

Nano Electrospray based Peptide Sequencing: From the last Millenium to Today

Matthias Wilm

EMBL - Heidelberg

The introduction of the quasi-static nano electrospray ion source in 1992 and the installation of encased collision cells in triple quadrupole machines allowed the extensive analysis of peptide mixtures by tandem MS. Having intensive fragment spectra at our disposal computer algorithms, the sequence-tag algorithm, were developed that allowed the first peptide identifications using translated open reading frames in DNA data bases and later EST data bases. From that point onwards protein characterization was increasingly dominated by mass spectrometric techniques, starting with protein identification over protein de-novo sequencing, characterization and specific detection of secondary modifications, automatic protein identification, massive on-line peptide sequencing, parallel sequencing to systematic peptide and protein quantitations.

Today, close to all molecular biological research is backed up by mass spectrometric investigations and it is not too far fetched to say that very often a high quality of the mass spectrometry department is a prerequisite for publicly perceiving a high quality of the biological research.