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Josip Lovric is the author of Introducing Proteomics: From Concepts to Sample Separation, Mass Spectrometry and Data Analysis, published by Wiley.

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Mass spectrometry based proteomics can routinely identify hundreds of proteins in a single LC-MS run, and methods have been developed for relative quantitation between differentially treated samples using stable isotopes. However, absolute quantitation has so far required addition of a labeled standard late in the experimental workflow, introducing variability due to sample preparation. Here ...

Absolute SILAC for Accurate Quantitation of Proteins in ...

INTRODUCTION. The explicit goal of proteomics is to identify and quantify all the proteins present in a cell at a specific moment. However, this is a significant challenge because unlike the genome, the proteins present in a system at any time are dynamic and of varying complexity.

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