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TALKS

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About these abstracts

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differential processing of proenkephalinergic and proopiomelanocortin (POMC) systems among controls, prolactin-secreting microadenomas, and non-secreting macroadenomas. We will present our discovery data on growth hormone (GH) isoforms, differentially expressed proteins ($n = 56$) between controls and macroadenomas, novel phosphoproteins, and oxidative stress nitroproteins (NS). All of these data profoundly impact on our knowledge of human neuroendocrinology.

S-39-3
Omics in precision medicine

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It has been estimated that only Alzheimer's disease (AD) alone, the most common form of dementia, will affect approximately 81 million individuals by 2040. To date, the actual cause and cascade of events in the progression of many neurological and neurodegenerative diseases have not been fully determined. Furthermore, there is no definitive blood test or simple diagnostic method for many of those diseases so far available. Fibril formation of proteins, together with a dysfunctional regulation of lipids and steroids, has been shown to play a fundamental role influencing various risk factors of neurodegeneration and pathogenesis. Recently, there has been a stronger focus on proteomics and metabolomics (e.g. lipidomic) studies with the hope of increasing our understanding of the underlying mechanisms leading to disease. Technological advancements in high-resolution mass spectrometry and rapid improvements in chromatographic techniques have led to quick expansion of the field of in this research. In this presentation, emphasis is given to the new developments in technologies and their applications in disease biomarker discovery.

S-39-2
Large-scale label-free clinical proteomics and phosphoproteomics for precision medicine

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The general goal of our clinical cancer proteomics efforts is to disclose tumor biology and drive improved diagnostics, treatment and management of cancer. To this end, we use label-free mass spectrometry-based proteomics that is optimally suited for large-scale clinical sample profiling. I will highlight our work in various cancer types with a focus on exosome proteomics for non-invasive diagnostics and phosphoproteomics for response prediction. More specifically, I will discuss our prostate cancer effort that made use of an innovative workflow for high-throughput extracellular vesicle proteomics applied to prostate cancer cell lines and urinary patient samples. Furthermore I will highlight our newly developed computational analysis approach for Integrative inferred kinase activity (INKA) analysis that can rank kinase activities in mass spectrometry-based phosphoproteome data derived from single samples. We show that INKA can uncover oncogenes, differential kinase activity and drug targets. We believe that cancer proteomics powered by precise measurements and dedicated analysis will realize the full potential of multi-parameter diagnostics and personalized medicine.

ShT-39-1
Semi-targeted metabolomic studies of methamphetamine's biotransformations and its impact on macrophage's secreted metabolome

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Methamphetamine (MA) is an illegal psychostimulant. Despite the prevalence of MA addiction, its effect on the innate immune system is not known. Several reports showed the effect of MA on various aspects of intracellular signaling, yet changes in intracellular and secreted metabolomes induced by MA in human monocyte derived macrophages (hMDM) has been understudied. In this study, we used a semi-targeted metabolomic approach to investigate the effect of MA on macrophages secreted metabolism. Culture supernatants from hMDM exposed to MA or controls were subjected to solid phase extraction (SPE, Plexa PCX) or liquid-liquid extraction and followed by reversed phase chromatography performed with two columns connected in-line (EC 50/2 Nucleodur C18 Pyramid, 3 μm and EC 150/2.1 Cogent, UDC-Cholesterol, 4 μm). A QTRAP 6500 MS/MS System with a Turbo Spray ion source (SCIEX, Framingham, MA, USA) working in multiple reaction monitoring mode (MRM) was used as a detection system. Selected MRM list was based on research papers, databases (e.g. HMDB, METLIN). During analytical work-flow, identity verification was found as the most critical step. It was performed using enhanced product ion mode (EPI) supported by a chemical characteristic of analytes (RPLC – polarity and SPE – acid-base properties). Results presented in this paper describe three novel aspects of metabolomic research. First, we present an attempt to analyze the metabolic secretome of hMDM exposed to Meth in comparison to non-exposed control cells. We measured 94 metabolites and identified 11 that were significantly different between control and Meth-exposed macrophages. Our new analytical approach, utilizing combined C18 and Cogent columns, allowed us to separate and identify OHMA isomers. Lastly, we have found two presumably unknown metabolites pending structural determination and confirmation. This work is supported by R01 DA043258 and P30 MH062261 grants from National Institutes of Health (USA).

ShT-39-2
Development of a diagnostic SARI test system based on protein microchip for detection and forecasting the severity of acute respiratory infections

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According to the World Health Organization (WHO), acute respiratory viral infections cause the overwhelming majority of all reported infectious diseases, yet methods for their molecular diagnosis are limited. The purpose of this study is to develop a multiparameter diagnostic assay, including a set of reagents, based on protein microchip technology, which allows personalized diagnosis of influenza-like illnesses and severe acute respiratory infections (SARI). Ideally, such diagnostics will be capable of determining etiological agents and providing prognostic