

MASS SPECTROMETRY: A KEY ANALYTICAL TECHNIQUE IN PROTEIN STUDIES

PETER ROEPSTORFF

*Department of Molecular Biology, Odense University,
DK-5230 Odense M, Denmark*

Electrospray ionisation (ESI) and matrix assisted laser desorption/ionisation (MALDI) mass spectrometry (MS) allow rapid, accurate and very sensitive molecular mass determination of peptides and proteins as well as molecular mass mapping of complex mixtures. In addition, sequence information on selected compounds in mixtures can be generated by collision induced dissociation or post source decay respectively. When the mass spectrometric information is combined with information derived by classical biochemistry techniques such as treatment with specific enzymes, use of specific protein interaction in affinity based procedures, and the use of information on protein sequences available in data bases, then the result is a multidimensional approach to protein studies.

Examples of applications of mass spectrometry from our recent protein studies will be given. These include:

- Correlation of sequence information with protein pattern as revealed by 2D-PAGE (Proteome analysis).
- Determination of protein modifications, e.g., glycosylation and phosphorylation.
- Investigation of enzyme specificity and reaction mechanisms.
- Generation of sufficient sequence information for cloning
- Protein sequencing supported by MS.
- Studies of protein function and interaction.

Finally present limitations and future challenges will be discussed.