

# Package ‘tenXplore’

October 16, 2018

**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** 1.2.0

**Author** Vince Carey

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

**Depends** R (>= 3.4), shiny, restfulSE (>= 0.99.12)

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

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**License** Artistic-2.0

**LazyLoad** yes

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

**VignetteBuilder** knitr

**RoxygenNote** 6.0.1.9000

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

**git\_branch** RELEASE\_3\_7

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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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tenx500

*tenx500: serialized full SummarizedExperiment for demonstration*

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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(remouse)
```

**Arguments**

remouse            optional SummarizedExperiment instance, assay data in memory

**Value**

shiny app invocation

**Examples**

```
tenXplore
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