

# Resource Summary Report

Generated by [NIF](#) on Aug 26, 2026

## pyranges

RRID:SCR\_024191

Type: Tool

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### Proper Citation

pyranges (RRID:SCR\_024191)

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### Resource Information

**URL:** <https://github.com/pyranges/pyranges>

**Proper Citation:** pyranges (RRID:SCR\_024191)

**Description:** Software application for efficient comparison of genomic intervals in Python.

**Resource Type:** data analysis software, data processing software, software application, software resource

**Defining Citation:** [PMID:31373614](#)

**Keywords:** comparison of genomic intervals, Python

**Availability:** Free, Available for download, Freely available,

**Resource Name:** pyranges

**Resource ID:** SCR\_024191

**Old URLs:** <https://sources.debian.org/src/python3-pyranges/>

**License:** MIT license

**Record Creation Time:** 20230824T050212+0000

**Record Last Update:** 20260821T194256+0000

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### Ratings and Alerts

No rating or validation information has been found for pyranges.

No alerts have been found for pyranges.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Feng X, et al. (2026) CRESCENT: a deep learning framework with multi-scale attention for detecting recurrent copy number alterations. Briefings in bioinformatics, 27(2).

Zigdon I, et al. (2026) Spatially resolved profiling of steroid nuclear receptors reveals a role for the disordered N-terminal domains in genome targeting and AP-1 interaction. Genome research, 36(7), 1386.

Sinitsyn S, et al. (2026) Current status of human endogenous retrovirus annotation. Briefings in bioinformatics, 27(1).

Lim CS, et al. (2025) RIBOSS detects novel translational events by combining long- and short-read transcriptome and translome profiling. Briefings in bioinformatics, 26(2).

Xu S, et al. (2024) Protocol to process crosslinking and immunoprecipitation data into annotated binding sites. STAR protocols, 5(2), 103040.

Benjamin KJM, et al. (2024) Analysis of gene expression in the postmortem brain of neurotypical Black Americans reveals contributions of genetic ancestry. Nature neuroscience, 27(6), 1064.

Chapman OS, et al. (2023) Circular extrachromosomal DNA promotes tumor heterogeneity in high-risk medulloblastoma. Nature genetics, 55(12), 2189.