Resource Summary Report

Generated by kravitz2 on Sep 5, 2026

IRanges

RRID:SCR_006420
Type: Tool

Proper Citation

IRanges (RRID:SCR_006420)

Resource Information

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

Proper Citation: IRanges (RRID:SCR_006420)

Description: Software tool for computing and annotating genomic ranges.Provides efficient low-level and highly reusable S4 classes for storing ranges of integers, RLE vectors (Run-Length Encoding), and, more generally, data that can be organized sequentially (formally defined as Vector objects), as well as views on these Vector objects. Efficient list-like classes are also provided for storing big collections of instances of the basic classes. All classes in the package use consistent naming and share the same rich and consistent Vector API as much as possible.

Abbreviations: IRanges

Synonyms: Infrastructure for manipulating intervals on sequences

Resource Type: software resource

Defining Citation: PMID:23950696

Keywords: Annotating genomic ranges, computing genomic ranges, genomic ranges, storing ranges of integers, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: IRanges

Resource ID: SCR_006420

Alternate IDs: OMICS_01163, biotools:iranges

Alternate URLs: https://bio.tools/iranges

License: Artistic License, v2

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260903T234827+0000

Ratings and Alerts

No rating or validation information has been found for IRanges.

No alerts have been found for IRanges.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 88 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Garinet S, et al. (2026) Cell-free DNA epigenomic profiling enables noninvasive detection and monitoring of translocation renal cell carcinoma. The Journal of clinical investigation, 136(3).

Avila TU, et al. (2026) Repeat expansions in C9orf72 rewire the 3D chromatin landscape in ALS. bioRxiv : the preprint server for biology.

Shastry A, et al. (2026) Confidence: a web app for cross-platform differential gene expression analysis, gene scoring, and enrichment analysis. Scientific reports, 16(1).

Jordá-Llorens JI, et al. (2026) CUT homeobox factors modulate chromatin accessibility in neurons. bioRxiv : the preprint server for biology.

Adey BN, et al. (2026) Pervasive Transcription in the Human Genome Exceeds Background Noise. Genome biology and evolution, 18(5).

Ferrando A, et al. (2026) SFPQ directs histone H3.3 deposition to R-loops in DNA repeats to protect genome stability. Nature communications, 17(1).

Damgaard F, et al. (2026) Distinct prophage infections in colorectal cancer-associated Bacteroides fragilis. Communications medicine, 6(1).

Ma J, et al. (2026) Runs of homozygosity reveal population dynamics and selection across global cattle. Journal of animal science and biotechnology, 17(1).

Repele A, et al. (2026) The differentiation of myeloid progenitors is effected by cascading waves of coordinated gene expression that remodel cellular physiology in a characteristic sequence. PLoS computational biology, 22(5), e1014276.

Palma LG, et al. (2025) Chromatin activity of I?B? mediates the exit from naïve pluripotency. eLife, 14.

Griend JAV, et al. (2025) RtmR is a membrane-embedded RRM-family RNA-binding protein that regulates biofilm formation. bioRxiv : the preprint server for biology.

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

Regner MJ, et al. (2025) Defining the regulatory logic of breast cancer using single-cell epigenetic and transcriptome profiling. Cell genomics, 5(2), 100765.

Bender A, et al. (2025) UHRF2 mediates resistance to DNA methylation reprogramming in primordial germ cells. Nature communications, 16(1), 7350.

Karami-Moalem S, et al. (2025) EMS-induced genomic variation and QTL-seq analysis of safflower spininess through whole genome sequencing (WGS). BMC genomics, 27(1), 115.

Luo X, et al. (2025) RNA-RNA Interactome Approaches Provide in vivo Evidence for a Critical Role of the Hfq Rim Face in sRNA-mRNA Pairing. bioRxiv : the preprint server for biology.

Chen X, et al. (2025) Long-Read Sequencing Outperforms Short-Read Sequencing in Detecting Most Structural Variations. Serican journal of medicine, 2(2).

Lin H, et al. (2025) Modular organization of enhancer network provides transcriptional robustness in mammalian development. Nucleic acids research, 53(2).

Kasan M, et al. (2025) Genomic and phenotypic stability of fusion-driven pediatric sarcoma cell lines. Nature communications, 16(1), 380.

Yang J, et al. (2025) Machine learning-augmented m6A-Seq analysis without a reference genome. Briefings in bioinformatics, 26(3).