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Welcome to the third issue of the HUPO 4th Annual World Congress Newsletter!

WHAT YOU CAN READ ABOUT!!! Featured in this edition are detailed information about the Pre-Congress Educational Sessions and biographies of four of our world renowned invited speakers. Should you desire additional information about any of our Congress speakers, it can be found on our website.

([www.hupo2005.com](http://www.hupo2005.com))

DON'T MISS IT!!! The HUPO 4th Annual World Congress in Munich has been received with great enthusiasm from academia and industry. We are proud to announce that the first 600 delegates from 45 countries have already registered to the meeting. We hope to see you at this truly international event!

**ABSTRACTS!!!** The Scientific Committee would like to thank all abstract submitters for the outstanding, high-caliber content of their abstracts. The Human Proteome Organisation is extremely excited about the future of this field! We look forward to hosting an interactive forum with so many of our world leaders and newsmakers.

### INTERESTING ABSTRACT INFORMATION BASED ON SUBMISSIONS:

#### Top 5 Abstract Categories

Medical, Clinical, Pharmaceutical and Disease Proteomics – Cancer Proteomics  
Clinical Biomarker Discovery  
Bioinformatics  
Model Organisms – Microbial Proteomes  
Functional Proteomics – Protein-Protein Interactions and Networks

#### Top 5 Countries of Submission

Germany  
United States  
Sweden  
P.R. China  
Italy

### Educational Program – Space is limited – Register Now!

Sunday, August 28th, 08:30-16:30

08:30–09:15	GEL-BASED PROTEOMICS : Two-Dimensional Electrophoresis and DIGE	R. Westermeier
09:15–10:15	NON-GEL BASED PROTEOMICS: Multi-Dimensional LC / MudPIT	P. Andren & H.-R. Hoepker
10:15-10:30	COFFEE BREAK	
10:30–12:00	PROTEIN IDENTIFICATION MALDI – Peptide Mass Fingerprinting Peptide Sequencing with LC-ESI MS/MS	P. Roepstorff & K. Hjernøe
12:00–12:30	LUNCH	
12:30–14:00	PTM PROTEOMICS Phospho-Proteomics Glycoproteomics	O.N. Jensen & M. R. Larsen
14:00–14:45	QUANTITATIVE PROTEOMICS by MS with and without Stable Isotopes / ICAT	B. Macek
14:45–15:00	COFFEE BREAK	
15:00-16:30	BIOINFORMATICS FOR PROTEOMICS	H. Hermjakob & R. Appel

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## UPDATES FROM OUR SPEAKERS



**Angelika Görg**

Technische Universität München, Vice President of the German Proteome Society, Munich, Germany

Since the early 1980's, Prof. Görg has had a long-standing involvement in the development and application of innovative one- and two dimensional electrophoresis techniques for a wide range of biochemical, medical, microbial and agricultural applications. Angelika Görg has been involved in developing and introducing the

technology of immobilized pH gradients (IPG) in 1982. Since that time, Prof Görg and co-workers have pioneered the development of 2-D electrophoresis technology with IPGs (IPG-Dalt) for proteome analysis, by introducing IPG strips cast on plastic backings, as well as narrow and wide pH range IPGs with long separation distances, and IPG gels for the separation of very alkaline proteins up to pH 12 (Electrophoresis 1988 & 2000; Proteomics 2004). This technology has been constantly refined and has become - in combination with mass spectrometry- the basis for the majority of the ongoing proteome projects. More recently, for the detection of low abundance proteins in micropreparative 2-D gels using narrow pH range IPGs in the first dimension, a simple prefractionation method according to pI using flat-bed Sephadex IEF has been introduced (Proteomics 2002).

Prof. Görg, former President of the German Electrophoresis Society (DEG) from 1992 to 2001, is currently Vice President of the German Society for Proteomic Research (DGPF) founded in 2001 and Council Member of the Human Proteome Organization (HUPO). Prof. Görg is Senior Editor of the Journal Proteomics (Wiley,

In recognition of her methodical work, Prof. Görg received scientific awards in Glasgow (1992) and Tokyo (1994) from the British and Japanese Electrophoresis Societies, respectively, and was awarded the Heinz-Maier-Leibnitz Medal in 2001, as well as the "Bundesverdienstkreuz am Bande" in 2003 in Munich.

In October 2004 at the 3rd World Congress of HUPO in Beijing, Prof. Görg received "in recognition of her indispensable contributions to the field of proteomic sciences" the Distinguished Achievement Award in Proteomics. After studying Biochemistry and Food Chemistry at the Universities of Tübingen and Stuttgart, Angelika Görg received her Ph.D. degree from the Technical University of Munich. In 1992, Dr. Görg was appointed Professor at the Technical University of Munich, and is now Head of the Proteomics Group.



**Matthias Mann**

University of Southern Denmark, Odense and Max-Planck Institute for Biochemistry, Martinsried, Germany

Matthias Mann, a German native, was trained in physics and mathematics and studied with John Fenn for his Ph.D. which he received from Yale University in 1989. After postdoctoral work with Peter Roepstorff in Denmark, he became group leader at the European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany. Since 1998

he has been full professor at the University of Southern Denmark, Odense where he is now the director of the Center for Experimental Bioinformatics (CEBI). From July 2005 he will be a director at the Max-Planck Institute for Biochemistry in Martinsried, near Munich.

Dr. Mann's work in mass spectrometry and proteomics stretches back for 20 years, starting with work on the electrospray ionization method and today encompasses a



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31<sup>st</sup>**

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wide spectrum of cell signaling problems which his group approaches with proteomic techniques. He has been elected member of the European Molecular Biology Laboratory (EMBO), visiting professor at Harvard Medical School as well as the Danish Society of Arts and Sciences. He is author or co-author of more than 250 publications and is the recipient of many international prizes.

Matthias Mann has been involved in mass spectrometry based proteomics from the very beginning. As a graduate student with John Fenn at Yale University, he was a member of the team that developed electrospray, a key technology that won the Nobel prize for John Fenn in 2002. Later, his group at the European Molecular Biology Laboratory pioneered a set of technologies consisting of the first algorithm to identify peptides in sequence databases by their mass spectrometric fragmentation spectra ('Peptide Sequence Tag' algorithm), a method to make small amounts of gel separated proteins amenable to mass spectrometry and a miniaturized, highly efficient version of electrospray working at extremely low flow rates ('nanoelectrospray'). This allowed extremely sensitive protein sequencing and resulted in the cloning of important biological molecules such as the catalytic subunit of telomerase and caspase-8. His group performed the first, large scale identification of proteins linking 'proteome' to genome for the first time. His group also initiated work on protein-protein interaction detection by mass spectrometry and first used mass spectrometry to characterize multi-protein complexes. Recently, Dr. Mann's group described a quantitative proteomics technology termed Stable Isotope Labeling with Amino acids in Cell culture or SILAC. The SILAC technology has been applied to signal dependent protein – protein interactions and to quantify relative changes in phosphorylation upon signaling. By comparing several states, SILAC has allowed the protein composition of the human nucleolus in response to perturbation to be determined and allowed mapping the time-order of activation in signaling pathways. These developments now allow proteomics to study dynamic processes.



**John R. Yates III**

Department of Cell Biology, SR11, The Scripps Research Institute, LaJolla, CA, United States

Mass spectrometry has emerged as a powerful technique for cellular proteomics, complementing traditional gene-by-gene approaches with a comprehensive description of the molecular factors contributing to a biologically relevant system. Their lab remains at the forefront of this field, developing new strategies to address more sophisticated

scientific questions through proteomics, such as how to quantify global changes in protein abundance for mammalian systems, how to characterize complex post-translational modifications, and what information can be gained by comparing the proteome with the transcriptome.

Quantitative mass spectrometry-based proteomics methods rely on strategies that introduce an internal isotopic standard for every protein to be characterized. The preferred method to introduce these standards is by metabolic labeling (i.e. providing an isotope-labeled amino acid in culture medium), however this approach has been limited to microorganisms and simple model organisms. Recently, their lab developed a method to generate <sup>15</sup>N-labeled proteins and peptides in *Rattus norvegicus* tissues, achieving atomic enrichment >90% in liver and plasma. There are countless possibilities for the application of this labeling strategy for comparative proteomic analyses of mammalian tissues, particularly for studying animal models of disease. In addition, a novel technique was developed for comparing the abundance of peptides with internal isotopic standards from tandem mass spectra. Whereas most quantitative proteomics approaches measure these differences at the level of the mass spectra of intact peptides, by instead quantifying the fragmented peptide,

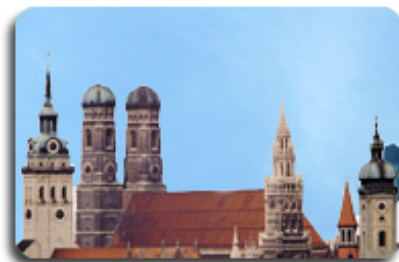


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the signal-to-noise and dynamic range of these measurements was improved dramatically.

The characterization of post-translational modifications also represents an emerging application of mass spectrometry-based proteomics. The modification of cellular factors by SUMO (Small Ubiquitin-related Modifier Protein) is an essential process in budding yeast, but the identities of the substrates remain largely unknown. Using proteomics techniques, 271 new SUMO targets were identified, illustrating for the first time the diverse roles that SUMO plays in regulating eukaryotic cells. This work also revealed coordinated SUMO modification of multiple proteins in well-defined macromolecular complexes. This intriguing result suggests that sumoylation may target protein complexes rather than individual proteins. Additional work in their lab focuses on characterizing the mechanism underpinning this observation.

Finally, in collaboration with Elizabeth Winzeler's lab in the department, a genome-wide comparison of global protein and mRNA transcript abundance was performed for several stages throughout the life cycle of *Plasmodium falciparum*. Previous work in other labs suggested there is little correlation between mRNA and protein abundance, however this comparison showed a significant correlation in *P. falciparum*, particularly when a delay between the synthesis of mRNA transcripts and proteins was considered. Interestingly, correlating mRNA and protein expression profiles for individual genes revealed particular families of functionally related genes that appeared to observe similar patterns of mRNA and protein accumulation. This gene-by-gene correlation analysis identified those genes that are most likely regulated by post-transcriptional controls, and will be useful for future studies to unravel the molecular mechanisms underlying this type of regulation.



**Mathias Uhlen**

Royal Institute of Technology (KTH), Stockholm, Sweden

Mathias Uhlen has for more than 25 years been working in the field of protein research. In the early eighties, he cloned and characterized the genes for protein A and protein G. These biomolecules are now extensively used for purification of antibodies to be used both in diagnostics and therapy. He also showed for the first time in 1983 that affinity tags can be used for purification of recombinant

proteins. Affinity tags are now widely used in research and industry and they have become one of the most important technical tools in the fields of protein engineering, proteomics and structural genomics. In the late eighties, Uhlen and colleagues published for the first time the use of magnetic microspheres with streptavidin for automated solid phase applications. Such laboratory systems based on streptavidin beads are now widely used both in research and diagnostics. In the early 1990's he established that using "protein engineering" new biomolecules, called Affibodies, could be selected and used for research, diagnostic and therapeutic purposes. Towards the end of the 1990's, Professor Uhlen led a research project to simplify the analysis of DNA that led to Pyrosequencing, a methodology that is currently used for genetic analysis in clinical research and forensic science. In the late 1990's, he was responsible for the set-up of a genome center at the Royal Institute of Technology which subsequently sequenced the whole genome of a pathogenic bacterium *Mycoplasma mycoides* and established a transcript profiling unit with "in-house" generated micro arrays. Since early 2000, Uhlen has focused his research on proteomics efforts and is currently responsible for the Swedish Human Protein Resource Project (HPR), the aim of which is to systematically map the human proteome using antibody-based proteomics ([www.hpr.se](http://www.hpr.se)). In 2004, he was elected chair of the HUPO Human Antibody Initiative (HAI).

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We look forward to welcoming you in Munich