

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 21, 2025

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

Funding:

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: 20250420T014327+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 65 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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.

Galanti L, et al. (2024) Dbf4-dependent kinase promotes cell cycle controlled resection of DNA double-strand breaks and repair by homologous recombination. *Nature communications*, 15(1), 2890.

Weinand K, et al. (2024) The chromatin landscape of pathogenic transcriptional cell states in rheumatoid arthritis. *Nature communications*, 15(1), 4650.

Bai X, et al. (2024) Joint inference of clonal structure using single-cell genome and transcriptome sequencing data. *NAR genomics and bioinformatics*, 6(1), lqae017.

Moqri M, et al. (2024) PRC2-AgeIndex as a universal biomarker of aging and rejuvenation. *Nature communications*, 15(1), 5956.

Gourmet L, et al. (2024) Immune evasion impacts the landscape of driver genes during cancer evolution. *Genome biology*, 25(1), 168.

Madsen AL, et al. (2024) Genetic architecture of oral glucose-stimulated insulin release provides biological insights into type 2 diabetes aetiology. *Nature metabolism*, 6(10), 1897.

Keenan CR, et al. (2024) Suv39h-catalyzed H3K9me3 is critical for euchromatic genome organization and the maintenance of gene transcription. *Genome research*, 34(4), 556.

Luo J, et al. (2024) p300/CBP degradation is required to disable the active AR enhanceosome in prostate cancer. *bioRxiv : the preprint server for biology*.

Demidov G, et al. (2024) Comprehensive reanalysis for CNVs in ES data from unsolved rare disease cases results in new diagnoses. *NPJ genomic medicine*, 9(1), 49.

Terekhanova NV, et al. (2023) Epigenetic regulation during cancer transitions across 11 tumour types. *Nature*, 623(7986), 432.

Gyenis A, et al. (2023) Genome-wide RNA polymerase stalling shapes the transcriptome during aging. *Nature genetics*, 55(2), 268.

Rogala S, et al. (2023) The lncRNA Sweetheart regulates compensatory cardiac hypertrophy after myocardial injury in murine males. *Nature communications*, 14(1), 7024.

Costeira R, et al. (2023) Hemin availability induces coordinated DNA methylation and gene expression changes in *Porphyromonas gingivalis*. *mSystems*, 8(4), e0119322.

Kovatcheva M, et al. (2023) Vitamin B12 is a limiting factor for induced cellular plasticity and tissue repair. *Nature metabolism*, 5(11), 1911.

Agostinho de Sousa J, et al. (2023) Epigenetic dynamics during capacitation of naïve human pluripotent stem cells. *Science advances*, 9(39), eadg1936.

Sriden N, et al. (2022) Large-scale comparative transcriptomic analysis of temperature-responsive genes in *Arabidopsis thaliana*. *Plant molecular biology*, 110(4-5), 425.

Fava VM, et al. (2022) A systems biology approach identifies candidate drugs to reduce mortality in severely ill patients with COVID-19. *Science advances*, 8(22), eabm2510.

Sun J, et al. (2022) CircSeqAlignTk: An R package for end-to-end analysis of RNA-seq data for circular genomes. *F1000Research*, 11, 1221.