Resource Summary Report

Generated by RRID on Apr 8, 2025

FindPeaks

RRID:SCR_010857
Type: Tool

Proper Citation

FindPeaks (RRID:SCR_010857)

Resource Information

URL: http://sourceforge.net/apps/mediawiki/vancouvershortr/index.php?title=FindPeaks

Proper Citation: FindPeaks (RRID:SCR_010857)

Description: Software application that can be used for converting Eland, Maq (.map), BED or other files into WIG files and identifying areas of enrichment (ChIP-Seq analysis).

Abbreviations: FindPeaks

Resource Type: software resource

Keywords: chip-seq

Funding: BC Cancer Agency ;
Michael Smith Foundation for Health Research

Resource Name: FindPeaks

Resource ID: SCR_010857

Alternate IDs: OMICS_00440

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250214T183139+0000

Ratings and Alerts

No rating or validation information has been found for FindPeaks.

No alerts have been found for FindPeaks.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 297 mentions in open access literature.

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

Zhou Z, et al. (2025) GnRH pulse generator activity in mouse models of polycystic ovary syndrome. eLife, 13.

Boubou Y, et al. (2025) Rural-urban transformation shapes oasis agriculture in Morocco's High Atlas Mountains. Scientific reports, 15(1), 3433.

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.

Han SY, et al. (2025) Multi-dimensional oscillatory activity of mouse GnRH neurons in vivo. eLife, 13.

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

Pindwarawala M, et al. (2025) Defective glycosylation and ELFN1 binding of mGluR6 congenital stationary night blindness mutants. Life science alliance, 8(3).

Nguyen CDK, et al. (2024) PRMT1 promotes epigenetic reprogramming associated with acquired chemoresistance in pancreatic cancer. Cell reports, 43(5), 114176.

Chandrasekaran V, et al. (2024) Bivalent chromatin accommodates survivin and BRG1/SWI complex to activate DNA damage response in CD4+ cells. Cell communication and signaling : CCS, 22(1), 440.

Liu B, et al. (2024) Nuclear respiratory factor 1 regulates super enhancer-controlled SPIDR to protect hepatocellular carcinoma cells from oxidative stress. BMC gastroenterology, 24(1), 97.

Vitarelli MdO, et al. (2024) Integrating high-throughput analysis to create an atlas of replication origins in Trypanosoma cruzi in the context of genome structure and variability. mBio, 15(4), e0031924.

Chan JD, et al. (2024) FOXO1 enhances CAR T cell stemness, metabolic fitness and

efficacy. Nature, 629(8010), 201.

Chapeau EA, et al. (2024) Direct and selective pharmacological disruption of the YAP-TEAD interface by IAG933 inhibits Hippo-dependent and RAS-MAPK-altered cancers. Nature cancer, 5(7), 1102.

Cipriano A, et al. (2024) Transcriptional and epigenetic characterization of a new in vitro platform to model the formation of human pharyngeal endoderm. Genome biology, 25(1), 211.

Lee HK, et al. (2024) STAT5B leukemic mutations, altering SH2 tyrosine 665, have opposing impacts on immune gene programs. bioRxiv : the preprint server for biology.

Parolia A, et al. (2024) NSD2 is a requisite subunit of the AR/FOXA1 neo-enhanceosome in promoting prostate tumorigenesis. bioRxiv : the preprint server for biology.

Helminen L, et al. (2024) Chromatin accessibility and pioneer factor FOXA1 restrict glucocorticoid receptor action in prostate cancer. Nucleic acids research, 52(2), 625.

Cheng S, et al. (2024) Review and Evaluate the Bioinformatics Analysis Strategies of ATAC-seq and CUT&Tag Data. Genomics, proteomics & bioinformatics, 22(3).

Povoleri GAM, et al. (2024) Identification of a transcription factor network regulating anti-TNF mediated IL10 expression in human CD4+ T cells. Discovery immunology, 3(1), kyae013.

Zhang Y, et al. (2024) MSC-derived mitochondria promote axonal regeneration via Atf3 gene up-regulation by ROS induced DNA double strand breaks at transcription initiation region. Cell communication and signaling : CCS, 22(1), 240.

Tremblay BJM, et al. (2024) Interplay between coding and non-coding regulation drives the Arabidopsis seed-to-seedling transition. Nature communications, 15(1), 1724.