CANCER SCIENCE INSTITUTE OF SINGAPORE

SEMINAR ANNOUNCEMENT

Matthias Mann



Professor and Director, Max-Planck Institute of Biochemistry, Munich and Novo Nordisk Foundation Center for Protein Research, Copenhagen

Proteomics in cell signalling and cancer research

Date: Wednesday, 10 February 2016

Time: 10am – 11am

Venue: CeLS Auditorium, Centre for Life Sciences
(28 Medical Drive, Singapore 117456)

Host: Dr. Dennis Kappei

Abstract:

Mass spectrometry based proteomics has advanced tremendously in the last few years. We describe a shotgun proteomics workflow that allows us to detect and quantify the large majority of the proteins expressed in a biological system such as cancer cell lines and even formalin-fixed, paraffin embedded material. This included streamlined and highly efficient sample preparation, analysis with very high sequencing speed using modern mass spectrometers and bioinformatic analysis using the MaxQuant and Perseus platforms. Efforts in our group have focused on 'single shot' analysis and we demonstrate very high coverage in this mode (Mann et al., Mol. Cell, 2013). We have also extended this concept to the analysis of interactomes (Hein et al. Cell 2015) and phosphorylation, where the 'EasyPhos' method now allows acquiring large numbers of phosphoproteomes, for instance for the analysis of in vivo signaling (Humphrey et al. Nat. Biotech, 2015). Together such developments make proteomics increasingly relevant to translational research as I will discuss in this talk.

Biography:

Matthias Mann studied physics and mathematics at Göttingen University in Germany and obtained his Ph.D. in chemical engineering at Yale University. Here he was decisively involved in the development of electrospray ionization, now a key technology of the life sciences. As a post-doctoral fellow and later as a professor for bioinformatics at the University of Southern Denmark in Odense, he developed, amongst others techniques, the first bioinformatics search algorithms for peptide fragmentation data and SILAC, a new method of quantitative proteomics and a breakthrough in the mapping of protein interactions. In 2005, Matthias Mann took up a director position at the Max-Planck-Institute of Biochemistry in Munich. Here his group continues to address a wide range of biological questions using proteomic technology, as well as to develop this technology. The group is also heavily involved in providing proteomic methods and tools to the community. Most prominently, they have provided the MaxQuant suite of computational proteomics algorithms. More recently his group used the SILAC technology in conjunction with MaxQuant to describe the first comprehensive identification and quantification of a proteome. In 2009 Dr. Mann was additionally appointed director of the proteomics department of the Novo Nordisk Foundation Center for Protein Research in Copenhagen. Matthias Mann has authored and co-authored more than 580 publications with a total citation count of more than 100,000, making him one of the most highly cited researchers worldwide. In 2012 he was awarded the Leibniz Prize from the German Research Foundation, the Ernst Schering Prize, the Louis-Jeantet Foundation Prize for Medicine and the Körber European Science Prize. In 2015 he has been awarded the Barry L. Karger Medal in Bioanalytical Chemistry and the Theodor Bücher Lecture and Medal.