



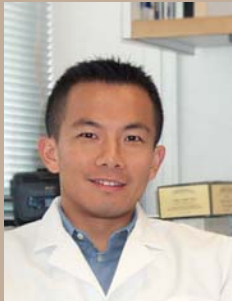
**NEW JERSEY  
MEDICAL SCHOOL**

University of Medicine & Dentistry of New Jersey

**CENTER FOR ADVANCED PROTEOMICS RESEARCH**

# Resources in Proteomics Research

Center for Advanced Proteomics  
Research  
MSB F602/604  
UMDNJ-New Jersey Medical School  
185 S. Orange Avenue  
Newark, NJ 07103



**Hong Li, Ph.D.**  
Director

Phone: 973-972-8396

Fax: 973-972-5594

Email: [liho2@umdnj.edu](mailto:liho2@umdnj.edu)

<http://www.umdnj.edu/proweb/>

*The CAPR is conveniently located in the MSB at the NJ Medical School, next to the Molecular Resource Facility and the Center for Human Genetics*

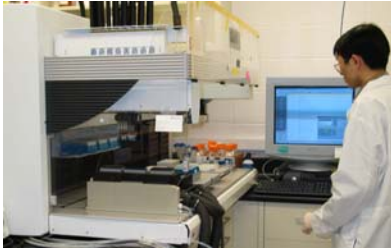


The Center for Advanced Proteomics Research (CAPR) is a core facility specializing in sensitive identification and purity determination of proteins and peptides. CAPR is equipped with state-of-the-art proteomics instruments and bioinformatics systems for protein structure and function analysis. Our instruments include a Waters QTOF electrospray tandem mass spectrometer and an ABI 4700 Proteomics Analyzer. Our philosophy is that the understanding of gene function in disease should include the characterization of protein expressions and their post-translational modifications. We welcome both large-scale research collaborations and routine fee-for-service based analysis. We look forward to helping you with your proteomic needs.

## Current Services

- Protein identification
- MS/MS sequencing
- Expression profiling
- 2D gel electrophoresis
- In-gel digestion
- Accurate mass measurement
- Purity determination

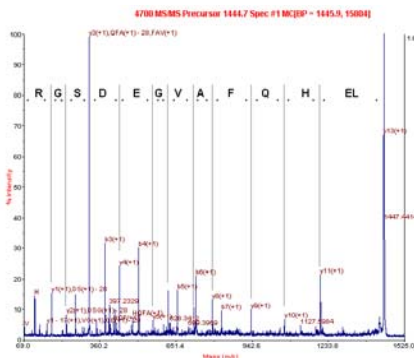




### Low Level Protein Identification

Proteins isolated on 1D or 2D gel electrophoresis can be submitted in the form of a coomassie or sypro ruby-stained gel band or spot. Trypsin breakdown of the proteins into peptides provides a means to identify proteins through peptide mass fingerprinting. High mass measurement accuracy on the ABI 4700 MALDI-TOF mass spectrometer can identify proteins at low ng and fmol levels. We use a TECAN robot to process trypsin digestion and sample spotting up to 96 samples/day.

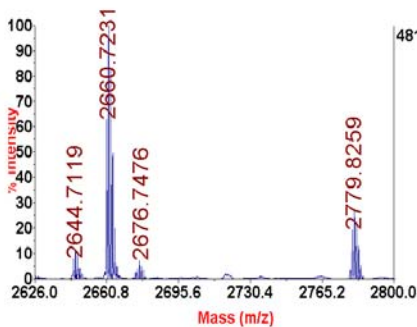
Category: Protein Identification  
 Service Order #: S002  
 Price: \$150.00



### Protein Mixture Identification by TOF/TOF LC/MS/MS

Proteins in complex mixtures obtained from sources such as immunoprecipitation and affinity purification can be denatured and digested with trypsin in solution. The resulting peptide mixtures are separated by LC Packings capillary HPLC and spotted onto a MALDI mass spectrometer plate via a Dionex Probot instrument. Selected peptides are sequenced on the ABI 4700 mass spectrometer and multiple proteins can be identified simultaneously.

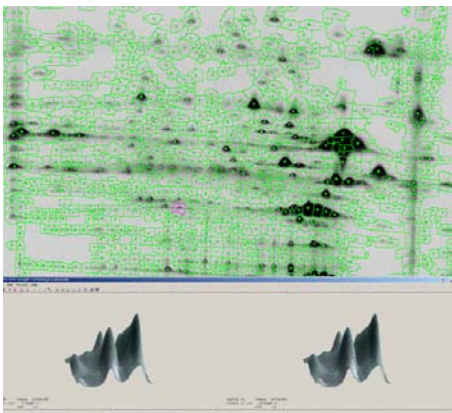
Category: Protein Identification  
 Service Order #: S004  
 Price: \$470.00



### Accurate Protein/Peptide Mass Measurement

Purified or semi-purified recombinant or biologically-isolated proteins and peptide molecular weight can be determined on a mass spectrometer with accuracy of up to 10 ppm for peptides and 0.1% for proteins. Isotopic resolution of up to 8,000 atomic mass unit can be obtained on the ABI 4700 mass spectrometer. Sample purity can be estimated. Similar services for nucleic acid and lipids are also available.

Category: Purity & MW Determination  
 Service Order #: S007  
 Price: \$50.00



### Bio-Rad Criterion 2D gel Electrophoresis

This is the classic method of choice for comparative analysis of protein expression among different biological conditions. It is also a powerful means to separated protein isoforms. We will provide guidance in sample preparation and data analysis. We visualize the gel stained with sypro ruby using an Amersham Typhoon imager to achieve the highest sensitivity and dynamic range. Both BioRad PDQuest and Amersham DeCyder software packages are available to expression analysis.

Category: 2D Gel Electrophoresis  
 Service Order #: S012  
 Price: \$160.00