

Description of the UPSprotx2 dataset

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This dataset results from a controlled relative quantification proteomics experiment where Sigma UPS1 human proteins were spiked in a similar yeast lysate in 2 different concentrations (with a ratio of 2). As a consequence, it can be used to benchmark the quality of a statistical analysis: in the ideal case, after the differential analysis, only and all the human proteins should be selected.

1 Preparation and digestion of proteins and peptides

TODO

2 Nano-LC-MS/MS analyses

TODO

3 Computational analyses

TODO