Dr Frode Berven

Frode S. Berven (Ph.D.) has been the head of the Proteomics Unit at University of Bergen since 2009. He has been working in the proteomics field for nine years, during his master, Ph.D, and post doctor position. During his post doctor period and in his current position, Berven has been focusing on biomarker discovery in the cerebrospinal fluid of multiple sclerosis patients using state of the art mass spectrometry based quantitative proteomics. From 2008 until June 2009 Berven did his research in quantitative proteomics at the Proteomics Platform at the Broad Institute of MIT and Harvard in the group of Steven Carr.

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: Thursday, June 10th in Auditorium 4 of BBB, kl. 09:00 – 10:00

Targeted protein quantification using mass spectrometry

There has always been a problem to quantify proteins with good enough specificity, reproducibility, accuracy and detection limit, especially in a multiplexed fashion. The usual way to do this is to use western-blotting or a global semi-quantitative mass spectrometry based method like iTRAQ or alternatively by using stained 2-DE gels. All of these approaches have limitations and drawbacks in this setting. An ELISA assays is a good alternative, but only exists for a few proteins. Now there is a new mass spectrometry method that has a great potential to fill this empty space, namely Stable Isotope Dilution Multiple Reaction Monitoring (SID-MRM). The principle of this method is to spike into each sample the same amount of heavy peptides that represents your target protein and use this as an internal standard in the analysis. The mass spectrometer is then set to only look for these peptides and will then increase its sensitivity dramatically. By using this technique, one can compare the relative ratio of many peptides (>100) representing many proteins (>30) between many samples in a fast, accurate, specific, sensitive and reproducible way. One can also get an absolute quantitative measurement for a protein, and tailor the assay to target only certain areas of a protein, for example areas with modifications or those unique for a protein isoform. The possibilities of SID-MRM will be presented.