

# Package ‘TabulaMurisData’

October 12, 2023

**Type** Package

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

**Version** 1.18.0

**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\_17

**git\_last\_commit** 766872b

**git\_last\_commit\_date** 2023-04-25

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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	<i>Tabula Muris 10x data</i>
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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
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**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  Tabula Muris SmartSeq2 data
```

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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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