

Package ‘muscData’

September 23, 2025

Version 1.23.0

Title Multi-sample multi-group scRNA-seq data

Description Data package containing a collection of multi-sample multi-group scRNA-seq datasets in SingleCellExperiment Bioconductor object format.

URL <https://github.com/HelenaLC/muscData>

BugReports <https://github.com/HelenaLC/muscData/issues>

License MIT + file LICENSE

Depends R (>= 3.6), ExperimentHub, SingleCellExperiment

Imports utils

Suggests BiocStyle, dplyr, DropletUtils, knitr, GEOquery, Matrix, matrixStats, methods, muscat, rmarkdown, R.utils, readxl, scater, scds, Seurat

biocViews ExperimentHub, ExperimentData, ExpressionData, GEO, Homo_sapiens_Data, ImmunoOncologyData, SingleCellData

VignetteBuilder knitr

RoxygenNote 6.1.1

git_url <https://git.bioconductor.org/packages/muscData>

git_branch devel

git_last_commit 60a7685

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-09-23

Author Helena L. Crowell [aut, cre]

Maintainer Helena L. Crowell <helena.crowell@uzh.ch>

Contents

Kang18_8vs8	2
Index	3

Kang18_8vs8

Kang18_8vs8 *dataset***Description**

- 10x droplet-based scRNA-seq PBMC data from 8 Lupus patients before and after 6h-treatment with INF-beta.
- The dataset contains 35635 features across 29065 cells, and no filtering or preprocessing has been applied.
- The original data is deposited in the Gene Expression Omnibus (GEO) under accession number GSE96583.

Usage

```
Kang18_8vs8(metadata = FALSE)
```

Arguments

metadata	logical value indicating whether ExperimentHub metadata (describing the overall dataset) should be returned only, or if the whole dataset should be loaded. Defaults to FALSE.
----------	--

Details

link to reference: <https://www.ncbi.nlm.nih.gov/pubmed/29227470>

link to raw data: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE96583>

Value

an object of class `SingleCellExperiment`.

Author(s)

Helena L. Crowell <helena.crowell@uzh.ch>

References

Kang et al. (2019). "Multiplexed droplet single-cell RNA-sequencing using natural genetic variation", *Nature Biotechnology* **36**, 89-94.

Examples

```
# load metadata only
Kang18_8vs8(metadata = TRUE)

# load SingleCellExperiment
Kang18_8vs8(metadata = FALSE)
```

Index

Kang18 (Kang18_8vs8), [2](#)
Kang18_8vs8, [2](#)