

# R documentation

of 'Exp1\_R2\_prot.Rd'

October 6, 2016

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Exp1\_R2\_prot

*Exp1\_R2\_prot dataset*

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## 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 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.

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.

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