

# Package: tenXplore (via r-universe)

November 18, 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

**Config/pak/sysreqs** libglpk-dev make libicu-dev libpng-dev libxml2-dev libssl-dev python3 zlib1g-dev

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/tenXplore>

**RemoteRef** HEAD

**RemoteSha** 4caaa52fa50429d940137bde033e21965e33b84

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

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**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"))
```

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

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**Description**

add/retrieve HSDS-based SE to/from cache

**Usage**

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

**Arguments**

cache *BiocFileCache-like cache*

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tenx500	<i>tenx500: serialized full SummarizedExperiment for demonstration</i>
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**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
```

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

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