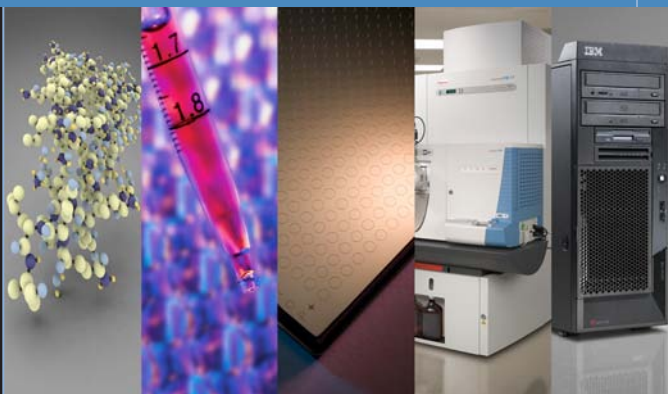


# VISIT THERMO AT ABRF 2005

**LEARN ABOUT  
PROTEOMICS<sup>n</sup>**  
THE COMPLETE SUITE OF  
THERMO SOLUTIONS  
FOR PROTEOMICS



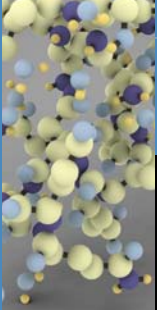
**Join us at ABRF in Savannah, Georgia  
February 5–8, 2005  
Booth 801**

Speak with our applications experts to  
learn more about Proteomics<sup>n</sup> solutions for:

- **Top-Down Protein Analysis**
- **High-Throughput Protein ID**
- **Ultra-sensitive PTM Characterization**
- **Biomarker Discovery and Validation**

Analyze • Detect • Measure • Control™

**Thermo**  
ELECTRON CORPORATION



## PROTEOMICS<sup>n</sup>

*The Complete Suite of Thermo Solutions for Proteomics*

- **Top-Down Protein Analysis**  
Finnigan™ LTQ FT™  
ProSight™ PTM Software
- **High-Throughput Protein ID**  
Finnigan vMALDI™ LTQ™  
ProteomeX™ LTQ  
SEQUEST® Sorcerer™
- **Ultra-sensitive PTM Characterization**  
Finnigan LTQ  
SEQUEST software  
BioWorks™ software
- **Biomarker Discovery software and Validation**  
Label-free Quantitation  
HeavyPeptides™ for AQUA®

## Attend our Lunchtime Technical Workshops

*All workshops take place from noon – 1:00 in room 105. Lunch will be served.*

### **Sunday: A New Label-Free Platform for Quantitative Proteomics**

*Avoid the cost and complexity of isotopic labels – this workshop will introduce a comprehensive new experimental workflow for confident identification and validation of biomarkers.*

Speaker: Dr. Leo Bonilla, Director, BRIMS Center, Thermo Electron Corporation

### **Monday: Massive Parallel Searching of MS/MS Data Using a Novel SEQUEST Accelerator**

*A new, configurable computer chip has been customized for SEQUEST database searching. Combined with proprietary indexing approaches, it is now possible to search more than 50 times faster than a conventional high-end PC.*

Speaker: Dr. Steve Gygi, Assistant Professor, Dept. of Cell Biology, Harvard Medical School

### **Tuesday: Top-Down Proteomics – A Definitive New Approach to Intact Protein Analysis**

*Top-down protein sequencing is the ultimate tool for protein characterization. This technique is now routinely achievable on an LC timescale, using a linear ion trap – FTICR hybrid mass spectrometer and ProSight PTM software.*

Speaker: Dr. Andrew Forbes, Center for Top-Down Proteomics, University of Illinois at Urbana-Champaign

***For complete information on our proteomics solutions, visit***

**[www.thermo.com/proteomics](http://www.thermo.com/proteomics)**

**Thermo**  
ELECTRON CORPORATION

# Technical Posters

Proteomics Applications from Thermo

---

## Sunday » February 6

- P64-S** *Phosphorylation Analysis with MALDI Using MS<sup>3</sup> on an Intermediate-Vacuum MALDI Source Coupled with a Linear Ion Trap Mass Spectrometer*; Mari Prieto-Conaway  
Identification of PTMs
- P76-S** *On-line Identification and Characterization of Glycopeptides Using Hybrid Ion Trap-Fourier Transform Mass Spectrometry*; Scott M. Peterman  
Carbohydrate Analysis
- P133-S** *Utilization of MS<sup>n</sup> Analysis of CAF-Labeled Peptides for Protein Sequencing on a MALDI-Ion Trap Mass Spectrometer*; Reid Asbury, GE Healthcare  
Protein Sequencing
- P171-S** *New Experimental Strategies for the Analysis of Multiply Phosphorylated Peptides by Linear Ion Trap Mass Spectrometry*; Zhiqi Hao  
Carbohydrate Analysis

## Monday » February 7

- P11-M** *Top-Down Analysis of Low Molecular Weight Human Plasma Proteome Using Hybrid Ion Trap-Fourier Transform Mass Spectrometry*; Jennifer N. Sutton  
Proteomics
- P131-M** *Automatic De Novo Sequencing Using Hybrid Ion Trap-Fourier Transform Mass Spectrometry*; Fernando Martin-Maroto  
Bioinformatics
- P134-M** *Automated Top-Down LC/MS<sup>n</sup> Approach for Identification and Characterization of Unknown Yeast Proteins*; Vlad Zabrouskov  
New Mass Spectrometry Protocol
- P185-M** *High-Throughput Identification of Serum Proteins Separated by 2D-DIGE Using Fast Intelligent Data-Dependent MALDI MS<sup>n</sup>*; Anthony Sullivan  
Proteomics

## Tuesday » February 8

- P66-T** *Top-Down Analysis of Intact Proteins for Site Determination of Post-Translational Modifications by High Resolution ECD FTMS*; Helmut Muenster  
Identification of PTMs
- P164-T** *Increased Sequence Coverage of Human CSF Proteins Produced by Limited Acid Hydrolysis and Proteolysis in Both Aqueous and Aqueous/Organic Solvent Systems*; Roger G. Biringer  
New Mass Spectrometry Protocol
- P195-T** *Identification and Differential Expression Analysis of Putative and Known Plasma Biomarkers for Human Myocardial Injury*; Tori Richmond  
Proteomics

# Thermo

ELECTRON CORPORATION

5225 Verona Road • Madison, WI 53711

**Address Service Requested**

PRESORTED  
FIRST CLASS  
U.S. POSTAGE  
**PAID**  
PERMIT NO. 688  
REDWOOD CITY, CA

**STOP BY BOOTH 801 AT ABRF TO  
WIN ONE OF THREE APPLE® IPOD®  
U2 SPECIAL EDITION PLAYERS**

