New Instruments and Services
Combining the best of quadrupole, Orbitrap, and ion trap mass analysis in a revolutionary Tribrid architecture, the Orbitrap Fusion Tribrid mass spectrometer features:

- Resolution up to **450,000** to remove spectral interferences
- **CID/HCD/ETD** detected by the Ion Trap or Orbitrap at any level of MSn for maximum experimental flexibility
- Dynamic Scan Management architecture lets every user easily get the maximum information from every sample
- Quick **polarity switch** between positive and negative mode.
The ParaCell is the new core technology for solariX XR, providing uncommon broadband ion stability resulting in resolution far superior to other detection schemes.

- Ultimate mass resolving power in excess of $\text{RP} = 10,000,000$
- FTICR technology providing unrivaled mass accuracy
- Apollo II Ion Funnel Electrospray Source enabling high ion transmission efficiency over a broad mass range
- Hybrid Qh Front End supporting CASI™ for enrichment of low abundant species
- Optimized ion optics for sensitivity and mass range coverage
- Proprietary ParaCell ICR cell with patented SIDEKICK™ ion accumulation system for high detection efficiency.
- Nanobay-E Acquisition electronics enabling data streaming for increased broad-band resolution
- Wide range of fragmentation techniques including CID and ECD
- **Dual ionization source**: MALDI source with Smartbeam II laser and ESI source
Application of Orbitrap Fusion

PROTEINS
Bottom-up Proteomics
Targeted Quantitation
Top-Down Proteomics
Intact Protein Characterization

Post Translational Modification Analysis:
Glycosylation
Phosphorylation

Relative Quantitation:
SILAC
TMT
Label-Free

GLYCANS
Glycan Identification & Characterization
2-AA Quantitation
Intact Glycoprotein Profiling
PTM Glycosylation

Application of 15T FT ICR

• High End Proteomics Studies (Top-down and Bottom-up workflows)
• PTM Investigation
• Accurate de novo sequencing
• Molecular Imaging of Tissue—Distribution of Drugs, Metabolites, and Biomarkers
• Petroleum Product Analysis
• Complex Environmental Sample Analysis
• Metabolomics Research
New Services:

- 2D LC/MSMS for Protein Identification and PTM Study
- Targeted Proteomics Quantitation
- Top-down Proteomics
- MALDI Tissue Imaging
High pH Fractionation with Low pH Separation

Waters Mclass 2D System
Dionex 3000 2D System

reverse-phase (C18)

Fraction

Pump 1

Pump 2

Trap

Analytical

reverse-phase (C18)

to waste

$60/fraction on the orbitrap XL
$75/fraction on the orbitrap Fusion

Slide courtesy of Nilini S. Ranbaduge
Multi-dimensional Separation

Fractionation (F)

pH 10.0

F1

pH 2.6

F2

F15

Gradient separation

Slide courtesy of Nilini S. Ranbaduge

$60/fraction on the orbitrap XL
$75/fraction on the orbitrap Fusion
Targeted Proteomics Quantitation

Full Scan

Targeted @ 479.2730^2 (SLVLfGlyTPSR )/516.7793^2 (SLVLC(CAM)TPSR)

MS/MS of 516.7793^2+ (SLVLC(CAM)TPSR)

MS/MS of 479.2730^2+ (SLVLfGlyTPSR )
Top-down v.s. Bottom-up Proteomics

A  Bottom-up MS approach

B  Top-down MS approach

(C) MS/MS fragmentation mechanism

http://eric.diluccio.fr/blog/2012/02/histone-modifications-and-cancers/

Circulation: Cardiovascular Genetics December 2011 vol. 4 no. 6 711

Trends in Biochemical Science; Volume 35, Issue 9, September 2010, Pages 522–529
Protein Identification by Top Down MS/MS

Parents ions (750 - 770, 15+)

Histone H4

ECD MS/MS
Protein Identification by Top Down MS/MS

Known Modification

Modification Detected

$500 on Fusion or ICR
**What is Imaging Mass Spectrometry?**

Imaging Mass Spectrometry is a technology that combines advanced analytical techniques for the analysis of biological molecules with spatial fidelity. An effective approach for imaging biological specimens in this way utilizes Matrix-Assisted Laser Desorption Ionization Mass Spectrometry (MALDI MS). Briefly, molecules of interest are embedded in an organic matrix compound that assists in the desorption and ionization of compounds on irradiation with a UV laser. The mass-to-charge ratio of the ions are measured using a mass spectrometer over an ordered array of ablated spots. Multiple analytes are measured simultaneously, capturing a representation or profile of the biological state of the molecules in that sample at a specific location on the tissue surface.
Problem
• Interference from Matrix
• Metabolites not Stable

Solutions:
• High Mass Accuracy (FT ICR)
• Changing Matrix
• Derivatization
• Using Product Ions for Scanning

$750/Sample on 15T ICR