

Package: picklerick (via r-universe)

June 16, 2026

Title Fast Single-Cell Format Conversion via SCX

Version 0.1.0

Description R bindings to the SCX streaming interop engine for single-cell genomics. Converts between H5Seurat, H5AD, and SCX internal formats via a memory-bounded streaming pipeline. Inspect file metadata without loading data into memory. No Python dependency.

License GPL-3

Imports methods, Matrix, jsonlite, S4Vectors, SingleCellExperiment, SummarizedExperiment

Suggests HDF5Array, rhdf5, Seurat, testthat (>= 3.0.0)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

SystemRequirements Cargo (rustup) >= 1.70

Config/pak/sysreqs zlib1g-dev libclang-dev

Repository <https://omnibenchmark.r-universe.dev>

Date/Publication 2026-06-16 21:49:08 UTC

RemoteUrl <https://github.com/btraven00/scx>

RemoteRef main

RemoteSha 0151c2f941fd808741ff5193ab8d35726fa0098a

RemoteSubdir r/picklerick