

Comparative proteomic investigations of biological protein samples using the quantitative Protein Sequence Tag (qPST) technology.

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The Protein Sequence Tag (PST) technology is a gel-free proteomic approach for the analysis of complex protein mixtures. It is applicable to a wide range of samples with different biochemical properties and involves a combination of highly reproducible chemical and enzymatic cleavage steps coupled with the tagging of amino groups using a proprietary labelling reagent. Subsequent peptide analysis and characterisation is achieved by in-depth LC-MS and LC-MS/MS investigations. PST has been further developed to allow for the differential quantitative analysis of complex proteomes through the development of the isotope labelled quantitative PST tags (qPST).

The performance of qPST was evaluated with *S. cerevisiae*, grown on either galactose or ethanol as carbon source. The data obtained from this application will be presented and demonstrate the robustness of the qPST approach in detecting quantitative changes in complex proteomes with

- (1) three replicate analyses showing a high reproducibility
- (2) low false positive rate
- (3) good correlation from the literature.

Subsequently, qPST was applied to the analysis of human plasma samples. The results demonstrating the robustness and utility of the qPST approach will be presented.

In summary, qPST is a powerful approach to discover biologically relevant biomarkers using differential quantitative protein analysis in complex proteomes of cells and body fluids. It provides accurate quantitative determination of differential expressed proteins and can be used to address comprehensive quantitative proteome analysis.