R documentation

of ‘`Exp2_R2_prot.Rd`’

October 6, 2016

`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.

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