**Recent Publications**

**CHESS: a New Human Gene Catalog Curated from Thousands of Large-Scale RNA Sequencing Experiments Reveals Extensive Transcriptional Noise**  

**Discovery and Quantification of Non-Human Proteins in Human Milk**  

**Alzheimer’s Disease Phenotype or Inflammatory Insult Does Not Alter Function of L-Type Amino Acid Transporter 1 in Mouse Blood-Brain Barrier and Primary Astrocytes**  

**Multiplex Assay for Quantification of Acute Phase Proteins and Immunoglobulin A in Dried Blood Spots**  

**Multiple-Enzyme-Digestion Strategy Improves Accuracy and Sensitivity of Label- and Standard-Free Absolute Quantification to a Level That Is Achievable by Analysis with Stable Isotope-Labeled Standard Spiking**  

**A rapid non-target screening method for determining prohibited substances in human urine using liquid chromatography/high-resolution tandem mass spectrometry**  

**Absolute quantification of targeted meat and allergenic protein additive peptide markers in meat products**  

**Tissue and plasma proteomics for early stage cancer detection**  

**Layers of regulation on cell-cycle gene expression in the budding yeast Saccharomyces cerevisiae**  

**Quantification of protein markers monitoring the preanalytical effect of blood storage time before plasma isolation using 15N metabolically labeled recombinant …**  

**Dysregulation of mucosal membrane transporters and drug metabolizing enzymes in ulcerative colitis**  

**Using Stepwise Pharmacogenomics and Proteomics to Predict Hepatitis C Treatment Response in Difficult to Treat Patient Populations**  

**Quantification of membrane transporter proteins in human lung and immortalized cell lines using targeted quantitative proteomic analysis by isotope dilution nanoLC-MS/MS.**  

**Stereocilia-staircase spacing is influenced by myosin III motors and their cargos espin-1 and espin-like**  

**A new mass spectrometry-based method for the quantification of histones in plasma from septic shock patients**  

**Improving selectivity and sensitivity of protein quantitation by LC–HR–MS/MS: determination of somatropin in rat plasma**  

**A crude-MS strategy for in-depth proteome analysis of the methane-oxidizing Methylocystis sp. strain SC2**  

**Biochemical characterization of human tissue kallikrein 15 and examination of its potential role in cancer**  
Expression profile of human tissue kallikrein 15 provides preliminary insights into its roles in the prostate and testis
Panagiota S. Filippou et al., Clinical Biochemistry (2018) – PMID: 29958881

Elucidation of chemical modifier reactivity towards peptides and proteins and the analysis of specific fragmentation by MALDI-CID-MS2.

Cerebrospinal Fluid C-Reactive Protein in Parkinson’s Disease: Associations with Motor and Non-motor Symptoms
Hossein Sanjari Moghaddam et al., NeuroMolecular Medicine (2018) – PMID: 29980980

Extracellular Prolyl Oligopeptidase Derived from Activated Microglia is a Potential Neuroprotection Target
Teemu A. Natunen et al., Basic & Clinical Pharmacology & Toxicology (2018) – PMID: 29998529

ProteomeTools: Systematic characterization of 21 post-translational protein modifications by LC-MS/MS using synthetic peptides

Quantification of Membrane Transporter Proteins in Human Lung and Immortalized Cell Lines Using Targeted Quantitative Proteomic Analysis by Isotope Dilution nanoLC-MS/MS

ProteomeTools: Systematic characterization of 21 post-translational protein modifications by LC-MS/MS using synthetic peptides

Targeted Mass Spectrometry-Based Assays for Relative Quantification of Thirty Brain-Related Proteins and their Clinical Applications

Parsing and Quantification of Raw Orbitrap Mass Spectrometer Data Using RawQuant

Analysis of Histone Modifications by Mass Spectrometry

Mining the Human Tissue Proteome for Protein Citrullination
Lee et al, Molecular and Cellular Proteomics (2018) – PMID: 29610271

Quantification of Urinary Protein Biomarkers of Autosomal Dominant Polycystic Kidney Disease by Parallel Reaction Monitoring

An MRM-Based Cytokeratin Marker Assay as a Tool for Cancer Studies: Application to Lung-Cancer Pleural Effusions

Quantitative Proteomics and SWATH-MS to Elucidate Peri-Receptor Mechanisms in Human Salt Taste Sensitivity

Prioritizing Popular Proteins in Liver Cancer: Remodelling One-Carbon Metabolism
Mora et al., J Proteome Res. (2017) – PMID: 28944671

Quantitation of 87 Proteins by nLC-MRM/MS in Human Plasma: Workflow for Large-scale Analysis of Biobank Samples
Rezeli et al., J Proteome Res. (2017) – PMID: 28738677

A Comparative VUV Absorption Mass-spectroscopy Study on Protonated Peptides of Different Size