

R documentation

of 'Exp2_R100_pept.Rd'

October 6, 2016

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.

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