

Resource Summary Report

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IRanges

RRID:SCR_006420

Type: Tool

Proper Citation

IRanges (RRID:SCR_006420)

Resource Information

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

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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: 20260725T190619+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 77 mentions in open access literature.

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

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.

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

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

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

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

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.

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.

Ahrend F, et al. (2025) Protocol for assembling, prioritizing, and characterizing piRNA clusters using the piRNA Cluster Builder. STAR protocols, 6(2), 103759.

Lynch AT, et al. (2025) HAND1 level controls the specification of multipotent cardiac and extraembryonic progenitors from human pluripotent stem cells. The EMBO journal, 44(9),

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

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

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.

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.

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

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

Hackley RK, et al. (2024) TbsP and TrmB jointly regulate gapII to influence cell development phenotypes in the archaeon *Haloferax volcanii*. *Molecular microbiology*, 121(4), 742.

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.