

# Package ‘multiWGCNadata’

February 18, 2025

**Type** Package

**Title** Data Package for multiWGCNA

**Version** 1.5.0

**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).

**License** Artistic-2.0

**VignetteBuilder** knitr

**Encoding** UTF-8

**LazyData** false

**Depends** ExperimentHub

**Imports** utils

**Suggests** BiocStyle, knitr, multiWGCNA, rmarkdown, SummarizedExperiment

**RoxygenNote** 7.2.3

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

**git\_branch** devel

**git\_last\_commit** 8baeb94

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multiWGCNAdata-package

*multiWGCNAdata available as R objects*

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### 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 have been parsed into list objects and are available in the ExperimentHub.

### 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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