Package 'TabulaMurisData'

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Type Package

Title 10x And SmartSeq2 Data From The Tabula Muris Consortium

Version 1.0.0

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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/).

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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

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R topics documented:

TabulaMurisData   *TabulaMurisData*

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, Stephen R. Quake, Tony Wyss-Coray, Spyros Darmanis: Single-cell transcriptomic characterization of 20 organs and tissues from individual mice creates a *Tabula Muris*. bioRxiv doi:10.1101/237446 (2017).

TabulaMurisDroplet   *Tabula Muris 10x data*

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, Stephen R. Quake, Tony Wyss-Coray, Spyros Darmanis: Single-cell transcriptomic characterization of 20 organs and tissues from individual mice creates a *Tabula Muris*. bioRxiv doi:10.1101/237446 (2017).

Examples

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

TabulaMurisSmartSeq2   *Tabula Muris SmartSeq2 data*

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, Stephen R. Quake, Tony Wyss-Coray, Spyros Darmanis: Single-cell transcriptomic characterization of 20 organs and tissues from individual mice creates a *Tabula Muris*. bioRxiv doi:10.1101/237446 (2017).

Examples

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

Index