

# Package ‘TENxXeniumData’

April 24, 2025

**Version** 1.4.0

**Title** Collection of Xenium spatial data by 10X genomics

**Description** Collection of Xenium spatial transcriptomics datasets provided by 10x Genomics, formatted into the Bioconductor classes, the SpatialExperiment or SpatialFeatureExperiment (SFE), to facilitate seamless integration into various applications, including examples, demonstrations, and tutorials. The constructed data objects include gene expression profiles, per-transcript location data, centroid, segmentation boundaries (e.g., cell or nucleus boundaries), and image.

**URL** <https://github.com/mrbakhsh/TENxXeniumData>

**BugReports** <https://github.com/mrbakhsh/TENxXeniumData/issues>

**License** MIT + file LICENSE

**Encoding** UTF-8

**biocViews** ExperimentData, ExperimentHub, SpatialData

**Depends** ExperimentHub

**Imports** SpatialExperiment, SpatialFeatureExperiment, BumpyMatrix, SummarizedExperiment, utils

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown

**RoxygenNote** 7.2.3

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

**git\_branch** RELEASE\_3\_21

**git\_last\_commit** 3ac7b04

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-04-24

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### Description

Collection of Xenium spatial transcriptomics datasets from 10X Genomics, formatted into the Bioconductor classes, the `SpatialExperiment` or `SpatialFeatureExperiment` (SFE). Such Datasets can be used as examples in packages, tutorials, or for testing purposes.

### Details

The following Xenium Spatial Transcriptomics datasets by 10X Genomics are currently available:

- `spe_mouse_brain`
- `sfe_mouse_brain`
- `spe_human_pancreas`
- `sfe_human_pancreas`

### Value

a `SpatialExperiment` or a `SpatialFeatureExperiment` data objects.

### Author(s)

Matineh Rahmatbakhsh

### Examples

```
# initialize hub instance
eh <- ExperimentHub()

# query for TENxXenium datasets
(q <- query(eh, "TENxXenium"))
```

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