

Resource Summary Report

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GenomicRanges

RRID:SCR_000025

Type: Tool

Proper Citation

GenomicRanges (RRID:SCR_000025)

Resource Information

URL: <http://www.bioconductor.org/packages/2.13/bioc/html/GenomicRanges.html>

Proper Citation: GenomicRanges (RRID:SCR_000025)

Description: Software package that defines general purpose containers for storing genomic intervals as well as more specialized containers for storing alignments against a reference genome.

Abbreviations: GenomicRanges

Synonyms: GenomicRanges - Representation and manipulation of genomic intervals

Resource Type: software resource

Keywords: genomic interval

Availability: Free, Available for download, Freely available

Resource Name: GenomicRanges

Resource ID: SCR_000025

Alternate IDs: SCR_018096, OMICS_01161

License: Artistic License, v2

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260808T185711+0000

Ratings and Alerts

No rating or validation information has been found for GenomicRanges.

No alerts have been found for GenomicRanges.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 56 mentions in open access literature.

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

Reed KSM, et al. (2026) Genome reorganization and its functional impact during breast cancer progression. *eLife*, 14.

Pradhan B, et al. (2026) Dynamic and Ongoing De Novo L1 Retrotransposition Contributes to Genome Plasticity and Intrapatient Heterogeneity in Ovarian Cancer. *Cancer research*, 86(4), 1073.

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.

Gadad SS, et al. (2026) X-linked cancer-associated polypeptide (XCP) from lncRNA1456 modulates PHF8 histone demethylase activity to regulate the epigenome, gene expression, and cellular pathways in breast cancer. *Oncogene*, 45(17), 1557.

Bassiouni R, et al. (2026) Integrated Single-Cell Whole-Genome Sequencing and Spatial Transcriptomics Reveal Intratumoral Heterogeneity in Ovarian Cancer. *Cancer research communications*, 6(5), 1020.

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).

Hu Q, et al. (2025) Circulating tumor DNA monitoring detects minimal residual disease and predicts outcomes in patients with esophageal adenocarcinoma or squamous cell carcinoma after esophagectomy. *BJC reports*, 3(1), 52.

Verrou KM, et al. (2025) Machine learning-based identification of a transcriptomic blood signature discriminating between systemic autoimmunity and infection. *Med (New York, N.Y.)*, 100840.

Zamuner FT, et al. (2025) Epigenetic profiling reveals key super-enhancer networks driving oncogenesis in HPV-positive HNSCC. *iScience*, 28(11), 113911.

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.

Gao Y, et al. (2025) Multimodal analyses reveal genes driving electrophysiological maturation of neurons in the primate prefrontal cortex. *Neuron*, 113(15), 2490.

Trendel J, et al. (2025) The human proteome with direct physical access to DNA. *Cell*, 188(16), 4424.

Köhne M, et al. (2025) *Satb1* directs the differentiation of TH17 cells through suppression of IL-2 expression. *Cell reports*, 44(7), 115866.

Li S, et al. (2025) HPV integration in head and neck cancer: downstream splicing events and expression ratios linked with poor outcomes. *Clinical cancer research : an official journal of the American Association for Cancer Research*.

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. *Cancer research communications*, 5(10), 1910.

Golov AK, et al. (2024) A genome-wide nucleosome-resolution map of promoter-centered interactions in human cells corroborates the enhancer-promoter looping model. *eLife*, 12.

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

Gustavsson EK, et al. (2024) The annotation of *GBA1* has been concealed by its protein-coding pseudogene *GBAP1*. *Science advances*, 10(26), eadk1296.

Lopes-Paciencia S, et al. (2024) A senescence restriction point acting on chromatin integrates oncogenic signals. *Cell reports*, 43(4), 114044.

Pinton A, et al. (2024) PHF6-altered T-ALL Harbor Epigenetic Repressive Switch at Bivalent Promoters and Respond to 5-Azacitidine and Venetoclax. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(1), 94.