbalanced genomes. *eLife*, 13.