

# PROTEOMICS AND METABOLOMICS CORE (PMC)

The Proteomics and Metabolomics Core (PMC) provides state-of-the-art mass spectral technology and support to all UTHSC campuses. It facilitates molecular-level discoveries that transform and advance our understanding of biological systems to solve challenging, relevant scientific questions in the life sciences.

## SERVICES

The PMC provides resources for the highest quality mass spectrometry (MS)-based analysis, supporting research needs in the field of proteomics. Services include:

- Consultations to optimize experiment design and to interpret generated data
- Identification of individual proteins in simple and highly complex protein mixtures
- Identification and mapping of post-translational and other modifications of proteins
- Differential protein expression analysis based on precursor ion quantification (SILAC, dimethyl labeling), reporter ion quantification (iTRAQ/TMT labeling), and precursor ion area detection (label-free analysis)
- Analysis of protein-protein interactions, and determination of the molecular masses of analytes

## 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 post-acquisition analysis of raw MS data include **Xcalibur/SII 4.3 Proteome Discoverer 2.4, PMI-Preview 3.5, PMI-Byonic 3.5, Compound Discoverer 2.1, Tracefinder 4.1, Lipidsearch 4.1**, and others.

## STAFF



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

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**For more information:**

**PROTEOMICS AND METABOLOMICS CORE**

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