Program

10.30 h : Bevezető (Dr. Hajós Péter, PE Analitikai Kémia Intézeti Tanszék)

10.35- 11.20 h :

Threading Protein Expressions into Disease Surveillance Strategies by Modern Analytical Methods

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Many of the modern approaches for studying disease compare steady state functions, such as repair, growth, and regulated gene expression within the various biological compartments organised by specialized function, be it mitochondria or blood vessels. The assignment of protein identities, which are linked to key biological mechanisms, which are associated with disease processes and disease progressions are an important area of this work. Today, the technology available for studying proteome expression and resolving exact protein and peptide identities in complex mixtures of biological samples allows global protein expression within cells, fluids, and tissue to be approached with confidence. This confidence is due in part to reproducible repetitive sampling and analysis technologies including robotics data acquisition and high level mass spectrometry including both laser-desorption and electrospray ionisation. The precision in defining differences between normal and diseased steady states is aided by the creation of compiled reference and master data sets and by new methods for multiplexing the analysis of samples in groups. The establishment of key representative reference proteome systems representing the dynamic changes in protein expression during disease will be vital to the interpretation of changes observed in specific samplings of disease states and specific cells obtained from these samples. The creation of reference databases of proteins linked to disease pathways will play an important role in furthering our understanding of the "proteome of disease". Examples will be given where protein expression patterns have been generated from compartments within tissue sections as well as clinical studies directed to drug action and biomarker developments.