

# Package ‘DAPARdata’

November 28, 2024

**Type** Package

**Title** Data accompanying the DAPAR and Prostar packages

**Version** 1.37.0

**Date** 2023-01-14

**Author** Samuel Wiczorek [cre,aut],  
Thomas Burger [aut],  
Enora Fremy [aut]

**Maintainer** Samuel Wiczorek <samuel.wiczorek@cea.fr>

**Description** Mass-spectrometry based UPS proteomics data sets from Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A.  
Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data Brief. 2015 Dec 17;6:286-94 and Gai Gianetto, Q., Combes, F., Ramus, C., Bruley, C., Coute, Y., Burger, T. (2016). Calibration plot for proteomics: A graphical tool to visually check the assumptions underlying FDR control in quantitative experiments. Proteomics, 16(1), 29-32.

**Depends** R (>= 4.4.0), MSnbase

**Suggests** knitr, DAPAR, BiocStyle

**Imports** utils

**License** GPL-2

**biocViews** ExperimentData, MassSpectrometryData, Proteome

**NeedsCompilation** no

**RoxygenNote** 7.2.3

**Encoding** UTF-8

**URL** <http://www.prostar-proteomics.org/>

**BugReports** <https://github.com/edyp-lab/DAPARdata/issues>

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/DAPARdata>

**git\_branch** devel

**git\_last\_commit** 6af47a5

**git\_last\_commit\_date** 2024-11-06

**Repository** Bioconductor 3.21

**Date/Publication** 2024-11-28

## Contents

DAPARdata . . . . .	2
Exp1_R25_pept . . . . .	3
Exp1_R25_prot . . . . .	4
Exp1_R2_pept . . . . .	5
Exp1_R2_prot . . . . .	6
Exp2_R100_pept . . . . .	7
Exp2_R100_prot . . . . .	8
Exp2_R10_pept . . . . .	9
Exp2_R10_prot . . . . .	10
Exp2_R2_pept . . . . .	11
Exp2_R2_prot . . . . .	12
<b>Index</b>	<b>13</b>

---

DAPARdata	<i>Lists the datasets embebbedin DAPARdata</i>
-----------	--

---

## Description

Lists the datasets embebbedin DAPARdata

## Usage

DAPARdata()

## Examples

DAPARdata()

---

`Exp1_R25_pept`*Exp1\_R25\_pept dataset*

---

**Description**

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Gai Gianetto et al. (2016) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 25 fmol and 10 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 2.5. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp1_R25_pept.txt`), or as a MSnSet structure (`Exp1_R25_pept`). In the latter case, the quantitative data are those of the raw intensities.

**Usage**

```
data(Exp1_R25_pept)
```

**Format**

An object of class `MSnSet` related to peptide quantification. It contains 6 samples divided into two conditions (25fmol and 10fmol) and 13918 peptides.

The data frame `exprs(Exp1_R25_pept)` contains six columns that are the quantitation of peptides for the six replicates.

The data frame `fData(Exp1_R25_pept)` contains the meta data about the peptides.

The data frame `pData(Exp1_R25_pept)` contains the experimental design and gives few informations about the samples.

**Value**

An object of class `MSnSet` related to peptides quantification.

**References**

Cox J., Hein M.Y., Lubner C.A., Paron I., Nagaraj N., Mann M. Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. *Mol Cell Proteomics*. 2014 Sep, 13(9):2513-26.

Giai Gianetto, Q., Combes, F., Ramus, C., Bruley, C., Coute, Y., Burger, T. (2016). Calibration plot for proteomics: A graphical tool to visually check the assumptions underlying FDR control in quantitative experiments. *Proteomics*, 16(1), 29-32.

---

Exp1\_R25\_prot

*Exp1\_R25\_prot dataset*

---

## Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Giai Gianetto et al. (2016) for details). It contains the abundance values of the different human and yeast proteins identified and quantified in these two conditions. The two conditions represent the measured abundances of proteins when respectively 25 fmol and 10 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 2.5. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp1_R25_prot.txt`), or as a MSnSet structure (`Exp1_R25_prot.MSnset`). In the latter case, the quantitative data are those of the raw intensities.

## Usage

```
data(Exp1_R25_prot)
```

## Format

An object of class `MSnSet` related to proteins quantification. It contains 6 samples divided into two conditions (25 fmol and 10 fmol) and 2384 proteins.

The data frame `exprs(Exp1_R25_prot)` contains six columns that are the quantitation of proteins for the six replicates.

The data frame `fData(Exp1_R25_prot)` contains the meta data about the proteins.

The data frame `pData(Exp1_R25_prot)` contains the experimental design and gives few informations about the samples.

## Value

An object of class `MSnSet` related to proteins quantification.

## References

Cox J., Hein M.Y., Lubner C.A., Paron I., Nagaraj N., Mann M. Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. *Mol Cell Proteomics*. 2014 Sep, 13(9):2513-26.

Giai Gianetto, Q., Combes, F., Ramus, C., Bruley, C., Coute, Y., Burger, T. (2016). Calibration plot for proteomics: A graphical tool to visually check the assumptions underlying FDR control in quantitative experiments. *Proteomics*, 16(1), 29-32.

---

Exp1\_R2\_pept

*Exp1\_R2\_pept dataset*

---

### Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Gaii Gianetto et al. (2016) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 5 fmol and 10 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 2. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp1_R2_pept.txt`), or as a MSnSet structure (`Exp1_R2_pept`). In the latter case, the quantitative data are those of the raw intensities.

### Usage

```
data(Exp1_R2_pept)
```

### Format

An object of class MSnSet related to peptide quantification. It contains 6 samples divided into two conditions (10fmol and 5fmol) and 14048 peptides.

The data frame `exprs(Exp1_R2_pept)` contains six columns that are the quantitation of peptides for the six replicates.

The data frame `fData(Exp1_R2_pept)` contains the meta data about the peptides.

The data frame `pData(Exp1_R2_pept)` contains the experimental design and gives few informations about the samples.

### Value

An object of class MSnSet related to peptides quantification.

### References

Cox J., Hein M.Y., Lubner C.A., Paron I., Nagaraj N., Mann M. Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. *Mol Cell Proteomics*. 2014 Sep, 13(9):2513-26.

Gaii Gianetto, Q., Combes, F., Ramus, C., Bruley, C., Coute, Y., Burger, T. (2016). Calibration plot for proteomics: A graphical tool to visually check the assumptions underlying FDR control in quantitative experiments. *Proteomics*, 16(1), 29-32.

---

Exp1\_R2\_prot

*Exp1\_R2\_prot dataset*

---

### Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Gaii Gianetto et al. (2016) for details). It contains the abundance values of the different human and yeast proteins identified and quantified in these two conditions. The two conditions represent the measured abundances of proteins when respectively 5 fmol and 10 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 2. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp1_R2_prot.txt`), or as a MSnSet structure (`Exp1_R2_prot.MSnset`). In the latter case, the quantitative data are those of the raw intensities.

### Usage

```
data(Exp1_R2_prot)
```

### Format

An object of class `MSnSet` related to proteins quantification. It contains 6 samples divided into two conditions (10fmol and 5fmol) and 2394 proteins.

The data frame `exprs(Exp1_R2_prot)` contains six columns that are the quantitation of proteins for the six replicates.

The data frame `fData(Exp1_R2_prot)` contains the meta data about the proteins.

The data frame `pData(Exp1_R2_prot)` contains the experimental design and gives few informations about the samples.

### Value

An object of class `MSnSet` related to proteins quantification.

### References

Cox J., Hein M.Y., Lubner C.A., Paron I., Nagaraj N., Mann M. Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. *Mol Cell Proteomics*. 2014 Sep, 13(9):2513-26.

Gaii Gianetto, Q., Combes, F., Ramus, C., Bruley, C., Coute, Y., Burger, T. (2016). Calibration plot for proteomics: A graphical tool to visually check the assumptions underlying FDR control in quantitative experiments. *Proteomics*, 16(1), 29-32.

---

`Exp2_R100_pept`*Exp2\_R100\_pept dataset*

---

## Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Ramus et al. (2015) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 1 fmol and 100 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 100. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp2_R100_pept.txt`), or as a `MSnSet` structure (`Exp2_R100_peptt.MSnset`). In the latter case, the quantitative data are those of the raw intensities.

## Usage

```
data(Exp2_R100_pept)
```

## Format

An object of class `MSnSet` related to peptides quantification. It contains 6 samples divided into two conditions (1 fmol and 100 fmol) and 5684 peptides.

The data frame `exprs(Exp2_R100_pept)` contains six columns that are the quantitation of peptides for the six replicates.

The data frame `fData(Exp2_R100_pept)` contains the meta data about the peptides

The data frame `pData(Exp2_R100_pept)` contains the experimental design and gives few informations about the samples.

## Value

An object of class `MSnSet` related to peptides quantification.

## References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. *Data Brief*. 2015 Dec 17;6:286-94. PMID: 26862574.

---

Exp2\_R100\_prot

*Exp2\_R100\_prot dataset*

---

## Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Ramus et al. (2015) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 1 fmol and 100 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 100. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp2_R100_prot.txt`), or as a MSnSet structure (`Exp2_R100_prot.MSnset`). In the latter case, the quantitative data are those of the raw intensities.

## Usage

```
data(Exp2_R100_prot)
```

## Format

An object of class MSnSet related to proteins quantification. It contains 6 samples divided into two conditions (1 fmol and 100 fmol) and 923 proteins.

The data frame `exprs(Exp2_R100_prot)` contains six columns that are the quantitation of proteins for the six replicates.

The data frame `fData(Exp2_R100_prot)` contains the meta data about the proteins.

The data frame `pData(Exp2_R100_prot)` contains the experimental design and gives few informations about the samples.

## Value

An object of class MSnSet related to proteins quantification.

## References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. *Data Brief*. 2015 Dec 17;6:286-94. PMID: 26862574.



---

Exp2\_R10\_pept

*Exp2\_R10\_pept dataset*

---

## Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Ramus et al. (2015) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 10 fmol and 100 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 10. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp2_R10_pept.txt`), or as a MSnSet structure (`Exp2_R10_pept.MSnset`). In the latter case, the quantitative data are those of the raw intensities.

## Usage

```
data(Exp2_R10_pept)
```

## Format

An object of class MSnSet related to peptides quantification. It contains 6 samples divided into two conditions (10 fmol and 100 fmol) and 5633 peptides.

The data frame `exprs(Exp2_R10_pept)` contains six columns that are the quantitation of peptides for the six replicates.

The data frame `fData(Exp2_R10_pept)` contains the meta data about the peptides.

The data frame `pData(Exp2_R10_pept)` contains the experimental design and gives few informations about the samples.

## Value

An object of class MSnSet related to peptides quantification.

## References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. *Data Brief*. 2015 Dec 17;6:286-94. PMID: 26862574.

---

`Exp2_R10_prot`*Exp2\_R10\_prot dataset*

---

## Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Ramus et al. (2015) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 10 fmol and 100 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 10. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp2_R10_prot.txt`), or as a MSnSet structure (`Exp2_R10_prot.MSnset`). In the latter case, the quantitative data are those of the raw intensities.

## Usage

```
data(Exp2_R10_prot)
```

## Format

An object of class MSnSet related to proteins quantification. It contains 6 samples divided into two conditions (10 fmol and 100 fmol) and 948 proteins.

The data frame `exprs(Exp2_R10_prot)` contains six columns that are the quantitation of proteins for the six replicates.

The data frame `fData(Exp2_R10_prot)` contains the meta data about the proteins.

The data frame `pData(Exp2_R10_prot)` contains the experimental design and gives few informations about the samples.

## Value

An object of class MSnSet related to proteins quantification.

## References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. *Data Brief*. 2015 Dec 17;6:286-94. PMID: 26862574.

---

Exp2\_R2\_pept

*Exp2\_R2\_pept dataset*

---

## Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Ramus et al. (2015) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 25 fmol and 50 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 2. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp2_R2_pept.txt`), or as a MSnSet structure (`Exp2_R2_pept.MSnset`). In the latter case, the quantitative data are those of the raw intensities.

## Usage

```
data(Exp2_R2_pept)
```

## Format

An object of class MSnSet related to peptides quantification. It contains 6 samples divided into two conditions (25fmol and 50fmol) and 5390 peptides.

The data frame `exprs(Exp2_R2_pept)` contains six columns that are the quantitation of peptides for the six replicates.

The data frame `fData(Exp2_R2_pept)` contains the meta data about the peptides

The data frame `pData(Exp2_R2_pept)` contains the experimental design and gives few informations about the samples.

## Value

An object of class MSnSet related to peptides quantification.

## References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. *Data Brief*. 2015 Dec 17;6:286-94. PMID: 26862574.

---

Exp2\_R2\_prot

*Exp2\_R2\_prot dataset*

---

### Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Ramus et al. (2015) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 25 fmol and 50 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 2. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see `inst/extdata/Exp2_R2_prot.txt`), or as a MSnSet structure (`Exp2_R2_prot.MSnset`). In the latter case, the quantitative data are those of the raw intensities.

### Usage

```
data(Exp2_R2_prot)
```

### Format

An object of class `MSnSet` related to proteins quantification. It contains 6 samples divided into two conditions (25 fmol and 50 fmol) and 948 proteins.

The data frame `exprs(Exp2_R2_prot)` contains six columns that are the quantitation of proteins for the six replicates.

The data frame `fData(Exp2_R2_prot)` contains the meta data about the proteins.

The data frame `pData(Exp2_R2_prot)` contains the experimental design and gives few informations about the samples.

### Value

An object of class `MSnSet` related to proteins quantification.

### References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. *Data Brief*. 2015 Dec 17;6:286-94. PMID: 26862574.

# Index

## \* datasets

Exp1\_R25\_pept, [3](#)  
Exp1\_R25\_prot, [4](#)  
Exp1\_R2\_pept, [5](#)  
Exp1\_R2\_prot, [6](#)  
Exp2\_R100\_pept, [7](#)  
Exp2\_R100\_prot, [8](#)  
Exp2\_R10\_pept, [9](#)  
Exp2\_R10\_prot, [10](#)  
Exp2\_R2\_pept, [11](#)  
Exp2\_R2\_prot, [12](#)

## \* data

Exp1\_R25\_pept, [3](#)  
Exp1\_R25\_prot, [4](#)  
Exp1\_R2\_pept, [5](#)  
Exp1\_R2\_prot, [6](#)  
Exp2\_R100\_pept, [7](#)  
Exp2\_R100\_prot, [8](#)  
Exp2\_R10\_pept, [9](#)  
Exp2\_R10\_prot, [10](#)  
Exp2\_R2\_pept, [11](#)  
Exp2\_R2\_prot, [12](#)

DAPARdata, [2](#)

Exp1\_R25\_pept, [3](#)  
Exp1\_R25\_prot, [4](#)  
Exp1\_R2\_pept, [5](#)  
Exp1\_R2\_prot, [6](#)  
Exp2\_R100\_pept, [7](#)  
Exp2\_R100\_prot, [8](#)  
Exp2\_R10\_pept, [9](#)  
Exp2\_R10\_prot, [10](#)  
Exp2\_R2\_pept, [11](#)  
Exp2\_R2\_prot, [12](#)