

# th ANNUAL WORLD CONGRESS

AUGUST 28 TO SEPTEMBER 1, 2005

Technical University of Munich, Germany

Downtown Munich Campus

**NEWSLETTER APRIL 2005** 

# From defining the proteome to understanding function



Bavarian State Opera



elcome to the second issue of the HUPO 4<sup>th</sup> Annual World Congress Newsletter! We are proud to introduce our honorary speakers in this issue and urge you to browse the congress Web Site (www.hupo2005.com) for upcoming updates on many of the

### **UPDATES FROM OUR HONORARY SPEAKERS**



#### John Fenn

Research Professor in the Department of Chemistry at Virginia Commonwealth University, Richmond Virginia, USA

My work in proteomics has been centered around the development of sensitive and precise methods for detecting, identifying and characterizing protein molecules. In particular I am now interested in determining the conformation of individual protein molecules and of non-covalently bound complexes containing two or more protein molecules. My primary tool in this endeavour Electrospray Ionization Mass Spectrometry, a technique which was developed in my laboratory.

Proteins are the workhorse molecules of living systems, responsible for the chemical and physical processes that constitute life. When one realizes that a single cell may contain more than 50,000 of these versatile molecules, and that sometimes they perform their tasks alone, and at other times in cooperation with one or more other molecules, one can begin to imagine the amount of information that must be accumulated before true understanding can be achieved. Describing in detail what an individual cell does and, how it does it, is akin to the problem of a visitor to a city of 50,000 people who wants to determine, and define in detail, the role of every person in that city. Moreover, that visitor doesn't speak the same language as the inhabitants.



We urge you to register to the congress and the education program now.

Seats are going fast!

Click here to register.



## Franz Hillenkamp

Institute of Medical Physics and Biophysics, University of Muenster Muenster, Germany

Co-inventor (together with Michael Karas) of Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI-MS) with ultraviolet as well as infrared lasers. We introduced MALDI-MS for the analysis of proteins/peptides, DNA/RNA, carbohydrates and glyco-conjugates as well as synthetic polymers. Special attention has also been paid to the MALDI-MS of non-covalently bound complexes.

Besides application of the technique to different classes of molecules we have conducted extensive research on the physicochemical mechanisms and processes underlying MALDI-MS.



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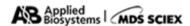
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Swiss-Prot's success story.

#### **Amos Bairoch**

Professor of Bioinformatics at the Department of Structural Biology and Bioinformatics University of Geneva Geneva, Switzerland

Heads the Swiss-Prot group (more than 75 collaborators) at the Swiss Institute of Bioinformatics. Amos Bairoch initiated the Swiss-Prot database in 1986. Today with near to 180,000 manually annotated sequences, Swiss-Prot is the most comprehensive database that connects protein sequences with the current knowledge in Life Sciences. The recent development of UniProt, a central resource on protein sequences created by joining information contained in Swiss-Prot, TrEMBL and American PIR databases is a measure of



Patrick H. O'Farrell

Professor of Biochemistry and Biophysics, University of California in San Francisco, California, United States

My interests in developmental biology have taken me in many directions. To examine developmental pathways, I developed high-resolution two-dimensional gel electrophoresis as a student. As a faculty, I abandoned what was to be the precursor of proteomics in favor of studies guided by genetics. Working in *Drosophila*, we contributed to the molecular dissection of embryonic patterning in the 80s. We then explored cell cycle mechanisms that control where and when cells divide during development.

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hupo2005@eventsintl.com

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