

Resource Summary Report

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BigWig and BigBed

RRID:SCR_007708

Type: Tool

Proper Citation

BigWig and BigBed (RRID:SCR_007708)

Resource Information

URL: http://hgdownload.cse.ucsc.edu/admin/exe/linux.x86_64/

Proper Citation: BigWig and BigBed (RRID:SCR_007708)

Description: Allow the high-performance display of next-generation sequencing experiment results in the UCSC Genome Browser.

Abbreviations: BigWig and BigBed

Resource Type: software resource

Resource Name: BigWig and BigBed

Resource ID: SCR_007708

Alternate IDs: OMICS_00626

Ratings and Alerts

No rating or validation information has been found for BigWig and BigBed.

No alerts have been found for BigWig and BigBed.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](https://www.fdi-lab.org/).

Cao K, et al. (2023) Integrated workflow for discovery of microprotein-coding small open reading frames. STAR protocols, 4(4), 102649.

Mau C, et al. (2023) How enhancers regulate wavelike gene expression patterns. eLife, 12.

Hu M, et al. (2022) Long non-coding RNA SNHG3 promotes prostate cancer progression by sponging microRNA-1827. Oncology letters, 24(2), 281.

Zou H, et al. (2022) Nuclear receptor ROR γ inverse agonists/antagonists display tissue- and gene-context selectivity through distinct activities in altering chromatin accessibility and master regulator SREBP2 occupancy. Pharmacological research, 182, 106324.

Almeida A, et al. (2022) Urinary extracellular vesicles contain mature transcriptome enriched in circular and long noncoding RNAs with functional significance in prostate cancer. Journal of extracellular vesicles, 11(5), e12210.

Richart L, et al. (2022) XIST loss impairs mammary stem cell differentiation and increases tumorigenicity through Mediator hyperactivation. Cell, 185(12), 2164.

Liu HY, et al. (2021) Dietary Conjugated Linoleic Acid Modulates the Hepatic Circadian Clock Program via PPAR γ /REV-ERB α -Mediated Chromatin Modification in Mice. Frontiers in nutrition, 8, 711398.

Detroja R, et al. (2021) ChiTaH: a fast and accurate tool for identifying known human chimeric sequences from high-throughput sequencing data. NAR genomics and bioinformatics, 3(4), lqab112.

Ishino K, et al. (2021) Hamster PIWI proteins bind to piRNAs with stage-specific size variations during oocyte maturation. Nucleic acids research, 49(5), 2700.

Costello KR, et al. (2021) Sequence features of retrotransposons allow for epigenetic variability. eLife, 10.

Williams J, et al. (2021) MethylationToActivity: a deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. Genome biology, 22(1), 24.

Golisz A, et al. (2021) Arabidopsis Spliceosome Factor SmD3 Modulates Immunity to Pseudomonas syringae Infection. Frontiers in plant science, 12, 765003.

Moretto F, et al. (2021) Transcription levels of a noncoding RNA orchestrate opposing regulatory and cell fate outcomes in yeast. Cell reports, 34(3), 108643.

Baunach M, et al. (2021) The Landscape of Recombination Events That Create

Nonribosomal Peptide Diversity. *Molecular biology and evolution*, 38(5), 2116.

Kotsantis P, et al. (2020) RTEL1 Regulates G4/R-Loops to Avert Replication-Transcription Collisions. *Cell reports*, 33(12), 108546.

Mutte SK, et al. (2020) High-resolution and Deep Phylogenetic Reconstruction of Ancestral States from Large Transcriptomic Data Sets. *Bio-protocol*, 10(6), e3566.

Gao T, et al. (2020) EnhancerAtlas 2.0: an updated resource with enhancer annotation in 586 tissue/cell types across nine species. *Nucleic acids research*, 48(D1), D58.

Rodger EJ, et al. (2019) Characterisation of DNA methylation changes in EBF3 and TBC1D16 associated with tumour progression and metastasis in multiple cancer types. *Clinical epigenetics*, 11(1), 114.

Cai D, et al. (2019) ROR γ is a targetable master regulator of cholesterol biosynthesis in a cancer subtype. *Nature communications*, 10(1), 4621.

Pegueroles C, et al. (2019) Transcriptomic analyses reveal groups of co-expressed, syntenic lncRNAs in four species of the genus *Caenorhabditis*. *RNA biology*, 16(3), 320.