

# Package ‘TabulaMurisData’

March 2, 2022

**Type** Package

**Title** 10x And SmartSeq2 Data From The Tabula Muris Consortium

**Version** 1.12.0

**Description** Access to processed 10x (droplet) and SmartSeq2  
(on FACS-sorted cells) single-cell RNA-seq data from the Tabula Muris  
consortium (<http://tabula-muris.ds.czbiohub.org/>).

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**biocViews** SingleCellData, ExperimentData, RNASeqData

**Depends** R (>= 3.5)

**Imports** ExperimentHub, utils

**Suggests** knitr, rmarkdown, BiocStyle, SingleCellExperiment, scran,  
scater, iSEE, testthat

**VignetteBuilder** knitr

**RoxygenNote** 6.1.0

**git\_url** <https://git.bioconductor.org/packages/TabulaMurisData>

**git\_branch** RELEASE\_3\_14

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**git\_last\_commit\_date** 2021-10-26

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## R topics documented:

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TabulaMurisData

*TabulaMurisData*


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### Description

This ExperimentHub package provides access to the 10x (droplet) and SmartSeq2 (on FACS-sorted cells) single-cell RNA-seq data from the Tabula Muris Consortium (<http://tabula-muris.ds.czbiohub.org/>)

### Author(s)

Charlotte Soneson

### References

The Tabula Muris Consortium: Single-cell transcriptomics of 20 mouse organs creates a *Tabula Muris*. Nature doi:10.1038/s41586-018-0590-4 (2018).

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TabulaMurisDroplet

*Tabula Muris 10x data*


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### Description

UMI counts from the 10x (droplet) single-cell RNA-seq data collected by the Tabula Muris Consortium. The object contains counts for 23,341 genes in 70,118 cells.

### Usage

```
TabulaMurisDroplet(metadata = FALSE)
```

### Arguments

metadata      Logical, whether only metadata should be returned

### Format

SingleCellExperiment

### Value

Returns a SingleCellExperiment object.

### Author(s)

Charlotte Soneson

## References

The Tabula Muris Consortium: Single-cell transcriptomics of 20 mouse organs creates a *Tabula Muris*. Nature doi:10.1038/s41586-018-0590-4 (2018).

## Examples

```
TabulaMurisDroplet(metadata = FALSE)
```

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|                      |                                    |
|----------------------|------------------------------------|
| TabulaMurisSmartSeq2 | <i>Tabula Muris SmartSeq2 data</i> |
|----------------------|------------------------------------|

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## Description

Read counts from the SmartSeq2 (on FACS-sorted cells) single-cell RNA-seq data collected by the Tabula Muris Consortium. The object contains counts for 23,433 features (23,341 genes and 92 ERCC spike-ins) in 53,760 cells.

## Usage

```
TabulaMurisSmartSeq2(metadata = FALSE)
```

## Arguments

|          |                                                   |
|----------|---------------------------------------------------|
| metadata | Logical, whether only metadata should be returned |
|----------|---------------------------------------------------|

## Format

SingleCellExperiment

## Value

Returns a SingleCellExperiment object.

## Author(s)

Charlotte Soneson

## References

The Tabula Muris Consortium: Single-cell transcriptomics of 20 mouse organs creates a *Tabula Muris*. Nature doi:10.1038/s41586-018-0590-4 (2018).

## Examples

```
TabulaMurisSmartSeq2(metadata = FALSE)
```

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## \* **datasets**

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