Package ‘ReactomeGSA.data’
August 8, 2024

Type Package
Title Companion data package for the ReactomeGSA package
Version 1.18.0
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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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 \texttt{EList} object containing the aggregated protein intensity values. Normalisation was already performed on the PSM level prior to protein-level aggregation.

Usage
\begin{verbatim}
griss_melanoma_proteomics
\end{verbatim}

Format
An object of class \texttt{EList} with 6456 rows and 20 columns.

Author(s)
Johannes Griss \texttt{<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 \texttt{ReactomeAnalysisResult-class} object.

Usage
\begin{verbatim}
griss_melanoma_result
\end{verbatim}

Format
An object of class \texttt{ReactomeAnalysisResult} of length 1.

Author(s)
Johannes Griss \texttt{<johannes.griss@meduniwien.ac.at>
References

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

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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