Resource Summary Report

Generated by NIF on Apr 22, 2025

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: software resource, data analysis software, data processing software, software toolkit, software application, 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: 20250422T055928+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 1881 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

Bastola S, et al. (2025) Endothelial-secreted Endocan activates PDGFRA and regulates vascularity and spatial phenotype in glioblastoma. Nature communications, 16(1), 471.

Cigrang M, et al. (2025) Pan-inhibition of super-enhancer-driven oncogenic transcription by next-generation synthetic ecteinascidins yields potent anti-cancer activity. Nature communications, 16(1), 512.

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

Aoi Y, et al. (2025) SPT5 regulates RNA polymerase II stability via Cullin 3-ARMC5 recognition. Science advances, 11(4), eadt5885.

Gur ER, et al. (2025) scATAC-seq generates more accurate and complete regulatory maps than bulk ATAC-seq. Scientific reports, 15(1), 3665.

Wang H, et al. (2025) BcWRKY25-BcWRKY33A-BcLRP1/BcCOW1 module promotes root development for improved salt tolerance in Bok choy. Horticulture research, 12(1), uhae280.

Chen L, et al. (2025) The DNA demethylase TET1 modifies the impact of maternal folic acid status on embryonic brain development. EMBO reports, 26(1), 175.

Zhang J, et al. (2025) Histone methyltransferases MLL2 and SETD1A/B play distinct roles in H3K4me3 deposition during the transition from totipotency to pluripotency. The EMBO journal, 44(2), 437.

Lechon T, et al. (2025) Regulation of meristem and hormone function revealed through analysis of directly-regulated SHOOT MERISTEMLESS target genes. Scientific reports, 15(1), 240.

Sasaki M, et al. (2025) Efficacy of CBP/p300 Dual Inhibitors against Derepression of KREMEN2 in cBAF-Deficient Cancers. Cancer research communications, 5(1), 24.

Jiang D, et al. (2025) Cytosine Methylation Changes the Preferred Cis-Regulatory Configuration of Arabidopsis WUSCHEL-Related Homeobox 14. International journal of molecular sciences, 26(2).

Zhao M, et al. (2025) Genetic variation in IL-4 activated tissue resident macrophages determines strain-specific synergistic responses to LPS epigenetically. Nature communications, 16(1), 1030.

Xiao R, et al. (2025) Deciphering Transcription in Cryptosporidium parvum: Polycistronic Gene Expression and Chromatin Accessibility. bioRxiv : the preprint server for biology.

Mestre-Fos S, et al. (2025) eIF3 engages with 3'-UTR termini of highly translated mRNAs. eLife, 13.

Bai C, et al. (2025) Multiomics analyses of the effects of LED white light on the ripening of apricot fruits. Journal of advanced research, 67, 1.

Hu ZC, et al. (2025) Evolution of a SHOOTMERISTEMLESS transcription factor binding site promotes fruit shape determination. Nature plants, 11(1), 23.

Naddaf E, et al. (2025) NLRP3 Inflammasome Activation and Altered Mitophagy Are Key Pathways in Inclusion Body Myositis. Journal of cachexia, sarcopenia and muscle, 16(1), e13672.

Lee J, et al. (2025) A chromosome-level genome assembly of wild silkmoth, Bombyx mandarina. Scientific data, 12(1), 27.

Duan S, et al. (2025) H3K56 acetylation regulates chromatin maturation following DNA replication. Nature communications, 16(1), 134.