

# Package ‘muscData’

October 16, 2025

**Version** 1.22.0

**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** RELEASE\_3\_21

**git\_last\_commit** 497deeb

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-10-16

**Author** Helena L. Crowell [aut, cre]

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

## Contents

|                       |   |
|-----------------------|---|
| Kang18_8vs8 . . . . . | 2 |
| Index                 | 3 |

---

|             |                            |
|-------------|----------------------------|
| Kang18_8vs8 | Kang18_8vs8 <i>dataset</i> |
|-------------|----------------------------|

---

### 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](mailto: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](#)