

Cell Biology

Analyze Proteins, lipids, and metabolites to provide insight into molecular biology of the cell.

CHARACTERIZE POST-TRANSLATIONAL
MODIFICATIONS SUCH AS
PHOSPHORYLATION AND GLYCOSYLATION

Investigate cell signaling pathways by analyzing changes in quantity and post-translational modification of specific signaling molecules.



Cancer Biomarker Discovery

Determine the differential expression of signature molecules in cancerous tissue.

QUANTIFY PROTEIN EXPRESSION USING
ISOBARIC TAGS FOR RELATIVE AND
ABSOLUTE QUANTIFICATION (ITRAQ)

Quantify protein expression using Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC), or by using semi-quantitative spectral count methodologies.



De-novo Peptide Sequencing

Offering peptide sequencing using algorithms to search the genomic sequence databases of hundreds of organisms.



Carolinan Medical Center

Uncompromising Excellence. Commitment to Care.



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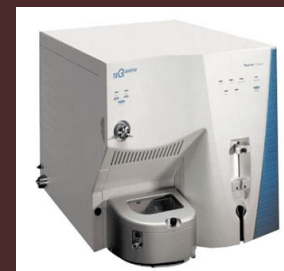
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Mass Spectrometry & Proteomics

CAROLINAS
MEDICAL CENTER

UNC-CHARLOTTE

CORE RESEARCH
FACILITY



Charlotte Region State-of-the-Art Mass Spectrometry & Proteomics Facility

LITQ-XL

LITQ-Oritrap ETD

TSQ-Quantum Ultra

Eksigent nano-2DLC

Waters ACQUITY UPLC

Waters NanoACQUITY UPLC

Mass Spectrometry combined with liquid chromatography pre-separation is used for identification of individual proteins at low femtomole concentrations with complex protein mixtures. Bioinformatics tools can be utilized to determine spectral count, allowing for semi-quantitative comparison of protein abundances among multiple samples.

The CMC/UNC-Charlotte Mass Spectrometry Core Facility is located in Cannon Research Center on the campus of Carolinas Medical Center. We can provide the biomedical research community with the most state-of-the-art technologies in mass spectrometry and proteomics applications. We welcome collaboration with researchers interested in the application of proteomics to their biomedical research.

Neuronal Disease

In brain, apply the proteomic approach to studies of the mechanisms involved in neuronal disease progression.

DIFFERENTIAL EXPRESSION OF NEUROTRANSMITTERS AND CO-FACTORS OF SIGNAL TRANSDUCTION MAY PROVIDE CLUES TO UNDERSTANDING NEURONAL DISEASE AS WELL AS THE PROTEIN REGULATION OF THE BRAIN

The differential expression profiling of small molecules, particularly molecules associated with one-carbon, is a fast growing field of study.



High-throughput Biomarker Validation

Validate putative candidates in studies with a larger number of samples utilizing selected ion monitoring (SIM) or multiple reaction monitoring (MRM)

IDENTIFY TARGETS WHICH CAN BE USED IN LARGER CLINICAL STUDIES WITH THE GOAL OF IDENTIFYING DIAGNOSTIC AND THERAPEUTIC STRATEGIES

Meta-genomics

This emerging discipline studies the genomics of an entire community of organisms with many potential applications to human health and disease. This field studies the human body as a host to microorganisms; as well as how microbes in the environment directly impact the livability of our environment. Utilizing proteomic techniques, further information can be determined as to how the microbial community affects human health and disease.

Microorganisms and Viruses

Analyze the changes in human tissues that reflect the responses and disruption of the host defense system.

THE HOST RESPONSE TO BACTERIA AND VIRUSES IN HUMAN DISEASES IS CRITICAL TO UNDERSTANDING THE DISEASES.

Analyze changes in microorganisms and viruses themselves using genomic databases and *de-novo* sequencing capabilities.



Phospho-signal Transduction

Phosphorylation is a key molecular event of cellular signal transduction. The low stoichiometry of this event makes it difficult to elucidate within the larger cellular protein complex

WE HAVE EXPERTISE IN THE APPLICATION OF PROTEOMIC STRATEGIES THAT ENRICH PHOSHOPEPTIDES VIA IMMOBILIZED METAL AFFINITY CHROMATOGRAPHY AND LC-MS/MS COMBINED WITH ELECTRON TRANSFER DISSOCIATION OR COLLISION

