

Resource Summary Report

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[rtracklayer](#)

RRID:SCR_021325

Type: Tool

Proper Citation

rtracklayer (RRID:SCR_021325)

Resource Information

URL: <https://bioconductor.org/packages/rtracklayer/>

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Description: Software R package for interfacing with genome browsers. Supports integration of existing genome browsers with experimental data analyses performed in R. R interface to genome annotation files and UCSC genome browser.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:19468054](#)

Keywords: Existing genome browsers integration, genome annotation files interface, interfacing with genome browsers

Funding: NHGRI P41 HG004059

Availability: Free, Available for download, Freely available

Resource Name: rtracklayer

Resource ID: SCR_021325

Alternate URLs: <https://github.com/lawremi/rtracklayer>

License URLs: <https://github.com/lawremi/rtracklayer/blob/master/LICENSE>

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260808T190522+0000

Ratings and Alerts

No rating or validation information has been found for rtracklayer.

No alerts have been found for rtracklayer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Sævarsson T, et al. (2026) Enhanced IFN γ response in dedifferentiated melanoma cells is due to chromatin remodeling as revealed by ATAC-seq. Cell communication and signaling : CCS, 24(1).

Hilgart E, et al. (2026) DNA Methylation Stochasticity Is Linked to Transcriptional Variability and Convergent Epigenetic Disruption across Genetic Subtypes of Acute Myeloid Leukemia. Cancer research, 86(13), 3325.

Ulmke PA, et al. (2026) Identification of novel genes with enriched expression in human intermediate progenitors reveals a key role for CDKN3 in cortical development. Stem cell reports, 103012.

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

Ahrend F, et al. (2025) Protocol for assembling, prioritizing, and characterizing piRNA clusters using the piRNA Cluster Builder. STAR protocols, 6(2), 103759.

Soni J, et al. (2025) Protocol for investigating intracellular microbial diversity using single-cell RNA-seq in immune cells of SARS-CoV-2-positive and recovered patients. STAR protocols, 6(1), 103546.

Bestehorn A, et al. (2025) Cytoplasmic mRNA decay controlling inflammatory gene expression is determined by pre-mRNA fate decision. Molecular cell, 85(4), 742.

Lykke-Andersen S, et al. (2024) Protocol for generating customizable and reproducible plots of sequencing coverage data using the seqNdisplayR package. STAR protocols, 5(2), 102960.

Chua EW, et al. (2024) A concise guide to essential R packages for analyses of DNA, RNA, and proteins. Molecules and cells, 47(11), 100120.

Pressl C, et al. (2024) Isolation and Molecular Profiling of Nuclei of Specific Neuronal Types from Human Cerebral Cortex and Striatum. Current protocols, 4(12), e70067.

Fait BW, et al. (2024) Spontaneously regenerative corticospinal neurons in mice. bioRxiv : the preprint server for biology.

Lehle JD, et al. (2024) An in vitro approach reveals molecular mechanisms underlying endocrine disruptor-induced epimutagenesis. eLife, 13.

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

Mandell JD, et al. (2023) Estimation of Neutral Mutation Rates and Quantification of Somatic Variant Selection Using *cancereffectsizer*. Cancer research, 83(4), 500.

de Tribolet-Hardy J, et al. (2023) Genetic features and genomic targets of human KRAB-zinc finger proteins. Genome research, 33(8), 1409.

Reynolds RH, et al. (2023) Local genetic correlations exist among neurodegenerative and neuropsychiatric diseases. NPJ Parkinson's disease, 9(1), 70.

Mohan DR, et al. (2023) β -Catenin-Driven Differentiation Is a Tissue-Specific Epigenetic Vulnerability in Adrenal Cancer. Cancer research, 83(13), 2123.

van Breugel ME, et al. (2023) Locus-specific proteome decoding reveals Fpt1 as a chromatin-associated negative regulator of RNA polymerase III assembly. Molecular cell, 83(23), 4205.

Sturgill D, et al. (2022) Protocol for base resolution mapping of ac4C using RedaC:T-seq. STAR protocols, 3(4), 101858.

Dong R, et al. (2022) svaRetro and svaNUMT: modular packages for annotating retrotransposed transcripts and nuclear integration of mitochondrial DNA in genome sequencing data. GigaByte (Hong Kong, China), 2022, gigabyte70.