

MASS SPECTROMETRY AND PROTEOMICS CORE

BIOTECHNOLOGY SCIENCES AND ENGINEERING (BSE) BUILDING | ROOM 3.108A

ABOUT

The **UTSA Mass Spectrometry and Proteomics Core** provides a range of high-resolution, high mass accuracy mass spectrometry-based services to identify and characterize a range of analytes from small organic molecules to proteins and other biomolecules; proteomics; and LC-MS/MS.

The core was established in 2010 with support from the National Institutes of Health through the Research Centers in Minority Institutions (RCMI) program of the National Institute on Minority Health and Health Disparities.

SERVICES

- » High-resolution, high mass accuracy mass analysis (HRMS)
 - Small molecules
 - Peptides and peptide sequencing
 - Proteins
 - Antibody mass analysis
 - Organometallic compounds
- » Proteomics-based analyses
 - SDS-PAGE, In-gel digest, Mascot
- » Customized analyses possible

INSTRUMENTATION

- maXis quadrupole time-of-flight (QTOF) high-resolution mass spectrometer with electrospray ionization (ESI) and atmospheric pressure chemical ionization (APCI) sources
- timsTOF Pro II QTOF high-resolution mass spectrometer with trapped ion mobility
- Orbitrap Exploris 480 high-resolution mass spectrometer and Vanquish Neo nanoUHPLC equipped with electrospray ionization and nanospray ion sources

CONTACT

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