

Resource Summary Report

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ChIPseeker

RRID:SCR_021322

Type: Tool

Proper Citation

ChIPseeker (RRID:SCR_021322)

Resource Information

URL: <https://bioconductor.org/packages/ChIPseeker/>

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Description: Software package to retrieve nearest genes around peak, annotate genomic region of peak, implements statistical methods for estimate significance of overlap among ChIP peak data sets, and incorporate GEO database for user to compare own dataset with those deposited in database. Several visualization functions are implemented to summarize coverage of peak experiment, average profile and heatmap of peaks binding to TSS regions, genomic annotation, distance to TSS, and overlap of peaks or genes.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:25765347](#)

Keywords: Retrieve nearest genes around peak, annotate genomic region of peak, overlap estimate significance, ChIP peak data sets

Availability: Free, Available for download, Freely available

Resource Name: ChIPseeker

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Ratings and Alerts

No rating or validation information has been found for ChIPseeker.

No alerts have been found for ChIPseeker.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 155 mentions in open access literature.

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

Xu H, et al. (2024) PP2A complex disruptor SET prompts widespread hypertranscription of growth-essential genes in the pancreatic cancer cells. *Science advances*, 10(4), eadk6633.

Huang Y, et al. (2024) Inhibition of CD38 enzymatic activity enhances CAR-T cell immune-therapeutic efficacy by repressing glycolytic metabolism. *Cell reports. Medicine*, 5(2), 101400.

Ho PJ, et al. (2024) Multi-omics integration identifies cell-state-specific repression by PBRM1-PIAS1 cooperation. *Cell genomics*, 4(1), 100471.

Hosseini M, et al. (2024) Metformin reduces the clonal fitness of Dnmt3aR878H hematopoietic stem and progenitor cells by reversing their aberrant metabolic and epigenetic state. *Research square*.

Zhang F, et al. (2024) Genetic and bioinformatic analyses reveal transcriptional networks underlying dual genomic coordination of mitochondrial biogenesis. *bioRxiv : the preprint server for biology*.

Hollin T, et al. (2024) Proteome-Wide Identification of RNA-dependent proteins and an emerging role for RNAs in *Plasmodium falciparum* protein complexes. *Nature communications*, 15(1), 1365.

Booms A, et al. (2024) Parkinson's disease risk enhancers in microglia. *iScience*, 27(2), 108921.

Chang J, et al. (2024) The dynamic landscape of chromatin accessibility and active regulatory elements in the mediobasal hypothalamus influences the seasonal activation of the reproductive axis in the male quail under long light exposure. *BMC genomics*, 25(1), 197.

Gaballa A, et al. (2024) PAF1c links S-phase progression to immune evasion and MYC function in pancreatic carcinoma. *Nature communications*, 15(1), 1446.

Carrick BH, et al. (2024) PUF partner interactions at a conserved interface shape the RNA-binding landscape and cell fate in *Caenorhabditis elegans*. *Developmental cell*, 59(5), 661.

Takahashi F, et al. (2024) Development of sexual dimorphism of skeletal muscles through the adrenal cortex, caused by androgen-induced global gene suppression. *Cell reports*, 43(2), 113715.

Hosseinzadeh L, et al. (2024) The androgen receptor interacts with GATA3 to transcriptionally regulate a luminal epithelial cell phenotype in breast cancer. *Genome biology*, 25(1), 44.

Li M, et al. (2024) From degraded to deciphered: ATAC-seq's application potential in forensic diagnosis. *International journal of legal medicine*.

Issa H, et al. (2023) Nanoparticle-mediated targeting of the fusion gene RUNX1/ETO in t(8;21)-positive acute myeloid leukaemia. *Leukemia*, 37(4), 820.

Zhao Y, et al. (2023) m6A mRNA Methylation Analysis Provides Novel Insights into Pigmentation in Sheep Skin. *Epigenetics*, 18(1), 2230662.

Arratia F, et al. (2023) Selective Concurrence of the Long Non-Coding RNA MALAT1 and the Polycomb Repressive Complex 2 to Promoter Regions of Active Genes in MCF7 Breast Cancer Cells. *Current issues in molecular biology*, 45(6), 4735.

Hendrickson PG, et al. (2023) Expression of the CIC-DUX4 fusion oncoprotein mimics human CIC-rearranged sarcoma in genetically engineered mouse models. *Research square*.

Craig AJ, et al. (2023) Genome-wide profiling of transcription factor activity in primary liver cancer using single-cell ATAC sequencing. *Cell reports*, 42(11), 113446.

Zhao Z, et al. (2023) An integrative single-cell multi-omics profiling of human pancreatic islets identifies T1D associated genes and regulatory signals. *Research square*.

Truong BT, et al. (2023) PRDM1 DNA-binding zinc finger domain is required for normal limb development and is disrupted in split hand/foot malformation. *Disease models & mechanisms*, 16(4).