Package 'multiWGCNAdata'

November 10, 2026

Type Package

Title Data Package for multiWGCNA

Version 1.10.0

biocViews ExperimentHub, ExpressionData, Homo_sapiens_Data, Mus_musculus_Data, RNASeqData, MicroarrayData

Description Stores expression profiling data from experiments compatible with the multiWGCNA R package. This includes human postmortem microarray data from patients and controls (GSE28521), astrocyte Ribotag RNA-seq data from EAE and wildtype mice (GSE100329), and mouse RNA-seq data from tau pathology (rTg4510) and wildtype control mice (GSE125957). These data can be accessed using the ExperimentHub workflow (see multiWGCNA vignettes).

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VignetteBuilder knitr

Encoding UTF-8

LazyData false

Depends ExperimentHub

Imports utils

Suggests BiocStyle, knitr, multiWGCNA, rmarkdown, SummarizedExperiment

RoxygenNote 7.2.3

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Author Dario Tommasini [aut, cre] (ORCID: <https://orcid.org/0000-0002-1214-6547>)

Maintainer Dario Tommasini <dtommasini0@gmail.com>

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multiWGCNAdata available as R objects

Description

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Details

See the vignette for examples of using these data in analyses.

browseVignettes("multiWGCNAdata")

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

Value

NA

Examples

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_se = eh_query[["EH8223"]]
astrocyte_se
```

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