

# Package ‘SCSBrainCellTypeCollection’

February 12, 2016

**Type** Package

**Title** anRichment-type collection of brain cell type-specific gene sets

**Version** 1.00

**Depends** anRichment

**Suggests** org.Hs.eg.db

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**Author** Peter Langfelder (R code); T. Grant Belgard (gene lists); Verge Genomics team

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**Description** This package contains gene sets with genes highly expressed in broad cell types as determined in single-cell sequencing by Zeisel et al., Science (2015).

**License** GPL-3

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SCSBrainCellTypeCollection

*Returns a collection containing gene sets of marker genes of broad brain cell types.*

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## Description

Returns a collection containing gene sets of marker genes of broad brain cell types. The gene sets were compiled from single cell sequencing data in mouse brains.

## Usage

```
SCSBrainCellTypeCollection(  
  organism = "human",  
  useHomology = TRUE,  
  addOldOrganismToSetNames = FALSE,  
  namePattern = ".convertedFrom.%o",  
  addOldOrganismToSetDescriptions = FALSE,  
  descriptionPattern = "(Converted from %o.)")
```

**Arguments**

organism	Character string specifying the organism. Can be common name (such as "human"), scientific name ("Homo sapiens"), or scientific shorthand ("Hs"). To see all recognized organisms, use function <a href="#">organismLabels</a> . If NULL or NA, gene sets in the collection will retain their original content and organism (in this case mouse).
useHomology	logical: should genes in non-human organisms be matched by homology information (where available)? If this is FALSE or the homology information is not available, genes will be matched by name.
addOldOrganismToSetNames	Logical: should an indication of the old organism be appended to the set name? This may be useful to indicate that the gene sets was originally constructed for a different organism and its content may not accurately reflect the new organism.
namePattern	Character string giving the pattern that is to be added to the set name. The characters "%o" will be substituted by the actual organism name.
addOldOrganismToSetDescriptions	Logical: should an indication of the old organism be appended to the set description?
descriptionPattern	Character string giving the pattern that is to be added to the set description. The characters "%o" will be substituted by the actual organism name.

**Details**

SCSBrainCellType gene sets were downloaded on December 14, 2015 and correspond to version 5.0.

**Value**

Collection of marker genes of broad brain cell types.

**Author(s)**

Code by Peter Langfelder, gene sets compiled by T. Grant Belgard from data published by Zeisel et al., Cell types in the mouse cortex and hippocampus revealed by single-cell RNA-seq, Science 19 Feb 2015 DOI: 10.1126/science.aaa1934.

**Examples**

```
## Not run:
collection = SCSBrainCellTypeCollection(organism = "mouse");
knownGroups(collection)

## End(Not run)
```

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