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Dipartimento di Scienze della Vita
Seconda Università degli Studi di Napoli - Caserta

Dipartimento di Scienza degli Alimenti
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REGISTRATION IS REQUIRED
the registration form is available at
http://isa.cnr.it/web-new/ita/eventi/eventi_6.htm
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organized by

Istituto di Scienze dell'Alimentazione
del CNR
e
Rete di Spettrometria di Massa
del CNR
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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.
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Workshop on

Recent Advances in Biological and Proteomic Mass Spectrometry

1 marzo 2004

Aula Bottazzi

Istituto di Scienze dell'Alimentazione
Consiglio Nazionale delle Ricerche

Via Roma 52 a/c - Avellino

PROGRAM

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

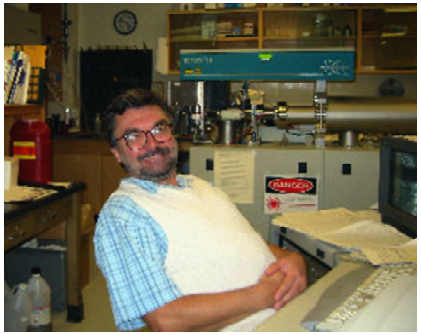
MALDI-TOF mass spectrometry: a technology platform for classical proteomics, proteomic profiling and biomarker discovery
Giovanna Tripepi
Bruker Daltonics S.r.l., Milano, Italia

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

Molecular profiling by mass spectrometry: an overiew
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 ether in space or time in 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 (ED)], 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.



ARPAD SOMOGYI

Affiliation and official address: Director of the Mass Spectrometry Facility, Department of Chemistry, University of Arizona, Tucson, AZ 85721
Education: (*degrees, dates, universities)* M.S., 1981, Chemistry, Lajos Kossuth, University, Debrecen, Hungary; Ph. D., 1984, Chemistry, Lajos Kossuth University, Debrecen, Hungary
Career/Employment: (*employers, positions and dates)* 1981-1983, Research Fellow of the Hungarian Academy of Sciences, Department of Chemistry, Lajos Kossuth University, Debrecen, Hungary; 1983-1987, Assistant Lecturer, Department of Chemistry, Lajos Kossuth University, Debrecen, Hungary; 1987-1991, Research Scientist, Mass Spectrometry Group, Central Research Institute for Chemistry of the Hungarian Academy of Sciences, Budapest, Hungary; 1992-1995, Post Doctoral Associate, Department of Chemistry, Virginia Commonwealth University, Richmond, VA; 1993-1995, Adjunct Faculty Member, Department of Chemistry, Virginia Commonwealth University, Richmond, VA; 1996, Post Doctoral Associate, Department of Chemistry, University of Arizona, Tucson, AZ; 1997- ,Director of Mass Spectrometry Facility, Department of Chemistry, University of Arizona, Tucson, AZ.
Current research interest: fragmentation mechanisms of protonated peptides in the gas phase by tandem mass spectrometry and theoretical methods; low energy ion-surface reactions between organic projectile ions and self-assembled monolayer surfaces by tandem mass spectrometry and theoretical methods; modelling organic environment and chemical reactions on Saturn's largest moon, Titan; gas-phase H / D exchange and chemical reactions some uranyl complexes; MALDI-TOF studies of non-soluble polyaromatic polymers
Publications: 56 papers in refereed journals; 67 communications to scientific meetings; 2 books.