

# Package ‘tenXplore’

April 16, 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** 1.24.0

**Author** Vince Carey

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

**Depends** R (>= 4.0), shiny, restfulSE (>= 0.99.12)

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

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

**License** Artistic-2.0

**LazyLoad** yes

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

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

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

**git\_branch** RELEASE\_3\_18

**git\_last\_commit** 9c4165a

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.18

**Date/Publication** 2024-04-15

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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()
```

**Value**

shiny app invocation

**Note**

Starts slowly as it sets up connection to HDF Server.

**Examples**

```
tenXplore
```

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