

2-DIMENSIONAL GEL ELECTROPHORESIS VERSUS QUANTITATIVE PROTEIN SEQUENCE TAGS (qPST™): A COMPARATIVE PROTEOMIC STUDY IN YEAST

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The quantitative Protein Sequence Tag (qPST) employs a peptide-labelling strategy using proprietary stable isotope tags. The procedure consists of a series of integrated steps including protein solubilisation, amino group labelling using different isotope labelled qPST-tags and enzymatic cleavage. The labelled peptide pairs are quantified in LC-MS by comparing the intensities of their monoisotopic peaks.

To evaluate the quantitative data obtained by qPST samples were analysed in parallel using 2D-gel electrophoresis.

Proteins were extracted from the yeast *S. cerevisiae* cultivated on rich medium containing either 2% galactose or 2% ethanol. Each protein extract was divided into two aliquots, one for each proteomic approach. 2DE-gels were silver-stained and analysed using Progenesis software. For qPST labelled-peptide pairs were quantified in LC-MS using a proprietary software package.

The two approaches displayed and identified a similar number of proteins (463 proteins with qPST and 457 proteins with 2DE). Approximately one third of the proteins identified with both approaches, one third were exclusively detected with qPST and one third were exclusively detected with 2DE. With 2DE, 73 identified proteins were found to be regulated at least 2-fold. With qPST, 56 identified proteins were found to be regulated at least 2-fold. Approximately two thirds of the regulations were detected with both approaches.

This study confirms that 2DE and qPST approaches are highly complementary with respect to the subset of proteins surveyed and analysed. It further shows that gel-free qPST profiling offers an accurate, efficient and effective solution for biomarker discovery and addresses proteins that are not amendable to gel-based approaches.

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