

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 analysis software, software application, software toolkit, software resource, data processing software, data visualization software

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: 20260812T044317+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 2806 mentions in open access literature.

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

Kumari B, et al. (2026) Single-cell exon deletion profiling reveals splicing events that shape gene expression and cell state dynamics. Nature communications, 17(1), 1218.

Torras-Llort M, et al. (2026) Phosphorylation of Barrier-to-Autointegration Factor (BAF) regulates anchoring of centromeric heterochromatin to the nuclear envelope (NE). Nucleic acids research, 54(3).

Shukla V, et al. (2026) Chromatin state architecture governs transcription factor accessibility across plant genomes. PLoS genetics, 22(1), e1012015.

Xiong Y, et al. (2026) Molecular and Chromatin Accessibility Programs Underlying Epithelial Injury and Impaired Regeneration in Neonatal Necrotizing Enterocolitis. Cellular and molecular gastroenterology and hepatology, 20(6), 101730.

Kong X, et al. (2026) OTX2 inhibits human pluripotent stem cell reprogramming toward 8-cell-like and morula-like states. Nature communications, 17(1), 1685.

Fang X, et al. (2026) The Disordered Region of ASXL1 Acts as an Auto-Regulator Through Condensation. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(17), e10999.

Li Y, et al. (2026) 3D epigenome architecture orchestrates cis and trans regulation of flowering time in rice. Genome biology, 27(1).

Tahiri G, et al. (2026) Coordinated gene family evolution shapes the genome of dimorphic Mucorales. Nature communications, 17(1).

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

Guo X, et al. (2026) VDLIN: A Deep Learning-Based Platform for Methylcobalamin-Inspired Immunomodulatory Compound Screening. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(7), e13775.

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

Yue Y, et al. (2026) ADA2 Forms Nuclear Condensates with GCN5 and ATP-Citrate Lyase (ACL) to Modulate H3K9 Acetylation at Genes Functioning in Rice Meristems. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(5), e13169.

Williams CAC, et al. (2026) SOX2 phosphorylation during mitosis limits genomic damage. *Genes & development*, 40(3-4), 185.

Tan K, et al. (2026) Near-complete genome assembly of a transformation-efficient elite inbred line LH244 and its comparison with B73. *Journal of integrative plant biology*, 68(2), 366.

Manivannan M, et al. (2026) Activated glucocorticoid receptor is an estrogen receptor silencer in ER+ metastatic breast cancer. *EMBO molecular medicine*, 18(1), 151.

Karlsson O, et al. (2026) Loss of SETDB1-mediated H3K9me3 in human neural progenitor cells leads to transcriptional activation of L1 retrotransposons. *Nucleic acids research*, 54(4).

Weir K, et al. (2026) Heterochronic transcription factor expression drives cone-dominant retina development in 13-lined ground squirrels. *eLife*, 14.

Holub E, et al. (2026) Effects of thymidylate synthase inhibitors differ in genomic uracilation and mutagenic potential. *Life science alliance*, 9(4).

Gorin A, et al. (2026) IFN γ -induced memory in human macrophages is sustained by the durability of cytokine signaling itself. *The Journal of experimental medicine*, 223(4).

Haase MAB, et al. (2026) Ancient co-option of LTR retrotransposons as yeast centromeres. *Nature*, 651(8107), 1004.