Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 27, 2025

ChIPpeakAnno

RRID:SCR_012828
Type: Tool

Proper Citation

ChIPpeakAnno (RRID:SCR_012828)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/ChIPpeakAnno.html

Proper Citation: ChIPpeakAnno (RRID:SCR_012828)

Description: Software package that includes functions to retrieve the sequences around the peak, obtain enriched Gene Ontology terms, find the nearest gene, exon, miRNA or custom features such as most conserved elements.

Abbreviations: ChIPpeakAnno

Resource Type: software resource

Funding:

Resource Name: ChIPpeakAnno

Resource ID: SCR_012828

Alternate IDs: OMICS_00804

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250420T014620+0000

Ratings and Alerts

No rating or validation information has been found for ChIPpeakAnno.

No alerts have been found for ChIPpeakAnno.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 396 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

King SE, et al. (2025) Prenatal maternal stress in rats alters the epigenetic and transcriptomic landscape of the maternal-fetal interface across four generations. Communications biology, 8(1), 38.

Klein L, et al. (2025) Spatial tumor immune heterogeneity facilitates subtype co-existence and therapy response in pancreatic cancer. Nature communications, 16(1), 335.

Zhao Y, et al. (2025) VISTA-induced tumor suppression by a four amino acid intracellular motif. bioRxiv : the preprint server for biology.

Malaymar Pinar D, et al. (2025) Nuclear Factor I Family Members are Key Transcription Factors Regulating Gene Expression. Molecular & cellular proteomics : MCP, 24(1), 100890.

De Felice D, et al. (2025) Rar?-Foxa1 signaling promotes luminal identity in prostate progenitors and is disrupted in prostate cancer. EMBO reports, 26(2), 443.

Zhang N, et al. (2025) Deciphering the molecular logic of WOX5 function in the root stem cell organizer. The EMBO journal, 44(1), 281.

Nshanian M, et al. (2025) Short-chain fatty acid metabolites propionate and butyrate are unique epigenetic regulatory elements linking diet, metabolism and gene expression. Nature metabolism, 7(1), 196.

Uckelmann M, et al. (2024) Dynamic PRC1-CBX8 stabilizes a porous structure of chromatin condensates. bioRxiv : the preprint server for biology.

Nshanian M, et al. (2024) Short-chain fatty acids propionate and butyrate control growth and differentiation linked to cellular metabolism. Research square.

Mancheno-Ferris A, et al. (2024) Crosstalk between chromatin and Shavenbaby defines transcriptional output along the Drosophila intestinal stem cell lineage. iScience, 27(1), 108624.

Yamanaka T, et al. (2024) The transcription factor NF-YA is crucial for neural progenitor maintenance during brain development. The Journal of biological chemistry, 300(2), 105629.

Hu S, et al. (2024) A continuum of zinc finger transcription factor retention on native chromatin underlies dynamic genome organization. Molecular systems biology, 20(7), 799.

Migale R, et al. (2024) FOXL2 interaction with different binding partners regulates the dynamics of ovarian development. Science advances, 10(12), eadl0788.

Cui Y, et al. (2024) Epigenetic regulation of H3K27me3 in laying hens with fatty liver hemorrhagic syndrome induced by high-energy and low-protein diets. BMC genomics, 25(1), 374.

Jalan M, et al. (2024) RAD52 resolves transcription-replication conflicts to mitigate R-loop induced genome instability. Nature communications, 15(1), 7776.

Yang T, et al. (2024) PWOs repress gene transcription by regulating chromatin structures in Arabidopsis. Nucleic acids research, 52(21), 12918.

Du K, et al. (2024) The chromatin remodeling factor OsINO80 promotes H3K27me3 and H3K9me2 deposition and maintains TE silencing in rice. Nature communications, 15(1), 10919.

Ban GI, et al. (2024) The COMPASS complex maintains the metastatic capacity imparted by a subpopulation of cells in UPS. iScience, 27(7), 110187.

Santini L, et al. (2024) FoxO transcription factors actuate the formative pluripotency specific gene expression programme. Nature communications, 15(1), 7879.

Smolko AE, et al. (2024) A MOZ-TIF2 leukemia mouse model displays KAT6-dependent H3K23 propionylation and overexpression of a set of active developmental genes. Proceedings of the National Academy of Sciences of the United States of America, 121(26), e2405905121.