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### Cancer Proteomics Core

Director: Towia Libermann

Location: 4 Blackfan Circle, HIM 208, Boston

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### Core Summary:

The Cancer Proteomics Core provides high-sensitivity, resolution, and throughput proteomics methods. The Core focuses on proteomic approaches to translational research based on analysis of patient materials such as blood, urine, and tumor tissue extracts.

### Personnel/Contact Information:

Director: Towia Libermann, Ph.D.

Phone: (617) 667-3393

Email: [tliberma@bidmc.harvard.edu](mailto:tliberma@bidmc.harvard.edu)

#### Other Staff:

Mass Spectrometry Proteomics: John Asara, Ph.D.

Phone: (617) 667-6182

Email: [jasara@bidmc.harvard.edu](mailto:jasara@bidmc.harvard.edu)

Clinical Proteomics: Dimitrios Spentzos, M.D.

Phone: (617) 667-0760

Email: [dspentzo@bidmc.harvard.edu](mailto:dspentzo@bidmc.harvard.edu)

Research Proteomics: Luiz Zerbini, Ph.D.

Phone: (617) 667-0760

Email: [lzerbini@bidmc.harvard.edu](mailto:lzerbini@bidmc.harvard.edu)

Bioinformatics: Hasan Otu, Ph.D.

Phone: (617) 667-0808

Email: [hotu@bidmc.harvard.edu](mailto:hotu@bidmc.harvard.edu)

### Facilities and Equipment:

Location of Core:

The facility is located at 4 Blackfan Circle, HIM 208, Boston.

Major Equipment:

Technologies deal for high-throughput screening of clinical samples.

- High-performance ABI 4700 MALDI-TOF/TOF mass spectrometer. Protein identification by extremely fast, automated MALDI-TOF peptide mass fingerprinting.
- Protein profiling and identification by SELDI (Surface-Enhanced Laser Desorption/Ionization) Time-Of-Flight mass spectrometer by Ciphergen. The Ciphergen Protein Chips® technology uses different chromatographic surfaces for separation, detection and analysis of complex mixtures of proteins at femtomole levels).

Detailed protein structural characterization using tandem mass spectrometry microcapillary

LC/MS/MS mode to fully characterize potential target proteins for sequence and post-translational modifications with lower throughput

- ABI QSTAR Pulsar Hybrid mass spectrometer for LC/MS/MS.
- Electro spray MS by Thermo Finnigan LCQ Deca Ion Trap Mass Spectrometer for LC/MS/MS.

High performance protein fractionation by Beckman PF2D LC Fractionation System.

High resolution LC by Dionex Nano LC Dual Gradient Capillary Separation System. The system will significantly increase the number of proteins that can be identified in clinical samples such as serum or tissue extracts and will be essential for identifying peptides with post-translational modifications and for separating isotope labeled proteins for protein quantitation.

Automated liquid handling by Beckman Biomek FX Robotic system.

Microarray Facility for protein and peptide microarrays utilizing an Amersham Lucidea arrayer. Hybridization stations by Amersham ASP automatic hybridization station, and a Biomicrosystems Maui automatic hybridization station. Arrays scanned by Perkin Elmer ScanArray Express HT Laser Scanner.

### Services:

#### Proteomics Services:

- Protein profiling of complex biological samples, eg. serum, urine, tissue, cell extracts.
  - Profiling by  $\mu$ LC/MS.
  - Multidimensional protein fractionation by  $\mu$ LC.
- Protein identification by  $\mu$ LC/MS/MS.
  - coomassie & silver stained gel bands.
- Identification of protein and peptide modifications.
  - phosphorylation sites.
  - protein modifications such as acetylation, methylation, and ubiquitination.
  - By  $\mu$ LC/MS/MS.
  - coomassie stain only, purified proteins.
- Relative quantitation by  $\mu$ LC/MS/MS
  - SILAC - stable isotope labeling of amino acids in cell culture which is a biosynthetic approach.
  - GIST - global internal standard technology, a post digestion peptide level labeling technique.
  - ICAT - isotope coded affinity tag -based protein profiling.
  - ITRAQ - isobaric peptide tagging system that enables you to label all primary amines, regardless of peptide class.

#### Bioinformatics Analyses Offered:

- Personalized consulting
- Customized data analysis and interpretation
- Web-based bioinformatics tools
- Comprehensive and innovative Bioinformatics and visualization tools
- Comprehensive annotation tools
- Identification of Global Relationships
- Incorporation of Biological Knowledge
- Pathway Analysis
- Publication ready figures
- The Bioinformatics Core is also responsible for software support and development.

### Fee Schedule/Rates:

#### Cancer Proteomics

Proteomics Price List	DF/HCC Members	Non-Members	Industry
Ciphergen	(plus 20%)	(plus 50%)	(plus 100%)
<b>protein chips</b>			
C533-0028	\$198.00	\$247.50	\$330.00
C533-0045	\$198.00	\$247.50	\$330.00
C533-0004	\$198.00	\$247.50	\$330.00
C533-0043	\$198.00	\$247.50	\$330.00
C553-0075	\$198.00	\$247.50	\$330.00
C554-0075	\$288.00	\$360.00	\$480.00
C553-0065	\$198.00	\$247.50	\$330.00
C554-0065	\$288.00	\$360.00	\$480.00
C533-0022	\$198.00	\$247.50	\$330.00
C554-0057	\$288.00	\$360.00	\$480.00
C554-0052	\$288.00	\$360.00	\$480.00
C554-0056	\$288.00	\$360.00	\$480.00
C573-0080	\$198.00	\$247.50	\$330.00
C574-0080-8	\$198.00	\$247.50	\$330.00
C574-0080-16	\$288.00	\$360.00	\$480.00
K100-0007	\$ 1,248.00	\$1,560.00	\$2,080.00
<b>PF2D</b>			
2D protein fractionation	\$660.00	\$825.00	\$1,100.00
<b>ABI MALDI/TOF-TOF</b>	(plus 30%)	(plus 50%)	(plus 150%)
protein identification	\$260.00	\$300.00	\$500.00
phosphorylation	\$390.00	\$450.00	\$750.00
<b>Protein Quantitation:</b>			
GIST, SILAC	contact core for prices		
SILAC	contact core for prices		
New AB relative	contact core for prices		
Note: prices for all services include initial consultation and bioinformatics			
Tier 1 analysis report.			
<b>BIOINFORMATICS</b>	(plus 20%)	(plus 50%)	(plus 100%)
additional support	\$65.00/hour	\$75.00/hour	\$100.00/hour
<b>PROTEOMIC PROJECT CONSULTATION</b>	included for all BIDMC & DF/HCC members	\$75.00/hour	\$100.00/hour

### Getting Started:

To access the core, please contact Towia Libermann at (617) 667-3393 or by email at [tliberma@bidmc.harvard.edu](mailto:tliberma@bidmc.harvard.edu).

### Departmental Web Link:

<http://www.dfhcc.harvard.edu/core-facilities/cancer-proteomics/>



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