

## **Mass spectrometric analysis of intact proteins: the dark side of deconvolution**

*Ágnes Gömöry, Károly Vékey, László Drahos*

1) Research Centre for Natural Sciences, Magyar Tudósok krt 2,  
H-1117 Budapest, Hungary

One of the most commonly used techniques for studying intact proteins, including monoclonal antibodies (MABs), is HPLC-MS. While studying pure, large amounts of protein is relatively easy, analyzing mixtures can be more complicated. The real challenge arises when small amounts of protein mixtures with large molecular masses are studied. In such cases, automatic evaluations (e.g. deconvolution of mass spectra) can yield incorrect results, making HPLC separation of the mixture increasingly important.

In this presentation, I will illustrate the process, problems, and difficulties of evaluating the mass spectra of proteins from small to complex antibody-drug conjugates. In the latter case, when the mixture is too complex, a reliable result can only be obtained using a detailed manual evaluation of the ion chromatograms and mass spectra.