Package ‘TabulaMurisData’

May 14, 2026

Type Package

Title 10x And SmartSeq2 Data From The Tabula Muris Consortium

Version 1.31.1

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, scrapper

VignetteBuilder knitr

Config/roxygen2/version 8.0.0

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Contents

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

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

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: 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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