Resource Summary Report

Generated by ASWG on Aug 4, 2026

genomicalignments

RRID:SCR_024236
Type: Tool

Proper Citation

genomicalignments (RRID:SCR_024236)

Resource Information

URL: https://bioconductor.org/packages/release/bioc/html/GenomicAlignments.html

Proper Citation: genomicalignments (RRID:SCR_024236)

Description: Software R package provides efficient containers for storing and manipulating short genomic alignments. This includes read counting, computing the coverage, junction detection, and working with the nucleotide content of the alignments.

Resource Type: software toolkit, software resource

Keywords: containers for storing and manipulating short genomic alignments, read counting, computing coverage, junction detection, working with nucleotide content of alignments.

Availability: Free, Available for download, Freely available,

Resource Name: genomicalignments

Resource ID: SCR_024236

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

Record Creation Time: 20230830T050216+0000

Record Last Update: 20260803T040902+0000

Ratings and Alerts

No rating or validation information has been found for genomicalignments.

No alerts have been found for genomicalignments.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 132 mentions in open access literature.

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

Candela ME, et al. (2025) Cryopreserved human alternatively activated macrophages promote resolution of acetaminophen-induced liver injury in mouse. NPJ Regenerative medicine, 10(1), 5.

Sudhindar PD, et al. (2025) Urinary renal epithelial cells can be used for NPHP1 phenotyping and a personalized therapeutic strategy. Journal of cell science, 138(20).

Ingham A, et al. (2025) CRAMP1-dependent histone H1 biogenesis is essential for topoisomerase II inhibitor tolerance. Molecular cell, 85(13), 2487.

Bearzatto B, et al. (2025) Rapid, user-friendly, cost-effective DNA and library Preparation methods for whole-genome sequencing of bacteria with varying cell wall composition and GC content using minimal DNA on the illumina platform. BMC genomics, 26(1), 396.

Zobel M, et al. (2025) A human CAGinSTEM platform for decoding HTT repeats' somatic instability links CAG interruption to HD pathology in neurons. Cell reports, 44(12), 116685.

Welti J, et al. (2025) NXP800 Activates the Unfolded Protein Response, Altering AR and E2F Function to Impact Castration-Resistant Prostate Cancer Growth. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(6), 1109.

Sudhindar PD, et al. (2025) Urine-derived renal epithelial cells for deep phenotyping and transcriptomic response to therapy in Fabry disease. Clinical science (London, England : 1979), 139(14), 791.

Dauban L, et al. (2025) Interactions between the genome and the nuclear lamina are multivalent and cooperative. Nature structural & molecular biology, 32(11), 2335.

Wu S, et al. (2025) Noncoding RNA Terc-53 and hyaluronan receptor Hmmr regulate aging in mice. Protein & cell, 16(1), 28.

Bhattacharya D, et al. (2025) Neuropathy-associated Tecpr2 mutation knock-in mice reveal endolysosomal loss of function phenotypes in neurons and microglia. Cell death & disease, 16(1), 775.

Ryan CW, et al. (2025) RNF2 Missense Variants Disrupt Polycomb Repression and Enable Ectopic Mesenchymal Lineage Conversion During Human Neural Differentiation. Research square.

Miyazawa H, et al. (2025) A noncanonical role of glycolytic metabolites controlling the timing of mouse embryo segmentation. Science advances, 11(38), eadz9606.

Galicia Aguirre C, et al. (2025) Cerulenin partially corrects the disrupted developmental transcriptomic signature in Huntington's disease striatal medium spiny neurons. Stem cells (Dayton, Ohio), 43(8).

Karakulak T, et al. (2025) Heterogeneous and novel transcript expression in single cells of patient-derived clear cell renal cell carcinoma organoids. Genome research, 35(4), 698.

Bhandare P, et al. (2025) Phenotypic screens identify SCAF1 as critical activator of RNAPII elongation and global transcription. Nucleic acids research, 53(4).

Chen Y, et al. (2025) A systematic benchmark of Nanopore long-read RNA sequencing for transcript-level analysis in human cell lines. Nature methods, 22(4), 801.

Ben Aribi H, et al. (2025) Efficient and easy gene expression and genetic variation data analysis and visualization using exvar. Scientific reports, 15(1), 12264.

Malik M, et al. (2025) Histone methyltransferase DOT1L maintains cell state and restricts cytotoxic potential of CD8 T cells. Science advances, 11(50), eadw1289.

Nguyen JH, et al. (2025) Developmental pyrethroid exposure disrupts molecular pathways for MAP kinase and circadian rhythms in mouse brain. Physiological genomics, 57(4), 240.

Shi Y, et al. (2025) Piezo1 senses hyphae and initiates host defense against pathogenic fungi. Cell reports, 44(6), 115839.