Dr Sander Piersma

Dr. Sander Piersma joined the OPL (OncoProteomics Laboratory) as a research associate at the start in April 2006. He studied Chemistry at the University of Amsterdam (1993), obtained his PhD in the Dept. of Enzymology at the Technical University of Delft (1998), and was a post-doc at the RIKEN Institute in Tokyo and at TNO. He worked as project leader at the Institute for Atomic and Molecular physics on development of imaging mass spectrometry. His research interest is development of innovative mass spectrometry-based proteomics for cancer research and biomarker discovery. At the OPL he is responsible for the nanoLC-LTQFTMS workflows. Furthermore, his focus is on chemical proteomics and secretome analysis.

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

Lecture: Wednesday, June 9th in Auditorium 4 of BBB, kl. 13:00 – 14:00

Label-free quantitation

Label-free quantitation is becoming a popular strategy for protein quantitation in large-scale proteomics experiments. Label-free proteomics comes in different flavours and can be MS1 (XIC and spectral intensity) or MS2 (spectral counting) based, but all approaches share one feature: no isotopic labelling is required for protein quantitation. Advantages over labelling based approaches such as iTRAQ and SILAC include cost (no labelling reagents required) and flexibility of experimental design (many vs many samples). Disadvantages include no multiplexing capability and demand for stable LC-MS/MS data acquisition.

The label-free quantitation block will include an overview of label-free protein quantitation strategies and data analysis and statistics approaches for detection of differential proteins in comparative proteomics experiments. Protein quantitation by spectral counting will be described in detail and a case study of our own research will be presented (Piersma et al. J Proteome Res. 2010 Apr 5;9(4):1913-22).