

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: 20260815T182139+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 [NIF](#) .

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.

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

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.

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.

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

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.

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.