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WELCOME to the fifth issue of the HUPO 4th Annual World Congress newsletter. In this edition, we feature updates from our speakers, provide you with Plenary details, introduce the final program so that you may plan your agenda in advance, and finally invite you to plan your tours and excursions in and around Munich.

UPDATES FROM OUR SPEAKERS



Erin O'Shea

Erin O'Shea is a Professor of Biochemistry and Biophysics at the University of California, San Francisco and an Investigator of the Howard Hughes Medical Institute. She received her undergraduate degree in biochemistry from Smith College and her Ph.D. in chemistry from the Massachusetts Institute of Technology. Her PhD work done with Peter Kim. She carried out her postdoctoral research with Robert Tjian at the University of California, Berkeley and with Ira Herskowitz at the University of California, San Francisco. Her honors include the National Academy of Sciences Award in Molecular Biology, a David and Lucile Packard Foundation Fellowship, a Presidential Faculty Fellow Award, the American Society for Cell Biology—Promega Early Career LifeScience Award, and the Irving Sigal Young Investigator Award from the Protein Society. She is a member of the American Academy of Microbiology, the American Academy of Arts and Sciences, and the National Academy of Sciences.

In collaboration with Jonathan Weissman's lab (HHMI, UCSF), Dr. O'Shea has developed reagents and methods to study the complete complement of proteins from budding yeast. Ultimately, they seek to be able to monitor dynamic changes in the protein abundance, localization, and post-translational modification of the proteome. To enable these studies, they have constructed two collections of ~5000 yeast strains, each expressing a single protein fused to an epitope tag for measurement of protein abundance (the TAP tag), or fused to the green fluorescent protein (GFP) to facilitate studies of protein localization. Two studies characterizing protein abundance and subcellular localization in the yeast proteome (Ghaemmaghami et al, Nature 2003; Huh et al, Nature 2003) have already been completed. They are now focused on the following studies: (1) characterizing protein lifetimes; (2) screening the proteome for protein kinase substrates; (3) investigating dynamic changes in protein subcellular localization.



Fuchu He

Fuchu He is a professor of Radiation Medicine at the Beijing Institute, the Director of China's National Center of Biomedical Analysis, and the President of the Institutes of Biomedical Sciences at Fudan University. He received his B.S. degree in Genetics from Fudan University, Shanghai in 1982 and earned his M.S. degree in Biochemistry and Ph.D. in Cell Biology from the Beijing Institute of Radiation Medicine.

Since 1997, through cooperation with analytic scientists, Prof. He has introduced and established a supporting technical platform for proteomics in China, and has carried out research on comparative proteomics about SARS-CoV, human fetal liver, and ES cell differentiation, and apoptosis initiation and metastasis of cancer cells. This team has found and characterized a series of protein sets associated with ES cell differentiation, apoptosis initiation and metastasis of cancer cells.

Recently, as the chief scientist, Dr. He initiated a series at the Chinese Human Proteome Programs, set up the Chinese Human Proteome Organization, directed the Beijing (National) Proteome Research Center, and then pioneered the international HUPO Human Liver Proteome Project (HLPP). He has been appointed as the Chair of HLPP Committee by HUPO council. He has also been a senior editor of PROTEMICS since 2002, and presided over the 3rd HUPO World Congress in 2004. His dedication and contribution to HLPP was remarkably applauded by international entities (Cyranoski D. China takes centre stage for liver proteome.

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Nature 425:441, 2003; Service RF. Public projects gear up to chart the protein landscape. Science 302:1316, 2003; Jia H. China pushes liver proteomics. Nature Biotech 22:136, 2004).

Beyond proteomics, his scientific achievements include: discovering and cloning hepatopoietin (HPO) from human fetal liver and characterizing its receptor and both autocrine and intracrine signal transduction pathways; discovering four periodic phenomena - namely "development-related evolution" of cytokines, "co-evolution" of cytokines and their receptors, "modulated evolution" of mRNA coding regions and their non-coding regions, and "slowing-down evolution" of molecules during phylogeny; establishing the most comprehensive gene expression profile of human fetal liver and annotating more than 100 human novel genes; and identifying ten susceptibility genes for chronic HBV infection and cancers.



Peter Roepstorff

Since 1975, Dr. Roepstorff has been a professor of Protein Chemistry at the Department of Biochemistry & Molecular Biology, University of Southern Denmark (formerly Odense University). He is also the director of the Danish Biotechnology Instrument Center (DABIC), which comprises fifteen research groups from five different universities. He graduated in Chemical Engineering from the Danish Technical University in 1966 and was a research associate at the Danish Institute for Protein Chemistry until 1975. From 1991-1995 he directed the Protein Engineering Research Centre under the Danish Biotechnology Programme and from 1995-1999 the research unit for Studies of Interaction, Structure, Function and Engineering of Macromolecules by NMR Spectroscopy under the same programme. In addition, from 1998 to 2002, he was director of the Center for Experimental Bioinformatics under the Danish National Research Foundation. He has published more than 350 papers on protein mass spectrometry and is member of the editorial boards of several journals on mass spectrometry and proteomics.

Dr. Roepstorff is one of the pioneers in protein mass spectrometry and proteomics. For more than 35 years his research focus has been on the use of mass spectrometry in protein chemistry. He is the founder of the Protein Research Group at the University of Southern Denmark, which has a long tradition for development of methodology for protein analysis by mass spectrometry and for development of bioinformatics tools for the use of mass spectrometry in protein chemistry.

His current research efforts include:

- Applications of mass spectrometry in proteomics research.
- Identification of proteins isolated from microorganisms and diseased tissue.
- Characterisation of post translationally modified proteins, including glycoproteins, phosphoproteins and truncated proteins.
- Membrane specific proteomics designed for transmembrane proteins and GPI anchored proteins
- Investigation of macromolecular complexes, such as protein-ligand, protein-protein and protein-DNA interactions.
- Development of bioinformatics tools to interface experimental data with database information



Richard Simpson

Professor Simpson received his PhD in biochemistry and chemistry at Melbourne University, Australia in 1974. After post-doctoral studies at the NIH, Bethesda, Maryland, he returned to Australia as a Research Fellow at St. Vincent's Institute of Medical Research, Melbourne. He is currently Head of the Joint Proteomics Laboratory of the Ludwig Institute for Cancer Research and the Walter and Eliza Hall Institute of Medical Research, a Research Professor at the University of Melbourne and Adjunct Professor at Yonsei University. He is a Vice-President of the Human Proteome Organization (HUPO), Chairperson of the HUPO Finance Committee and President of the Asia-Oceania HUPO Executive Committee. On a national level, Professor Simpson is President of the internationally-recognized Lorne Conference on Protein Structure and Function and President of the newly-formed Australasian Proteomic Society (APS).



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Tour Information

If you are interested in visiting Munich and its surroundings and wish to plan your tours in advance, you are invited to visit our supplier's [Autobus Oberbayern website](#)

Vouchers for these tours will be available for purchase in the registration area as well as at your hotel's concierge.

Professor Simpson has made major contributions to the field of analytical protein chemistry and pioneered many microsequencing strategies that have been developed further in protein micro analysis and proteomics. He has made key contributions to the field of cytokine receptor biology including the determination of the stoichiometry of the IL-6 receptor system and, more recently, he and his colleagues have determined the three-dimensional structure (by X-ray crystallography) of the ectodomain of the human IL-6 receptor. Recently, he has developed a major program in proteomic analysis of colorectal cancer, especially in the area of novel biomarker discovery. He is on a number of editorial boards, including the Journal of Biological Chemistry, Biochem. Biophys. Acta, Biochemistry Journal (UK) and Proteomics (Senior Editor). Professor Simpson was elected an Honorary Member of the American Society of Biochemistry and Molecular Biology in 1996, awarded the AMRAD Pharmacia Medal from the Australian Society for Biochemistry & Molecular Biology, and was an elected councilor of the Protein Society (1993-1996). In 1995 Professor Simpson was elected Fellow of the Australian Academy of Technological Sciences and Engineering (FTSE) and in 2003 was awarded the Centenary Medal from the Australian Government "For service to Australian society in research and development". He has published over 300 research publications and holds 16 patents. With the Cold Spring Harbor Laboratory Press, Professor Simpson has written a leading text book on proteomics – Proteins and Proteomics: A Laboratory Manual (2003) and, more recently, edited the book Purifying Proteins for Proteomics: A Laboratory Manual (2004).

CONGRESS PLENARY SESSIONS

We are pleased to present the following Plenary Sessions. For complete details of the congress program, please visit www.hupo2005.com/week.htm

We invite you read more about the content of the 9 Plenary sessions.

An Organized Effort in Proteomics: The HUPO Initiatives	S. Hanash
Proteomics Plenary Lectures	D. Hochstrasser, P. Bork, J. van Oostrum, M. Uhlen
Pioneers in Proteomics	P.O. Farrell, J. Fenn, F. Hillenkamp, A. Bairoch
Proteomics Technologies	J. Yates, A. Görg, R. Zubarev
Subproteomes	J. Bergeron, M. Mann, J. Vandekerckhove, A. Heck
Model Organisms	E. O'Shea, M. Hecker, H. Barbier-Brygoo, A. Slabas
Interaction Proteome	F.U. Hartl, B. Küster, W. Kolch
European and International Collaboration in Proteomic Research	A. Abbott, E. Mann, J. Fenn, M. Mann, H. Langen
System Biology	R. Aebersold, S. Brunak, L. Serrano

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Please do visit our website www.hupo2005.com to get all important congress information!

We look forward to welcoming you in Munich