

# Package ‘TENxXeniumData’

November 26, 2024

**Version** 1.2.0

**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>

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TENxXeniumData

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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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