Workshop on

Recent Advances in Biological and Proteomic Mass Spectrometry

1 marzo 2004

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Istituto di Scienze dell’Alimentazione
Consiglio Nazionale delle Ricerche

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Bruker Daltonics è uno dei principali produttori di spettrometri di massa e accessori per la ricerca in ambito chimico, biochimico e farmaceutico. La linea di prodotti include FT-MS, MALDI-TOF e MALDI-TOF/TOF, LC/ESI-Trappola ionica, ESI-TOF e ESI-Q-q-TOF, sistemi automatizzati per la preparazione del campione e software dedicati all’analisi nelle Scienze della Vita.
14.30 WELCOME ADDRESS
Arturo Leone
Direttore - Istituto di Scienze dell’Alimentazione (ISA) del CNR, Avellino

15.00 1st SESSION
The role of SID* ion activation technique in biological mass spectrometry
Arpad Somogyi
Mass Spectrometry Facility, Department of Chemistry, University of Arizona, Tucson, USA

16.00
FTMS as a most flexible, high-performance MS/MS technique: a comparison of Q-CID, ECD and IRMPD
Arnd Ingendoh
Bruker Daltonik GmbH, Bremen, Germany

16.45 COFFEE BREAK

17.15 2nd SESSION
MALDI-TOF mass spectrometry: a technology platform for classical proteomics, proteomic profiling and biomarker discovery
Giovanna Tripepi
Bruker Daltonics S.r.l., Milano, Italia

Recent advances in casein phosphoproteome
Luca Picariello
ISA/C.N.R., Avellino

Molecular profiling by mass spectrometry: an overview
Antonio Malorni
CESMA-ProBio/ISA/C.N.R., Avellino

19.00 Visit to CeSMa-ProBio labs

* With the development of soft ionization techniques, such as electrospray ionization (ESI) and matrix assisted laser desorption/ionization, biological samples, including proteins, peptides, oligosaccharides and DNAs, are now routinely investigated by mass spectrometry in many laboratories all over the world. To obtain structural information, such as protein and DNA sequences, fragmentation of smaller units of bigger biomolecules (that are usually generated by enzymatic digestion) is crucial and of primary importance. Because the ESI and MALDI ionization techniques do not provide enough internal energy to the ionic species, so-called ion activation methods are necessary to initiate and/or enhance fragmentation. The technique that is used to get structural information via fragmentation of a selected ion is called tandem mass spectrometry (MS/MS). In MS/MS, an ion of particular interest is selected either in space or in time as a mass spectrometer, the ion than is activated in a different region or subsequent time, and finally the fragments are analyzed by a subsequent mass measurement. The resulted MS/MS spectra are strongly dependent on the way the selected ion is activated. Ion activation is provided by different collisions of the selected ion and an “activating” target that can be either small gas molecules [He, Ar, Xe; high and low energy collision induced dissociation (CID)], photons [infrared multiphoton dissociation (IRMPD) or blackbody infrared radiative dissociation (BIRD)], electron [electron capture dissociation (ECD)], and a surface [surface-induced dissociation (SID)]. Although in most of the commercially available instruments, high or low energy CID is used as ion activation method, in certain cases, CID does not provide enough energy to efficiently fragment a selected ion. SID, however, can provide higher energies that lead to more fragments with a more controllable fashion. Obviously, the success of protein identification strongly depends on the number of fragments in the tandem MS/MS mass spectra: fragment rich spectra make sequencing more reliable. The present talk will focus on SID, which is a relatively unique but powerful ion activation method. Following a discussion on some general features of SID, examples will be shown to demonstrate and justify the usefulness of SID in biological mass spectrometry.