Package 'ReactomeGSA.data'

March 4, 2025

Type Package

Title Companion data package for the ReactomeGSA package

Version 1.21.0

Description Companion data sets to showcase the functionality of the ReactomeGSA package. This package contains proteomics and RNA-seq data of the melanoma B-cell induction study by Griss et al. and scRNA-seq data from Jerby-Arnon et al.

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Encoding UTF-8

Depends R (>= 3.6), limma, edgeR, ReactomeGSA, Seurat

RoxygenNote 6.1.1

biocViews ExpressionData, RNASeqData, Proteome, Homo_sapiens_Data

BugReports https://github.com/reactome/ReactomeGSA.data

URL https://github.com/reactome/ReactomeGSA.data/issues

git_url https://git.bioconductor.org/packages/ReactomeGSA.data

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Contents

`griss_melanoma_proteomics` *Proteomics intensity-based quantitation data from the B-Cell melanoma induction study by Griss et al.*

Description

The data is available as a `EList` object containing the aggregated protein intensity values. Normalisation was already performed on the PSM level prior to protein-level aggregation.

Usage

```
griss_melanoma_proteomics
```

Format

An object of class `EList` with 6456 rows and 20 columns.

Author(s)

Johannes Griss <johannes.griss@meduniwien.ac.at>

References

Griss et al., Nat Commun. 2019 10(1):4186. doi: 10.1038/s41467-019-12160-2

`griss_melanoma_result` *Example Camera result created based on the melanoma induction study by Griss et al.*

Description

The result is stored as a `ReactomeAnalysisResult-class` object.

Usage

```
griss_melanoma_result
```

Format

An object of class `ReactomeAnalysisResult` of length 1.

Author(s)

Johannes Griss <johannes.griss@meduniwien.ac.at>

References

Griss et al., Nat Commun. 2019 10(1):4186. doi: 10.1038/s41467-019-12160-2

`griss_melanoma_rnaseq` *Raw RNA-seq read counts from the B-Cell melanoma induction study by Griss et al.*

Description

The data is available as a `DGEList` object containing read counts per gene.

Usage

```
griss_melanoma_rnaseq
```

Format

An object of class `DGEList` with 58237 rows and 16 columns.

Author(s)

Johannes Griss <johannes.griss@meduniwien.ac.at>

References

Griss et al., Nat Commun. 2019 10(1):4186. doi: 10.1038/s41467-019-12160-2

`jerby_b_cells` *Example Seurat object containing B cells extracted from the single-cell RNA-seq dataset published by Jerby-Arnon et al.*

Description

This result is stored as a `Seurat` object.

Usage

```
jerby_b_cells
```

Format

An object of class `Seurat` with 23686 rows and 920 columns.

References

Jerby-Arnon et al., Cell 2018 1;175(4):984-997.e24. doi:10.1016/j.cell.2018.09.006

Index