

Application of Kingdon, Penning and Paul ion traps for determination of protein mixture compositions and protein primary structures

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Kingdon, Penning and Paul ion traps invented correspondingly in 1923, 1936 and 1956 have played essential role in 20th century physics- test of the validity of quantum electrodynamics, tests of symmetry properties of fundamental laws-particle-antiparticle (electron-positron), the electric dipole moment of the neutron, ion spectroscopy, hyromagnetic ratio, comparison of masses $m(p^+)/m(e^-)$ $m(CO^+)/m(N_2^+)$ frequency and time standards, dusty plasma and so on. All three traps are playing extremely important role in modern mass spectrometry and especially in its biological applications. Paul trap applied was the first to be used in mass spectrometry. It consists of three cylindrical electrodes of hyperbolic shape to which RF voltage and high frequency and amplitude is applied. It can trap ions of different mass to charge (m/z) ratio and measure m/z by consecutive ejection of different m/z ions from the trap using the property of ion instability in such traps at some conditions. Penning trap is a Paul trap (frequently with cylindrical instead of hyperbolic electrodes) in magnetic field applied parallel to the trap axes. It has started to be used in mass spectrometry in 1974 in the frame of Fourier transform (FT) ion cyclotron resonance (FT ICR) mass spectrometry. In FT ICR mass spectrometry ions are trapped by the combination of electric and magnetic fields. RF field is used to excite their cyclotron motion, whose frequency depends on m/z . The time domain signal induced by synchronously moving ions is detected and subjected by FT transformation resulting in mass spectra. FT ICR method provides currently the highest mass resolution and accuracy of mass measurements. High magnetic field from superconducting solenoid is needed for their operation. The powerfulness of Paul and Penning traps in mass spectrometry is based on their ability to cause fragmentation of trapped ions inside traps and measure fragmentation product mass spectra. Different fragmentation techniques were developed and implemented in mass spectrometry utilizing ion traps. Paul and Penning traps are used routinely with modern nondestructive methods of biomacromolecule ionization for peptides and proteins mixture analyses and determination of amino acid sequences in peptides and proteins as well as for characterization of proteins secondary structures by H/D exchange method. Kingdon trap has been introduced to mass spectrometry two years ago. Like FT ICR it utilizes FT method but does not need magnetic field for operation.