

THE PROTEIN SEQUENCE TAG (PST[®]) TECHNOLOGY: A GEL-FREE PROTEOMIC APPROACH FOR BROAD APPLICATION

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Recently, we introduced the Protein Sequence Tag technology (PST[®]), a gel-free technology for proteomics investigations. This approach was shown to be highly effective for protein identification using a crude mitochondrial fraction from *S. cerevisiae*, also in comparison to other technologies (1).

Here, we present results from further investigations on samples with quite different biochemical properties to highlight the broad applicability of the PST technology. Further comparisons to alternative proteomics methods were also undertaken.

For instance, we used highly enriched membrane fractions for such investigations, namely the membrane fraction of yeast mitochondria and the total membrane fraction of neuronal stem cells of mice. A high proportion of the found proteins (148 and 173, resp.) were identified as transmembrane or membrane-associated ones (80 and 50%, for each membrane fraction, resp.), partly with more than 5 transmembrane domains.

Another investigated sample was the nuclear extract of epithelial cells of mice. With the PST technology, we identified about 40% more proteins as with the 1DE-PMF approach (170 versus 124 proteins), whereby in both cases the proportion of nuclear proteins was about 70%. The 2DE approach identified even a quite lower number of proteins.

Human plasma, depleted from the 6 most abundant proteins, was applied to this procedure, too. Here, the number of identified proteins was in a similar range as found using the MudPIT approach.

The PST technology is currently extended to provide also quantitative protein data (for details, see abstract entitled "Quantitative Protein Sequence Tag and Tandem Mass Tag Technologies as gel-free procedures for mass spectrometry based quantitative proteomic analyses"). This quantitative feature, combined with the presented broad applicability, makes the PST approach to be a valuable tool in proteomics investigations.

- (1) Kuhn, K., Thompson, A., Prinz, T., Müller, J., Baumann, C., Schmidt, G., Neumann, T., and Hamon, C. (2003) Isolation of N-terminal protein sequence tags from cyanogen bromide cleaved proteins as a novel approach to investigate hydrophobic proteins. *J. Prot. Res.* 2, 598-609.