

# VCU Research spotlights....

Chemical and Proteomic Mass Spectrometry Core Facility

February 2012

Virginia Commonwealth University

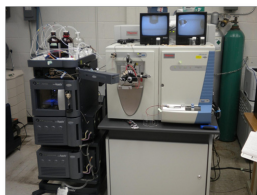
The Chemical and Proteomic Mass Spectrometry Core Facility is available to help meet your mass analysis needs. We are equipped for basic mass measurement of small or large molecules as well as proteomics experiments, ranging from simple protein identification to identifications of proteins in complex mixtures, analysis of post-translational modifications, and quantitation via iTRAQ labeling. Our instrumentation is state-of-the-art, with most purchased within the last two years. We have software for data analysis, and we return proteomics analyses to investigators using the Scaffold program.

## Services

- Basic Mass Measurement
- ESI-MS/MS
- LC-MS
- Exact Mass Measurement
- Protein Identification

## Instrumentation

**LTQ-OrbitrapVelos**, used for proteomics experiments. Provides extremely high sensitivity and mass accuracy. Fronted with a Waters nanoAcquity UPLC, which also has an SCX trap column, allowing MudPIT experiments for analysis of complex mixtures. Quantitation can be done via iTRAQ labeling. Post-translational modification analysis is also performed with this instrument.



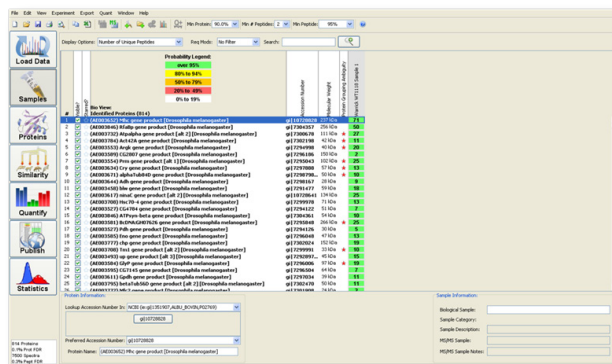
**QToF2** from Waters, used for basic mass measurement. Set up for direct infusion ESI. Samples must be free of salts and detergents.



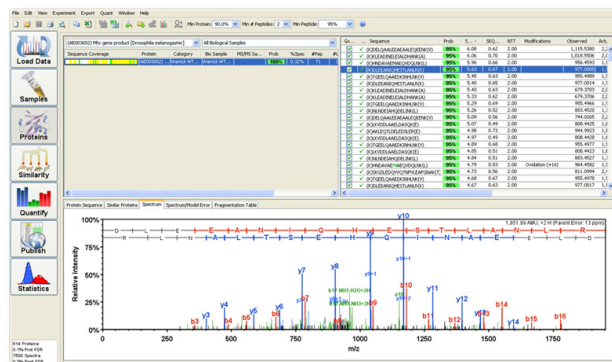
**5800 MALDI TOF-TOF** from AB Sciex bridges the gap. Small molecule samples with solubility issues or contamination with salts and detergents can be analyzed with this instrument. In addition, less complex proteomics samples (such as gel bands) can be separated with an offline LC and MALDI spotter, then analyzed with the 5800. It is also set up for quantitation with iTRAQ reagents.



## Results



Sample Scaffold file of a MudPIT run. Over 800 proteins were detected in 9 SCX fractionations. Investigators receive this list of proteins detected and peptides detected for each protein. Samples are run against species-specific databases, if one exists, or against NCBI's non-redundant database.



Double-clicking on a particular protein shows all the peptides detected within that protein. Investigators can view a map of where the peptides are within the protein sequence, view the fragmentation spectra, look at the probability scores, and more.

Contact Us! We offer a wide range of mass spectrometric services, from basic mass measurement to complex proteome analyses. We encourage investigators to contact the Mass Spec Core regarding their experimental needs, so that we can discuss how to get the best results for you.

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For more information, please visit <http://www.chemistry.vcu.edu/research/spect.html>

