

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

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260919T195132+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 43 mentions in open access literature.

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

Thienger P, et al. (2026) A Double-Negative Prostate Cancer Subtype Is Vulnerable to SWI/SNF-Targeting Degradable Molecules. *Cancer research*, 86(7), 1570.

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. *Nature methods*, 23(5), 946.

Hehl M, et al. (2026) Exonuclease ISG20 inhibits human cytomegalovirus replication by inducing an innate immune defense signature. *PLoS pathogens*, 22(1), e1013856.

Rodriguez-Carballo E, et al. (2026) OCT4 enhances the firing efficiency of late DNA replication origins in mouse embryonic stem cells. *Nature communications*, 17(1), 1686.

Roginski P, et al. (2026) Impact of GC content on de novo gene birth. *Nature communications*, 17(1), 1268.

Friske JD, et al. (2026) A Conserved Enhancer Locus in Extrachromosomal DNA and Homogeneously Staining Regions Activates MYC Transcription in Group 3 Medulloblastoma. *Cancer research*, 86(13), 3160.

Yang Y, et al. (2026) Targeting Wnt/ β -catenin and circadian regulator restores PRC2/EZH2-controlled chromatin bivalency and suppresses cell state diversity. *The Journal of clinical investigation*, 136(9).

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.

Lu Y, et al. (2025) Functional Genetic Screens Reveal Key Pathways Instructing the Molecular Phenotypes of Tumor-Associated Macrophages. *Cancer immunology research*, 13(12), 2054.

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.

Zou H, et al. (2023) Natural compounds ursolic acid and digoxin exhibit inhibitory activities to cancer cells in ROR γ -dependent and -independent manner. Frontiers in pharmacology, 14, 1146741.

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

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.

Krzyszton M, et al. (2022) Analysis of mRNA-derived siRNAs in mutants of mRNA maturation and surveillance pathways in *Arabidopsis thaliana*. Scientific reports, 12(1), 1474.