# Package 'ReactomeGSA.data'

November 10, 2026

**Type** Package

**Title** Companion data package for the ReactomeGSA package

**Version** 1.26.0

**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

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

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## 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

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

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## 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

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

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## 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

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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.*

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## 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

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