

# Package ‘muscData’

July 2, 2024

**Version** 1.19.0

**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** 0662add

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**Repository** Bioconductor 3.20

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`Kang18_8vs8``Kang18_8vs8 dataset`

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### 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

<code>metadata</code>	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.
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### 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)

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### 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)
```

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