Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

bsgenome

RRID:SCR_024230
Type: Tool

Proper Citation

bsgenome (RRID:SCR_024230)

Resource Information

URL: https://bioconductor.org/packages/BSgenome/

Proper Citation: bsgenome (RRID:SCR_024230)

Description: Software R package provides infrastructure shared by all the Biostrings-based genome data packages.

Resource Type: software resource, software toolkit

Keywords: infrastructure shared, Biostrings-based genome data packages,

Availability: Free, Available for download, Freely available,

Resource Name: bsgenome

Resource ID: SCR_024230

Alternate URLs: https://sources.debian.org/src/r-bioc-bsgenome/

Record Creation Time: 20230830T050216+0000

Record Last Update: 20260912T200115+0000

Ratings and Alerts

No rating or validation information has been found for bsgenome.

No alerts have been found for bsgenome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Nguyen TDT, et al. (2026) Pan-Cancer Single-Cell RNA Sequencing Analysis Refines Multi-Origin Monocyte and Macrophage Lineages. Cancer immunology research, 14(2), 350.

Huffman BM, et al. (2026) A Phase II Trial of Niraparib in Patients with Advanced Pancreatic Cancer Harboring Pathogenic Variants in ATM, BRCA1, BRCA2, PALB2, and CHEK2. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1666.

Mars JC, et al. (2025) Nuclear RNA cap-chaperones eIF4E and NCBP2 govern distinct fates for 1000s of mRNAs uncovering an unexpected regulatory point in gene expression. bioRxiv : the preprint server for biology.

Zheng Y, et al. (2025) Aberrant homeodomain-DNA cooperative dimerization underlies distinct developmental defects in two dominant CRX retinopathy models. Genome research, 35(2), 242.

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

Das G, et al. (2025) LncPTPred: predicting lncRNA-protein interaction based on crosslinking and immunoprecipitation (CLIP-Seq) data. Briefings in bioinformatics, 26(4).

Ver Heul AM, et al. (2025) RAG suppresses group 2 innate lymphoid cells. eLife, 13.

D'Ignazio L, et al. (2025) A hexamer tandem repeat RNA embedded within an SVA retrotransposon drives R-loop formation and neurodegeneration. Cell reports, 44(7), 115812.

Subramani PG, et al. (2024) Conserved role of hnRNPL in alternative splicing of epigenetic modifiers enables B cell activation. EMBO reports, 25(6), 2662.

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.

Plitt G, et al. (2024) The Genomic Landscape of Benign and Malignant Thyroid Tumors from Individuals Carrying Germline PTEN Variants Is Distinct from Sporadic Thyroid Cancers. Cancer research, 84(21), 3657.

Li J, et al. (2023) Genome instability footprint under rapamycin and hydroxyurea treatments. PLoS genetics, 19(11), e1011012.

Lu Z, et al. (2021) TSSr: an R package for comprehensive analyses of TSS sequencing data. NAR genomics and bioinformatics, 3(4), lqab108.