

Resource Summary Report

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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

Resource Name: ChIPpeakAnno

Resource ID: SCR_012828

Alternate IDs: OMICS_00804

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260725T190741+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 448 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Nitsch S, et al. (2026) H4K16 acylations destabilize chromatin architecture and facilitate transcriptional response during metabolic perturbations. *Molecular cell*, 86(1), 24.

Trendel J, et al. (2025) The human proteome with direct physical access to DNA. *Cell*, 188(16), 4424.

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

Luan Y, et al. (2025) Insufficient gene expression and lost gene regulatory network may underlie the mechanism of Hirschsprung Disease in 5p-syndrome. *Heliyon*, 11(3), e42079.

Tobias IC, et al. (2025) A Sox2 enhancer cluster regulates region-specific neural fates from mouse embryonic stem cells. *G3 (Bethesda, Md.)*, 15(4).

Wang H, et al. (2025) MYC Binding Near Transcriptional End Sites Regulates Basal Gene Expression, Read-Through Transcription, and Intragenic Contacts. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(31), e14601.

Lyu W, et al. (2025) Enalapril mitigates senescence and aging-related phenotypes in human cells and mice via pSmad1/5/9-driven antioxidative genes. *eLife*, 14.

Lu RJ, et al. (2025) Aging murine peritoneal macrophages undergo female-specific remodeling driven by hormone-dependent and independent mechanisms. *bioRxiv : the preprint server for biology*.

Floros KV, et al. (2025) Targeting SUMOylation promotes cBAF complex stabilization and disruption of the SS18::SSX transcriptome in synovial sarcoma. *Nature communications*, 16(1), 9761.

Yoshido A, et al. (2025) DOT1L inhibition exerts the anti-tumor effect by activating interferon signaling in breast cancer cells. *Clinical epigenetics*, 17(1), 201.

Zhao Y, et al. (2025) A Four Amino Acid Intracellular Motif of VISTA Blocks Growth Receptor Signaling in Cancer Cells to Induce Tumor Suppression. *Cancer research*, 85(18), 3399.

Gallardo A, et al. (2025) BMAL1-TRIM28 represses transposable elements independently of CLOCK in pluripotent cells. *Nature communications*, 16(1), 8250.

Guo N, et al. (2025) EZH2 variants derived from cryptic splice sites govern distinct epigenetic patterns during embryonic development. *Nucleic acids research*, 53(17).

Leismann J, et al. (2025) DNA methylation at retrotransposons protects the germline by preventing NRF1-mediated activation. *EMBO reports*, 26(17), 4312.

Zhao J, et al. (2025) Brain 5-hydroxymethylcytosine alterations are associated with Alzheimer's disease neuropathology. *Nature communications*, 16(1), 2842.

Otsuka K, et al. (2025) KRAB zinc-finger proteins regulate endogenous retroviruses to sculpt germline transcriptomes and genome evolution. *Genome research*, 35(3), 417.

Wang Y, et al. (2025) Mutation of SMARCA4 Induces Cancer Cell-Intrinsic Defects in the Enhancer Landscape and Resistance to Immunotherapy. *Cancer research*, 85(11), 1997.

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.

Liu Y, et al. (2025) Identification of HES4 as a novel prognostic marker and therapeutic target in hepatocellular carcinoma. *Discover oncology*, 16(1), 156.

Ferreira MA, et al. (2025) The immune NIK1/RPL10/LIMYB signaling module regulates photosynthesis and translation under biotic and abiotic stresses. *Nature communications*, 16(1), 4433.