Package ‘ReactomeGSA.data’

April 16, 2024

Type Package
Title Companion data package for the ReactomeGSA package
Version 1.16.1
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.
License Artistic-2.0
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
git_branch RELEASE_3_18
git_last_commit 56f5b0b
git_last_commit_date 2023-11-08
Repository Bioconductor 3.18
Date/Publication 2024-04-16
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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_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

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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

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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.

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