Abstract Carol Nilsson lecture: 2004-04-15, kl 18:15.

Title: High Resolution Mass Spectrometry for Structural Proteomics

With the understanding that describing complete genome sequences alone would not fulfill its expectations, the science of proteomics was born. Proteins are the functional mediators of many cellular processes, and changes in protein expression and/or structure may reflect cellular states. By comparing any organism's genome sequence to its proteome, it is obvious that the number of proteins outstrips the number of genes. This discrepancy is especially pronounced in higher organisms. One reason for the larger number of proteins is the existence of protein post-translational modifications. New techniques are being developed for targeting protein modifications such as phosphorylation and glycosylation, through visual comparison of two-dimensional gels and structural characterization by mass spectrometry. Through a donation made by the Knut and Alice Wallenberg Foundation, a technical platform for high-throughput analysis of protein post-translational modifications by Fourier transform ion cyclotron resonance mass spectrometry will be made available in Göteborg (serving southern Sweden) and Uppsala (serving northern Sweden). Examination of proteome-wide pattern changes in phosphorylation or glycosylation in diseased tissues can increase our understanding of pathophysiological mechanisms and identify novel therapeutic targets. Examples of these techniques will be described from the realm of clinical neuroscience, including neuro-oncology and neurodegeneration.