Professor Bernhard Küster

Prof. Küster holds the Chair for Bioanalytics at the Technical University Munich. He obtained a PhD in Biochemistry from the University of Oxford in 1997 for which he won the Mattauch-Herzog Award of the German Mass Spectrometry Society. He did a postdoc funded by an EMBO long-term fellowship at the EMBL in Heidelberg in the laboratory of Matthias Mann and was later appointed Research Associate Professor at Odense University, Denmark. Between 2000 and 2007, Prof. Küster served in a number of functions at Cellzome, Heidelberg, most recently as Vice President Analytical Sciences and Informatics. Research in his laboratory focuses on the development of affinity-based and quantitative mass spectrometry approaches and their application to functional and chemical proteomics as well as biomarker discovery.

During the "Quantitative Proteomic Course" in Bergen June 7th – 11th 2010, he will give two lectures that will be free to attend for people at UiB.

Lecture 1: Monday, June 7th in the Conference room of BBB, kl. 13:00 – 14:00

Chemical modification of peptides and proteins for quantitative mass spectrometry

Quantitative mass spectrometry for proteomics can be divided into approaches that either utilise the MS intensity directly or employ stable isotope labelling to compare the relative quantities of two or more samples. Stable isotopes may be introduced into peptides metabolically, enzymatically or chemically. In this one hour lecture, I will give an overview about the most commonly used chemical labelling strategies including some of the underlying ideas and chemical principles. A focus will be placed on commercially available reagents and those that are easily performed in the laboratory.

Lecture 2: Tuesday, June 8th in Auditorium 4 of BBB, kl. 09:00 – 10:00

Example applications of iTRAQ and TMT labelling for quantitative proteomics

Among the many choices for stable isotope labelling for quantitative mass spectrometry, methods that allow multiplexing of samples are particularly attractive. In particular, the commercially available reagents iTRAQ and TMT enable any laboratory to take advantage of this technology. In this lecture, I will give examples from my laboratory for the application of this technology including the proteome wide selectivity profiling of kinase inhibitors and the analysis of protein-protein interactions.