

# Package ‘LRcellTypeMarkers’

December 7, 2023

**Type** Package

**Title** Marker gene information for LRcell R Bioconductor package

**Version** 1.10.0

**Date** 2020-02-25

**BugReports** <https://github.com/marvinquiet/LRcellTypeMarkers/issues>

**GitURL** <https://github.com/marvinquiet/LRcellTypeMarkers>

**Description** This is an external ExperimentData package for LRcell. This data package contains the gene enrichment scores calculated from scRNA-seq dataset which indicates the gene enrichment of each cell type in certain brain region. LRcell package is used to identify specific sub-cell types that drives the changes observed in a bulk RNA-seq differential gene expression experiment. For more details, please visit: <https://github.com/marvinquiet/LRcell>.

**License** MIT + file LICENSE

**Encoding** UTF-8

**biocViews** ExperimentData, ExperimentHub, RNASeqData, SingleCellData, ExpressionData, PackageTypeData

**Depends** R (>= 4.1)

**Imports** ExperimentHub

**Suggests** LRcell, BiocStyle, knitr, rmarkdown, roxygen2, testthat

**VignetteBuilder** knitr

**RoxygenNote** 7.1.1

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

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

**git\_last\_commit** cede01c

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**Repository** Bioconductor 3.18

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### Description

This is an external ExperimentData package for LRcell. This data package contains the gene enrichment scores calculated from scRNA-seq dataset which indicates the gene enrichment of each cell type in certain brain region. LRcell package is used to identify specific sub-cell types that drives the changes observed in a bulk RNA-seq differential gene expression experiment. For more details, please visit: <https://github.com/marvinquiet/LRcell>.

### Details

See the vignette for examples of extracting and using these data.

`browseVignettes("LRcellTypeMarkers")`

Details of how these data were created are in the scripts/ directory of the source package.

The current release includes the following datasets:

**Mouse Whole Brain Marker Genes** Gene enrichment scores calculated from Mouse Adult Whole Brain scRNA-seq dataset. The dataset contains 15,976 common genes among 9 brain regions. According to original cell type annotation, we computed the gene enrichment scores for each brain region. The 9 brain regions are: Frontal Cortex (EH4548), Cerebellum (EH4549), Entopeduncular (EH4550), Globus Pallidus (EH4551), Posterior Cortex (EH4552), Striatum (EH4553), Substantia Nigra (EH4554), Thalamus (EH4555) and Hippocampus (EH4556).

**Human Prefrontal Cortex Marker Genes** Gene enrichment scores calculated from healthy human prefrontal cortex scRNA-seq dataset (EH4557). Original paper annotated the cell types based on prior knowledge which contains 26 valid sub-cell types (clusters).

### References

Saunders et al. (2018). Molecular Diversity and Specializations among the Cells of the Adult Mouse Brain. *Cell* 174(4), 1015-1030

Nagy et al. (2020) Single-nucleus transcriptomics of the prefrontal cortex in major depressive disorder implicates oligodendrocyte precursor cells and excitatory neurons. *Nature Neuroscience* 1-11

**Examples**

```
library(ExperimentHub)
eh <- ExperimentHub()
myfiles <- query(eh, "LRcellTypeMarkers")
## download resource
myfiles[[1]] ## load the first resource
myfiles[['EH4548']] ## load by EH id
```

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