

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

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

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260801T190340+0000

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 32 mentions in open access literature.

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

Han AL, et al. (2025) Estradiol (E2) concentration shapes the chromatin binding landscape of estrogen receptor alpha. *The Journal of biological chemistry*, 301(7), 108499.

Huang C, et al. (2025) A comparative genomic analysis at the chromosomal-level reveals evolutionary patterns of aphid chromosomes. *Communications biology*, 8(1), 427.

O'Dwyer MR, et al. (2025) Nucleosome fibre topology guides transcription factor binding to enhancers. *Nature*, 638(8049), 251.

López A, et al. (2025) Evaluating restriction enzyme selection for reduced representation sequencing in conservation genomics. *Molecular ecology resources*, 25(5), e13865.

Jia Z, et al. (2025) Protocol to perform assay for chromatin-bound condensates by exploratory sequencing in mouse embryonic stem cells. *STAR protocols*, 6(3), 104067.

Cummins M, et al. (2024) The Evolution of Ultraconserved Elements in Vertebrates. *Molecular biology and evolution*, 41(7).

Stutzman AV, et al. (2024) Heterochromatic 3D genome organization is directed by HP1a- and H3K9-dependent and independent mechanisms. *Molecular cell*, 84(11), 2017.

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.

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.

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.

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.

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.

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.

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.

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.

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