

# Package ‘HCADData’

November 18, 2025

**Type** Package

**Title** Accessing The Datasets Of The Human Cell Atlas in R/Bioconductor

**Version** 1.27.0

**Description** This package allows a direct access to the dataset generated by the Human Cell Atlas project for further processing in R and Bioconductor, in the comfortable format of SingleCellExperiment objects (available in other formats here: <http://preview.data.humancellatlas.org/>).

**License** MIT + file LICENSE

**Encoding** UTF-8

**biocViews** RNASeqData, SingleCellData, ExperimentData, ExpressionData, ExperimentHub

**Depends** R (>= 3.6), SingleCellExperiment

**Imports** ExperimentHub, AnnotationHub, HDF5Array, utils

**Suggests** knitr, rmarkdown, BiocStyle, scran (>= 1.11.4), BiocSingular, scater, scuttle, Rtsne, igraph, iSEE, testthat

**URL** <https://github.com/federicomarini/HCADData>

**VignetteBuilder** knitr

**RoxygenNote** 7.3.2

**Roxygen** list(markdown = TRUE)

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

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**Author** Federico Marini [aut, cre] (ORCID:  
<<https://orcid.org/0000-0003-3252-7758>>)

**Maintainer** Federico Marini <marinif@uni-mainz.de>

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|          |                                                     |
|----------|-----------------------------------------------------|
| HCADData | <i>Download data from the HCA via ExperimentHub</i> |
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## Description

Download HDF5 (dense assay) and RDS (row and column annotations) files from the HCA via ExperimentHub, composing them together as a SingleCellExperiment object

## Usage

```
HCADData(dataset = NULL, as.sparse = TRUE)
```

## Arguments

|           |                                                                                                                                                                                                         |
|-----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dataset   | A character string: which dataset should be retrieved?                                                                                                                                                  |
| as.sparse | Logical, specifies whether the underlying HDF5 dataset should be treated as sparse or not - will be passed to the call to HDF5Array(). Defaults to TRUE, i.e. by using the DelayedArray infrastructure. |

## Details

This current release includes the following datasets:

**Census of Immune Cells - Umbilical cord blood** UMI counts from the 10x (droplet) single-cell RNA-seq data. The object contains counts for 33694 genes in 384000 cells.

**Census of Immune Cells - Bone marrow** UMI counts from the 10x (droplet) single-cell RNA-seq data. The object contains counts for 33694 genes in 378000 cells.

## Value

A SingleCellExperiment object with a HDF5Matrix in the counts assay, containing the UMI counts for each gene in each cell. Row- and column-level metadata are also provided.

## Examples

```
HCADData()
sce_cordblood <- HCADData("ica_cord_blood")
```

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HCADData-pkg*HCADData: Accessing The Datasets Of The Human Cell Atlas in R/Bioconductor*

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**Description**

HCADData is an ExperimentHub package which provides access to the single-cell RNA-seq data from the Human Cell Atlas project (<https://www.humancellatlas.org>)

**Author(s)**

Federico Marini <[marinif@uni-mainz.de](mailto:marinif@uni-mainz.de)>

**References**

If you use the data in this package, please refer to the original sources (Human Cell Atlas Data Portal, <https://preview.data.humancellatlas.org>) as well (plus the related publications, which will be listed here when they will be out), which are licensed under a Creative Commons Attribution 4.0 International License.

**See Also**

Useful links:

- <https://github.com/federicomarini/HCADData>

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