

Resource Summary Report

Generated by [nidm-terms](#) on Aug 23, 2026

pyranges

RRID:SCR_024191

Type: Tool

Proper Citation

pyranges (RRID:SCR_024191)

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

Ratings and Alerts

No rating or validation information has been found for pyranges.

No alerts have been found for pyranges.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

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.