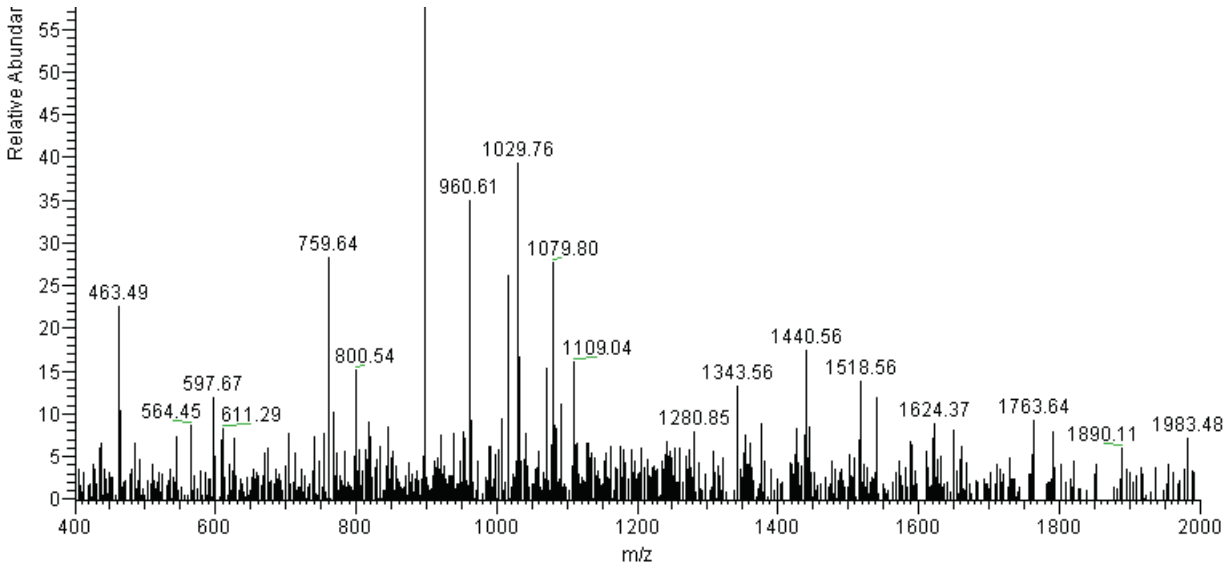
Proteomics and Metabolomics Core (PMC)

A University of Tennessee Health Science Center Institutional Core



MISSION

The PMC Core's mission is to provide the UTHSC campuses with state-of-the-art mass spectral technology and support to facilitate molecular-level discoveries that transform and advance our understanding of biological systems to solve challenging, relevant scientific questions in the life sciences.

INTRODUCTION AND SERVICES

In 2015, The Proteomics and Metabolomics Core (PMC) was established at UTHSC in Memphis, TN. The Core was created to provide resources for the highest quality mass spectrometry (MS)-based analysis supporting research needs in the fields of proteomics, metabolic profiling and metabolomics. The Core provides consultations to optimize experiment design and to interpret generated data. Services include identification and absolute or differential quantification of metabolites, drugs, and other small molecules in body fluids, cell and tissue extracts, identification of individual proteins in simple and highly complex protein mixtures, identification and mapping of posttranslational and other modifications of proteins, differential protein expression analysis based on precursor ion quantification (SILAC, dimethyl labelling), reporter ion quantification (iTRAQ/TMT labelling), and precursor ion area detection (label-free analysis), analysis of protein-protein interactions, and determination of the molecular masses of analytes.

The Metabolic Phenotyping MS facility (MPMS) within the PMC offers characterization of absolute and relative quantification of metabolites, such as those associated with glucose, lipid and protein metabolism, as well as specialized metabolite analyses.

EQUIPMENT AND SOFTWARE

The Core is equipped with a **Thermo Orbitrap Fusion Lumos mass spectrometer**- a tribrid mass spectrometer combining a Quadrupole, a Dual Linear Ion Trap, and Orbitrap mass analyzers able to perform CID, HCD, or ETD fragmentation, operate in parallel mode, and provide excellent resolution (500,000 FWHM @m/z 200), accuracy (1 ppm), sensitivity (quantification of 1 attomole at CV<15%), and high scan rate (20 Hz). The instrument operates in line with an ultra-HPLC system- Ultimate 3000RSLC Nano for nano-flow applications or Vanquish for micro-flow applications.

The software tools for system operation/data acquisition and postacquisition analysis of raw MS data include **Xcalibur/SII 4.1, Proteome Discoverer 2.2, PMI-Preview 2.14, PMI-Byonic 2.14, Compound Discoverer 2.1, Tracefinder 4.1, Lipidsearch 4.1**, and others.

The MPMS facility is also equipped with an **Agilent-7000C, QQQ gas chromatograph/Mass selective Detector (GC-MS/MS)**, a revolutionary advanced system with high efficiency & resolution, mass accuracy with low-to-high detection limits. Software tools include NIST 2014 MS Library Bundle & Mass Hunter Software program to enable absolute quantitative & mass accuracy detection (including isotope mass accuracy for isotope analysis).

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CORE DIRECTORS

David Kakhniashvili, PhD, is the director of the PMC at UTHSC. He earned his MS in Chemistry at Tbilisi State University (Rep. Georgia) and Ph.D. in Biochemistry at the Institute of Protein Research of Russian Academy of Sciences. Dr. Kakhniashvili has multiple publications in the field of proteomics related to red blood cells and sickle cell disease. He joined the UTHSC team in 2015.

Michelle Puchowicz, PhD, is the director of the MPMS facility within the PMC. She brings expertise in small molecule targeted metabolomics and stable isotopomer analysis through mass spectrometry based phenotyping techniques. These applications enable the identification of regulatory mechanisms that impact metabolism. Dr. Puchowicz earned a PhD in Nutritional Biochemistry from Case Western Reserve University and has over 17 years of collaborative expertise in the field of metabolism and whole body energetics. She joined the Division of Pediatric Obesity Program Team at UTHSC Memphis in summer of 2017.

STAFF

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