

# R documentation

of 'Exp1\_R2\_pept.Rd'

October 6, 2016

---

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 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 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.

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.

# Index

\*Topic **datasets**

Exp1\_R2\_pept, 1

\*Topic **data**

Exp1\_R2\_pept, 1

Exp1\_R2\_pept, 1

MSnSet, 1