

# Package ‘tenXplore’

November 22, 2024

**Title** ontological exploration of scRNA-seq of 1.3 million mouse neurons from 10x genomics

**Description**

Perform ontological exploration of scRNA-seq of 1.3 million mouse neurons from 10x genomics.

**Version** 1.29.0

**Author** Vince Carey

**Suggests** org.Hs.eg.db, testthat, knitr, rmarkdown, BiocStyle

**Depends** R (>= 4.0), shiny

**Imports** methods, ontoProc (>= 0.99.7), SummarizedExperiment, AnnotationDbi, matrixStats, org.Mm.eg.db, stats, utils, BiocFileCache

**Maintainer** VJ Carey <stvjc@channing.harvard.edu>

**License** Artistic-2.0

**LazyLoad** yes

**biocViews** ImmunoOncology, DimensionReduction, PrincipalComponent, Transcriptomics, SingleCell

**VignetteBuilder** knitr

**RoxygenNote** 7.3.2

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

**git\_branch** devel

**git\_last\_commit** 4caaa52

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-11-21

## Contents

CellTypes	2
se1.3M	2
tenx500	3
tenXplore	3

**Index****4**

---

CellTypes *cellTypes: data.frame with ids and terms*

---

**Description**

cellTypes: data.frame with ids and terms

**Usage**

```
CellTypes
```

**Format**

TermSet instance

**Source**

efo.owl, August 2017, subclasses of [http://www.ebi.ac.uk/efo/EFO\\_0000324](http://www.ebi.ac.uk/efo/EFO_0000324)

**Examples**

```
data(CellTypes)
head(slot(CellTypes, "cleanFrame"))
```

---

se1.3M *add/retrieve HSDS-based SE to/from cache*

---

**Description**

add/retrieve HSDS-based SE to/from cache

**Usage**

```
se1.3M(cache = BiocFileCache::BiocFileCache())
```

**Arguments**

cache *BiocFileCache-like cache*

---

tenx500	<i>tenx500: serialized full SummarizedExperiment for demonstration</i>
---------	--

---

**Description**

tenx500: serialized full SummarizedExperiment for demonstration

**Usage**

```
tenx500
```

**Format**

SummarizedExperiment instance

**Source**

restfulSE se1.3M pared down to 500 samples, assay materialized and assigned

**Examples**

```
data(tenx500)
tenx500
```

---

tenXplore	<i>basic shiny interface to 10x data with ontological setup for cell selection</i>
-----------	--

---

**Description**

basic shiny interface to 10x data with ontological setup for cell selection

**Usage**

```
tenXplore()
```

**Value**

shiny app invocation

**Note**

Starts slowly as it sets up connection to HDF Server.

**Examples**

```
tenXplore
```

# Index

\* **datasets**

CellTypes, [2](#)

tenx500, [3](#)

CellTypes, [2](#)

se1.3M, [2](#)

tenx500, [3](#)

tenXplore, [3](#)