

## Mississippi INBRE Proteomics Core Facility Equipment



### **Waters Xevo G2-S Mass Spectrometer**

Xevo® G2-S Quadrupole Time-of-Flight Mass Spectrometer is designed for scientists who need to identify, quantify and confirm the broadest range of compounds in complex and challenging samples. Its StepWave™ ion optics provides unsurpassed levels of durable sensitivity. With UPLC/MS<sup>E</sup> data acquisition, the Xevo G2-S OToF comprehensively catalogs complex samples in a single analysis. The Xevo G2-S OToF has fast data directed analysis (FastDDA), which allows full structural characterization of unknown compounds. It's Universal Ion Source Architecture enables the most extensive range of interface capabilities to service the broadest range of applications.



### **LTQ Velos Mass Spectrometer**

The Thermo Scientific™ LTQ XL™ Linear Ion Trap Mass Spectrometer is a mass spectrometer that offers multiple dissociation techniques, PQD, ETD and CID. Pulsed Q Collision Induced Dissociation (PQD™) is a proprietary technique that eliminates the low mass cut-off concern inherent with all ion traps. This results in extensive coverage for predicted and unpredicted metabolites, and the ability to perform peptide quantification using iTRAQ™ labels.



### **LTQ OrbiTrap Velos Mass Spectrometer**

The Thermo Scientific™ LTQ OrbiTrap Velos XL™ Hybrid Ion Trap-Orbitrap can perform a range of applications, including protein identification, biomarker discovery, de novo sequencing, and metabolite profiling. The instrument is a Fourier Transform Mass Spectrometer (FTMS) based on Thermo Scientific™ LTQ XL™ linear ion trap and Orbitrap mass spectrometer technologies. To enhance the flexibility of fragmentation experiments for advanced proteomics and small molecule research, the instrument features an HCD collision cell.



## **Applied Biosystems MALDI TOF/TOF 4700**

The MALDI TOF/TOF4700 combines high throughput matrix-assisted laser desorption ionization (MALDI) with true MS/MS capabilities. With TOF/TOF optics, it provides reproducible, high-energy fragmentation patterns for accurate protein identification.

\*Information obtained from product websites