Package ‘ReactomeGSA.data’
July 25, 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.
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_19
git_last_commit c254d39
git_last_commit_date 2024-04-30
Repository Bioconductor 3.19
Date/Publication 2024-07-25
Author Johannes Griss [aut, cre] (<https://orcid.org/0000-0003-2206-9511>)
Maintainer Johannes Griss <johannes.griss@meduniwien.ac.at>

Contents

<table>
<thead>
<tr>
<th>File</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>griss_melanoma_proteomics</td>
<td>2</td>
</tr>
<tr>
<td>griss_melanoma_result</td>
<td>2</td>
</tr>
<tr>
<td>griss_melanoma_rnaseq</td>
<td>3</td>
</tr>
<tr>
<td>jerby_b_cells</td>
<td>3</td>
</tr>
</tbody>
</table>

Index 4
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

---

**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.

References
Index

* datasets
  griss_melanoma_proteomics, 2
  griss_melanoma_result, 2
  griss_melanoma_rnaseq, 3
  jerby_b_cells, 3

DGEList, 3

EList, 2

griss_melanoma_proteomics, 2
griss_melanoma_result, 2
griss_melanoma_rnaseq, 3

jerby_b_cells, 3