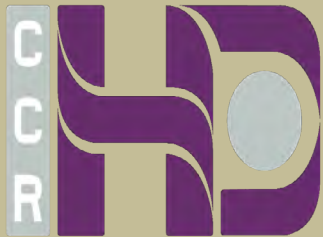


Translational Proteomics Center



Loyda M Melendez, PhD
Professor
Department of Microbiology
School of Medicine
Core Director
University of Puerto Rico Medical Sciences

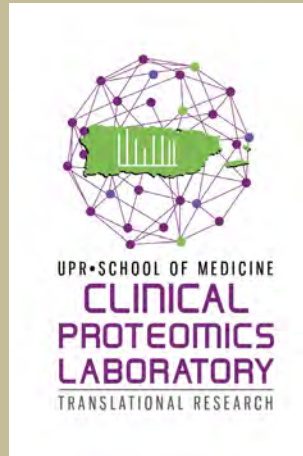


Center for Collaborative Research
in Health Disparities



January 29-30, 2020
Little Rock, AR, (USA)





Clinical Proteomics Laboratory San Juan, Puerto Rico



Horacio Serrano Rivera, PhD
Professor
School of Medicine
Internal Medicine Department
University of Puerto Rico

January 29-30, 2020
Little Rock, AR, (USA)





Coat of Arms



Commonwealth of Puerto Rico



Outline

- RCMI Research Infrastructure Core
 - Translational Proteomics Center
 - Genomics Translational Research Unit
 - Tropical and Emerging Infectious Diseases
 - Molecular Neurogenetics and Bioimaging
 - Integrated Informatics
- INBRE Centralized Instrumentation Core
- Clinical Proteomics Laboratory
 - Dr. Horacio Serrano



Center for Collaborative Research
in Health Disparities



Research Infrastructure Core



Genomic Service
Main suite: 1,400 sq ft



Tropical and Emerging Infectious
Diseases Research Service
1,445 sq ft



Integrated Informatic Service
599 sq ft



Neurogenetics and Bioimaging Service
926.96 sq ft



Proteomics Service
1,168.25 sq ft



Genomics Service
Satellite suite: 1,560 sq ft

Mission

- Center for collaborative research in health disparities (CCRHD)
 - To contribute to the national **infrastructure and the capacity** for research in the health sciences by supporting basic, behavioral and clinical studies in health disparities that affect the Puerto Rican population.

The Research Infrastructure Core (RIC) functions synergistically to **maximize the quality and productivity of the Research Projects** and the pilot projects funded by the CCRHD.

Vision

- Vision of the CCRHD
 - To create a collaborative center recognized as a model of excellence in promoting research in minority health and health disparities, contributing to a diverse biomedical research workforce and interacting with the community to improve health of Puerto Rican population.

RIC Aims	Direction	
<p>To combine Bioinformatics, Health Informatics and Operational Informatics resources into one Integrated Informatics Service</p>	<p>Abiel Roche-Lima, PhD Associate Professor</p>	
<p>To deliver high-end services to support Genomics and Proteomics research</p>	<p>Carmen L. Cadilla, PhD / Loyda M. Melendez, PhD Professor Department of Biochemistry / Department of Microbiology</p>	 
<p>To provide state-of-the-art Neurogenetics and Bio-imaging services</p>	<p>Mark Miller, PhD Professor Department of Anatomy</p>	
<p>To provide access to key resources for Tropical and Emerging Infectious Diseases research.</p>	<p>Adelfa Serrano, PhD Professor Department of Microbiology</p>	

Translational Proteomics Center (TPC)

Mission

- Provide an **integrated platform for biomarker discovery and protein identification and quantitation** to interface between basic and clinical research conducted in Puerto Rico for the diagnosis and therapeutic monitoring of human diseases.
- **Integrate** Genomics, Bioinformatics (Ingenuity Pathways), Metabolomics (INBRE), and Emergent Infectious Disease Cores with Proteomics Platform.
- **Provide TPC services with new methodologies** on quantitative proteomics such as: TMT labelling.
- Promote **validation strategies** including: Imaging (Core in Neurobiology), ELISAs (TPC,TEID), Kinetic assays (TPC, TEID) and Flow cytometry (CCC).
- **Provide workshops and trainings through the INBRE program** and Increase users and visits to the TPC, as well as supported projects.

Research Resources



UPR School of Medicine Interdepartmental Seminar Series

"State of the Art Resources Available to UPR MSC

Investigators through RCMI and INBRE Supported Facilities"



Loyda Meléndez, PhD
Professor
Microbiology Department
Translational Proteomic
Center Director



Carmen L. Cadilla PhD
Professor
Biochemistry Department
Genomics Translational
Research Unit Director



Nataliya Choma, PhD
Adjunct Professor
Biochemistry Department
INBRE Metabolomics Core
Director



Adelfa Serrano, PhD
Professor
Microbiology Department
Tropical and Emerging
Infectious Diseases Core



Mark Miller, PhD
Professor
Institute of Neurobiology
Neurogenetics and
Bioimaging Director



Abiel Roche-Lima, PhD
Assistant Professor
Bioinformatics Core
Director

Tuesday, December 5, 2017 at 12:00pm
Amphitheater 6th Floor, Guillermo Arbona
Building UPR- Medical Sciences Campus



SPONSORED BY THE RCMI AND INBRE PROGRAMS, Departments of Biochemistry and Physiology





1st day: 29 participants

PROTEOMIC WORKSHOP

March 12-13, 2018

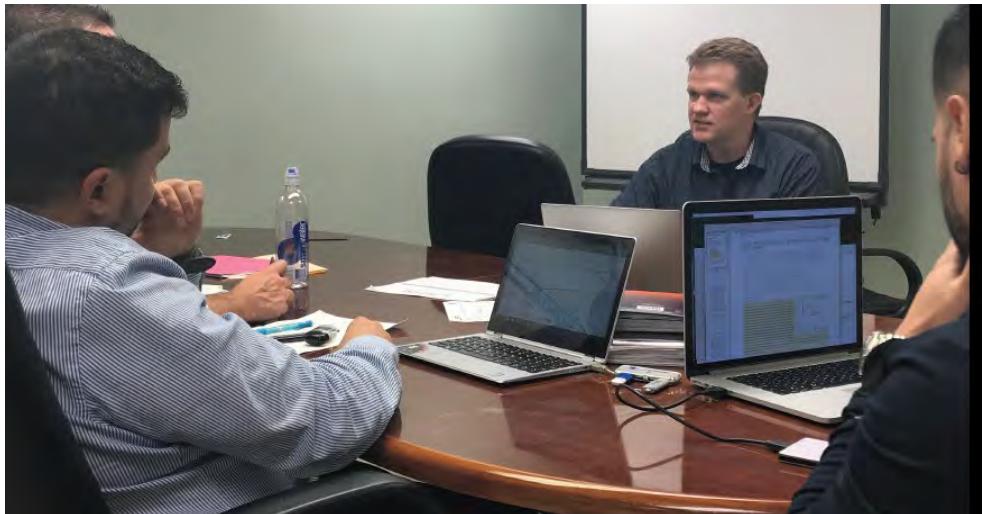
University of Puerto Rico, Medical Sciences Campus

Coordinator: Loyda Melendez

CRI Core

Evaluation Report

2nd day: 11 participants,
individual meetings with
students and faculty working
in proteomics related
projects

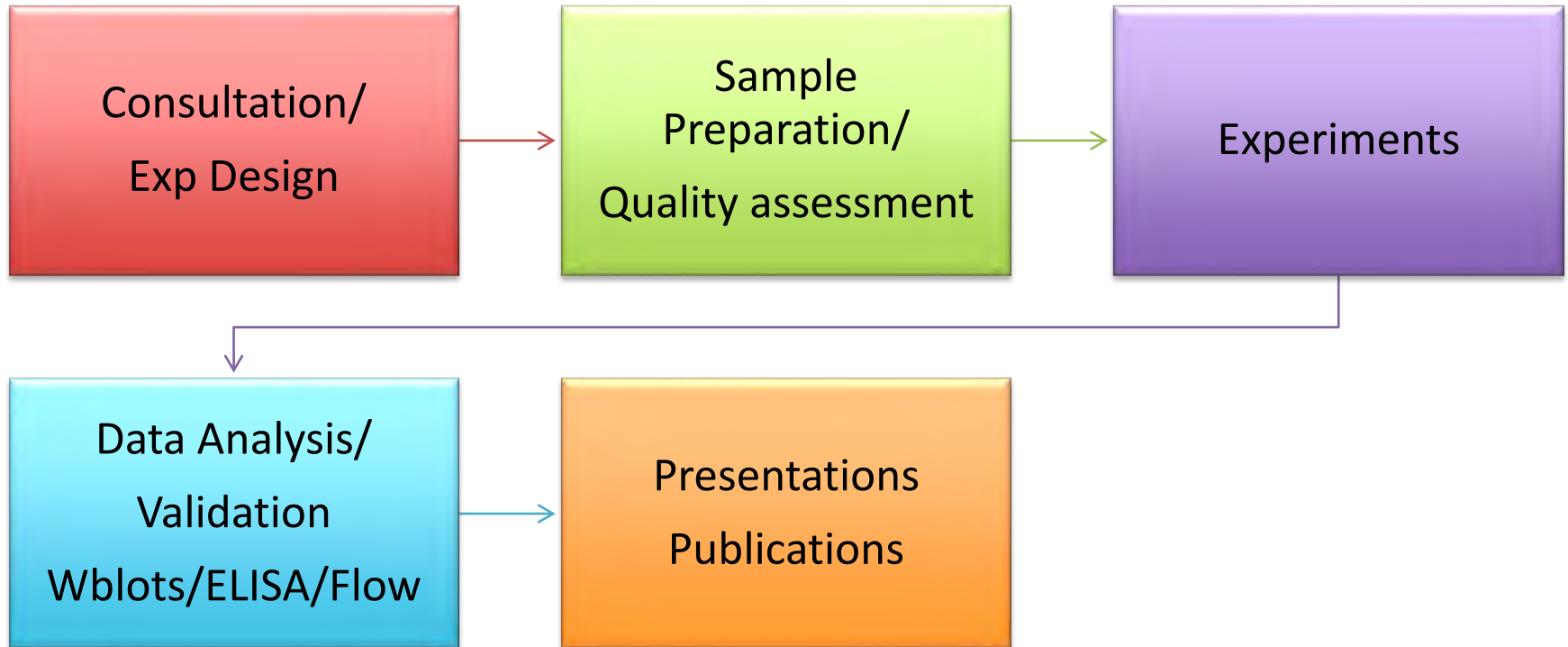


Evaluation & Tracking Team

Prepared by

Nicole M. Ortiz Vega, MS
Sharon M. Alvalle Vélez, MS

Method of Operation



Translational Proteomics Center

Loyda M Melendez, MT, MS, PhD



Service Leader
Loyda M Melendez, PhD

Ana Rodriguez, MS



Research Associate
Ana Rodriguez, MS

Supported by RCMi

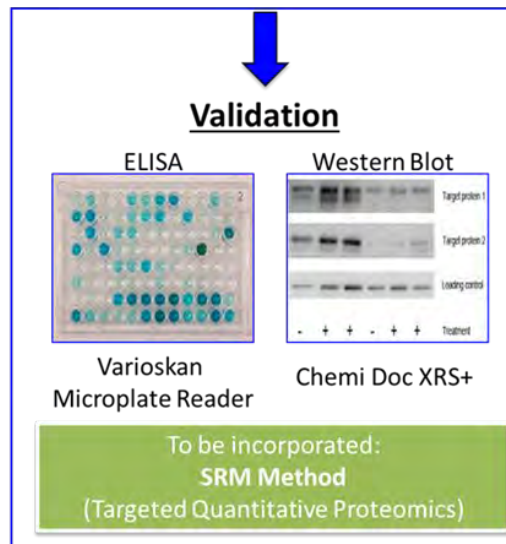
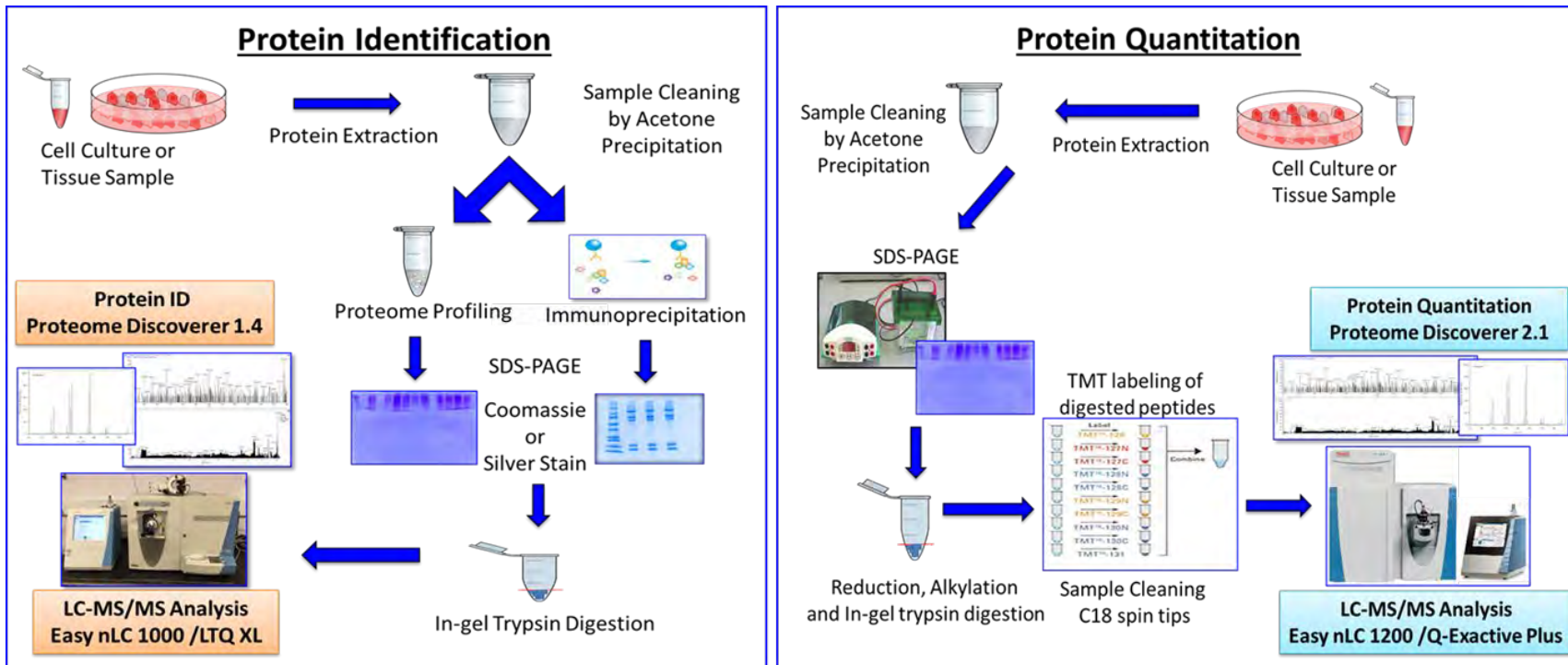
Yadira Cantres, BS



Research Assistant
Yadira Cantres, BS

Supported by CCC

Services Provided



#	Service Provided	Fee for Services
1	Initial Consultation	Free
2	Experimental design and power analyses	\$30/hr
3	Processing of complex clinical samples (BCA, Calibration curve)	\$35/sample
4	Depletion of most abundant proteins from clinical samples*	\$35/sample
5	Protein fractionation	\$35/sample
6	Protein Separation: ✓ One-dimensional SDS PAGE ✓ Gel staining (Coomassie or Silver)	\$ 50/Gel
7	Immunoprecipitation** **Investigators must provide antibodies of their preferences and the lysis buffer.	\$ 150
8	Sample Processing for Mass Spectrometry: ✓ Enzymatic digestion (in-gel) ✓ Peptide Extractions	\$ 15/Sample
9	Protein Identification: ✓ Analysis by LC-MS/MS (Easy-nLC-LTQ XL) ✓ Sequest HT Data Search	\$ 20/Sample
10	Quantitative Proteomics: ✓ Peptide tagging (iTRAQ/TMT labeling) ✓ Analysis by LC-MS/MS (Q-Exactive Plus) ✓ Sequest HT and Mascot Data Search ✓ SILAC	\$ 100/Sample
11	Protein Validation by Fluorometry/ELISA * Investigators provide ELISA Kits costs.	\$ 50
12	Protein Validation by Western Blot (WB) ✓ Investigators provide Antibodies of their preference.	\$ 75 \$ 15 (Re-Blot)
13	Ingenuity Pathway Analysis for Validated Proteins ✓ The software is also available for users Free independent analysis.	\$ 50
14	Consulting and Final Report	Free
15	Proteomics Abstract and Manuscripts Revision	Free

List of Services

http://rcmi.rcm.upr.edu/resreso/corefacnetwork/tpc/guides_prot

SALE!!!
25% discount x
INBRE users

INBRE CENTRALIZED RESEARCH INSTRUMENTATION CORE (CRI)

1. **Translational Proteomics Center— Dr. Loyda M. Melendez, RCMI - UPR Medical Sciences Campus**
2. Genomics Translational Research Unit – Dr. Carmen L.Cadilla, RCMI, PRCTRC - UPR Medical Sciences Campus
3. Metabolomics Research Core – Dr. Nataliya Chorna, INBRE - UPR Medical Sciences Campus
4. Sequencing Genomic Facility (SGf)— Dr. Riccardo Papa, INBRE and UPR Rio Piedras, NSF.
5. Protein Structure and Dynamics –Dr. Juan Lopez Garriga, NSF, INBRE. UPR Mayaguez Campus
6. In-Vitro Biotesting Facility (ChemTox)– Dr. Beatriz Zayas, INBRE and Universidad Metropolitana.

CRI Core Goals & Aims

- The overall goal of the PR-INBRE Centralized Research Instrumentation (CRI) Cores is to integrate and empower investigators and students from Tier 1, Tier 2 Primarily Undergraduate Institutions (PUIs) and Outreach Institutions by providing mentorship and scientific support.
- Specific Aim 1: Reinforce and enhance access to state-of-the-art core research instrumentation for nurturing new and expanding established research collaborations between the CRI investigators, students, and faculty from Puerto Rico, the Caribbean, and other IDeA states.

CRI Core Goals & Aims (cont.)

- Specific Aim 2: Ensure the effective dissemination of CRI Cores technologies via **theoretical and practical workshops, mentoring researchers** in experimental design and best practices in the use of the resources that are available to them.
- Specific Aim 3: Create an **alliance of CRI Core users**.

PROTEOMICS facilities

Comprehensive Cancer Center, Lab #5



- Lab 1,200 sq. ft.
- Instrumentation Room
- Chemical Room
- Cell culture Room
- Cold Room
- Emergency outlets



Tissue Culture Room



Cold Rooms



Storage of
reagents
clinical samples
and reagents
that need low
temperatures.

Chemical Room



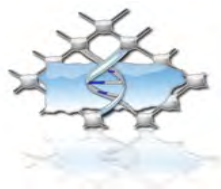
Mass Spectrometry Room

New Technology Quantitative LC/MS/MS Analysis

Protein
Quantitation
System



Thermo Easy n-LC 1200 coupled
to the Thermo Q-Exactive Plus Mass Spectrometer

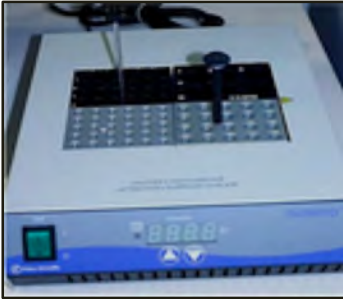


Puerto Rico IDeA Network Biomedical Research Excellence

PRINBRE
BIOMEDICAL RESEARCH EXCELLENCE

Instrumentation Protein ID

Enzyme Digestion – Peptide Extraction – LC/MS/MS Analysis



Digital Dry Bath

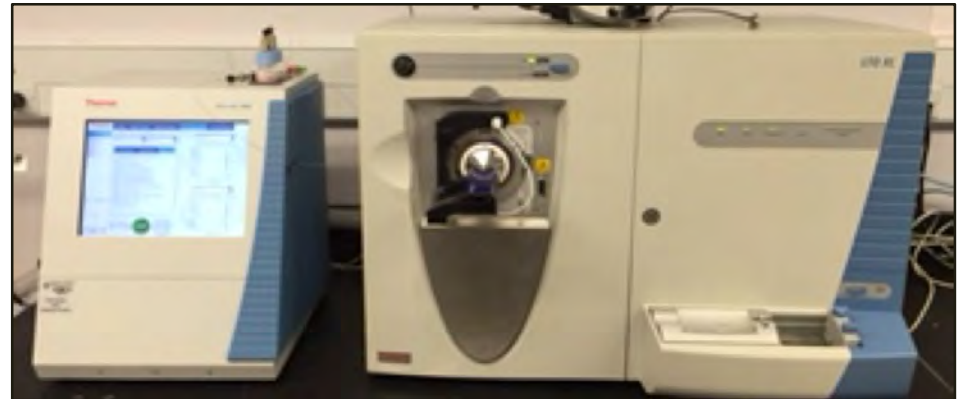


Sorvall Legend Micro 21R &
17 Centrifuges

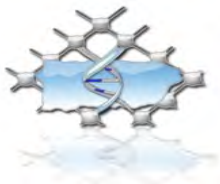


miVac DNA Concentrator Integrated
system & Savant Speed Vac Plus

Protein
Identification
System



Thermo Easy n-LC 1000 coupled
to the Thermo LTQ XL Mass Spectrometer



Puerto Rico IDEa Network Biomedical Research Excellence

PRINBRE
DISCOVER

Instrumentation Protein Validation

Electrophoresis – Western Blot – ELISA



Electrophoresis Station



Turbo Trans Blot Transfer System



Varioskan Flash Spectral Reader



Bio Rad Gel Doc XR+

The Translational Proteomics Center provides training, resources, and tools for new and established investigators seeking to use innovative approaches of proteomics to their research, as well as to undergraduate and graduate students in the biomedical field

Data Analysis



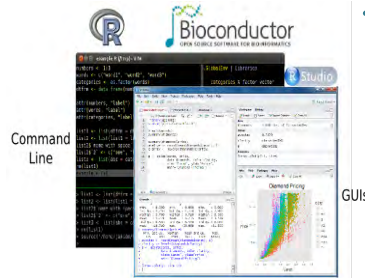
Proteome Discoverer 2.2

Mass Informatics Platform for Protein Scientists

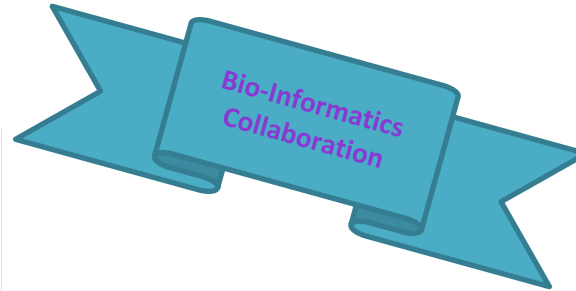
© Copyright 2009-2017 Thermo Fisher Scientific Inc. All rights reserved.
This program is protected by copyright law and international treaties as described in Help>About.



**Raw Data Analysis
(1,080 proteins/
sample pool)**



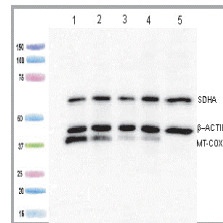
Limma R Statistics



**INGENUITY
PATHWAY ANALYSIS**



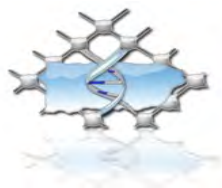
**Ingenuity Pathway
Analyses**



**Western Blot Analyses for
Validation**

Proteomics analysis programs

Program	Application
Image Lab™ Version 5.1	Software for acquisition and analysis of gel (Electrophoresis) and blot images (Western Blots).
SKanIt RE for Varioskan Flash Version 2.4.3	Software provides method setup, data acquisition, data processing, and reporting for Varioskan Flash instrument. Recommended for ELISA and other biological assays.
Xcalibur Version 2.2	Software provides method setup, data acquisition, data processing, and reporting for LC/MS/MS analysis.
Proteome Discoverer Version 1.4 and 2.1	Software for protein identification and quantitation in complex biological samples. Used with the analysis of raw data files of the LC/MS/MS analysis.
Ingenuity Pathway Analysis	Software helps in the research process of the data obtained. Answer biological questions as: What biological pathways do the identified proteins participate in? or What is the effect of known protein modifications?



Puerto Rico IDEa Network Biomedical Research Excellence

PRINBRE
BIOINFORM

Translational Proteomics

Users / Visits 2018-2019

<i>RCMI Facility</i>	<i>Month</i>	<i>Jul 2018</i>	<i>Aug 2018</i>	<i>Sep 2018</i>	<i>Oct 2018</i>	<i>Nov 2018</i>	<i>Dec 2018</i>	<i>Jan 2019</i>	<i>Feb 2019</i>	<i>Mar 2019</i>	<i>Apr 2019</i>	<i>May 2018</i>	<i>Jun 2019</i>	<i>Total</i>
<i>Translational Proteomics Center (TPC)</i>	<i>Service Tickets- Requested</i>	0	4	1	2	3	1	1	4	4	0	2	2	22
	<i>Service Tickets- Resolved</i>	0	1	4	1	3	0	3	2	0	0	4	2	18
	<i>Instrument Use- Bar coding data</i>	17	40	25	26	17	10	15	23	37	19	24	19	253
	<i>Unique Users (per Month)</i>	8	10	10	8	8	5	6	10	11	7	10	7	24*

July to June 2019

296 visits in total by 24* users between July to June 2019.

Impacted Projects- UPR-MSC

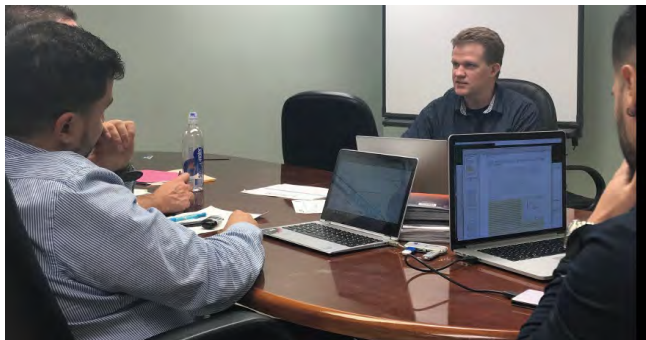
Project	Area	Investigator	Students / Postdocs
Adopting a Precision Medicine Paradigm in Caribbean Hispanics of Puerto Rico	Heart	Jorge Duconge, PhD	1
Upstream regulation and Downstream Effectors of c-MYC in Ovarian Cancer	Cancer	Pablo Vivas, PhD	1
Vaccine Development against Infectious Diseases	Infectious	Miguel Otero, PhD	2
Targeting Breast Cancer Progression	Cancer	Suranganie F. Dharmawardhane, PhD	2
Targeting Monocyte/Macrophage Cathepsin B in HIV-1 Neurocognitive Disorders	Infectious	Loyda M Melendez, PhD	4

Impacted Projects- Other UPR projects

Project	Area	Investigator
Novel Rac inhibitors as potential therapeutics for metastatic breast cancer: Phosphoproteomics analyses	Cancer	Surangami Dharmawardhane
Exosome-mediated soluble insulin receptor secretion correlates with HAND.	Infectious	Yamil Gerena and Valerie Wojna
mTOR related genes in cisplatin-resistant ovarian cancer PRCCC	Cancer	Pablo Vivas
Biomolecular Analyses of Hypospadias According to Severity.	Physio	Horacio Serrano/ Juan Carlos Jorge
Study of Proteins associated to stress in yeast for the discovery of antifungal treatment in humans.	Infectious	Jose Rodriguez-Medina
Combining High-Throughput Omics methods to Understand Cervical Microbiome Dynamics for Cancer Prevention among High-Risk Hispanics	Infectious	Filipa Godoy
HIV vaccine development	Infectious	Abel Baerga
Nicotine receptors and addiction	Drug abuse	José Lasalde

Special Activities 2019-20

Activities	Topics	Resources
Seminars and Webinar	Proteomics and Viral infections. Jan, 2019	Dr. Melendez
Trainings	Proteomics training to graduate and undergraduate students March, 2019	Core staff
Workshops	Quantitative Proteomics and Protein Bioinformatics. May, 2019	Dr. Bryan Ballif Dr. Emilio Camafeita Dr. Inmaculada Jorge
Course	Special Topics in Proteomics Feb-March, 2020	Drs. Melendez, Serrano, Ballif, Weintraub, Camafeita, Jorge



Outcomes: Presentations

Meetings	Place	Format
Human Proteome Organization (HUPO). September 30, 2018.	Orlando, Florida,	Poster
ABRCMS. Oct 2018.	Washington DC	Poster
PR Neuroscience. Nov 2018.	Puerto Rico	Poster
Society for Neuroscience. Nov 1-7, 2018.	San Diego, CA.	Poster
HIVDART and Emerging viruses. 27-29 November, 2018.	Miami , Florida,	Oral
Society on Neuroimmune Pharmacology 25th Scientific Conference. April 9-13, 2019.	Portland, OR	Oral and Poster
American Society for Mass Spectrometry. June 4, 2019 (ASMS)	Atlanta, GA	2 Posters
Cerebral Vascular Biology Conference, June 25-28, 2019	Miami, FL	Oral

Manuscripts

1. Rosario-Rodríguez LJ, Colón K, Borges-Vélez G, Negrón K, Meléndez LM. 2018. Dimethyl fumarate prevents lysosomal disruption and cathepsin B secretion from HIV infected macrophages. *J Neuroimmune Pharmacol*. 2018 Jul 9. doi: 10.1007/s11481-018-9794-5. PMID:29987592.
2. Rosas-Vidal L, Lozada V, Cantres-Rosario Y, Vega-Medina A, Melendez L, and Quirk G. 2018. Alteration of BDNF in the medial prefrontal cortex and the ventral hippocampus impairs extinction of avoidance. *Neuropsychopharmacology*. 2018 Dec;43(13):2636-2644. doi: 10.1038/s41386-018-0176-8. Epub 2018 Aug 11. PMID: 30127343.
3. Cantres-Rosario YM, Ortiz-Rodríguez SC, Santos-Figueroa AG, Plaud M, Negron K, Cotto B, Langford D, Melendez LM. *HIV infection induces extracellular cathepsin B uptake and damage to neurons*. *Sci Rep*. 2019 May 29;9(1):8006. doi: 10.1038/s41598-019-44463-1. PMID: 3114275
4. Vélez- López O., Gorantla S., Segarra Marrero A., Andino Norat MC, Álvarez M, Skolasky RL, Meléndez LM. 2019. Sigma-1r antagonist bd1047 prior to cocaine reduces cathepsin B secretion in HIV-1 infected macrophages. *J Neuroimmune Pharmacology* Jun;14(2):226-240. doi: 10.1007/s11481-018-9807-4. Epub 2018 Oct 10. PMID: 30306495
5. Vélez-López O, Carrasquillo-Carrión K, Salgado-Ramírez CA, Cantres-Rosario Y, Machín-Martínez E, Álvarez-Ríos MA, Roche-Lima A & Meléndez LM. Quantitative Proteomics of HIV-1 Infected Macrophages exposed to Cocaine following Sigma-1 Receptor Modulation. To be submitted to *J of Proteome Research*.
6. Zenon-Melendez CN, Roche-Lima A, Carrasquillo-Carrión K, Cantres Rosario Y, Roman E & Meléndez LM. Cathepsin B/SAPC secreted by HIV-infected macrophages share common and distinct pathways of neuronal apoptosis. To be submitted to *J of Proteome Research*.

Contact

Loyda M Melendez, PhD
Service Lead
Translational Proteomics Center

Comprehensive Cancer Center
Lab #5

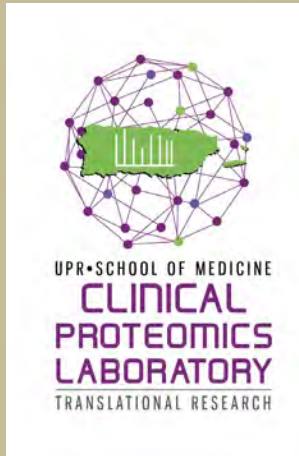
loyda.melendez@upr.edu

Cell 787-467-2328

Websites:

1. <http://rcmi.rcm.upr.edu/?q=proteomic-page>
2. https://md.rcm.upr.edu/micro/dt_team/dr-loyda-melendez/





Clinical Proteomics Laboratory San Juan, Puerto Rico



**Horacio Serrano Rivera, PhD
Professor
Internal Medicine Department
University of Puerto Rico**

January 29-30, 2020
Litter Rock, AR (USA)





The creation of this laboratory was an initiative developed through the Department of Internal Medicine of the School of Medicine, Medical Sciences Campus, University of Puerto Rico

Clinical Proteomics Laboratory

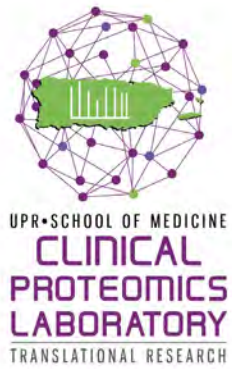
- Mission

- To provide support in proteomics to **clinical research faculty and students** by supporting clinical studies in health disparities that affect the Puerto Rican population.
- To promote translational research by applying proteomics approach.

We rely on existing platforms in the RCMI Translational Proteomic CORE directed by Dr. Loyda Meléndez



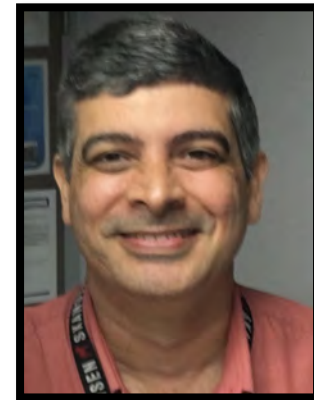
Clinical Proteomics Facility

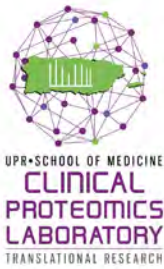




On a technical level we have a chemist and statistician as part of the staff.

Eric Miranda, MPH,
Research Assistant
eric.miranda@upr.edu



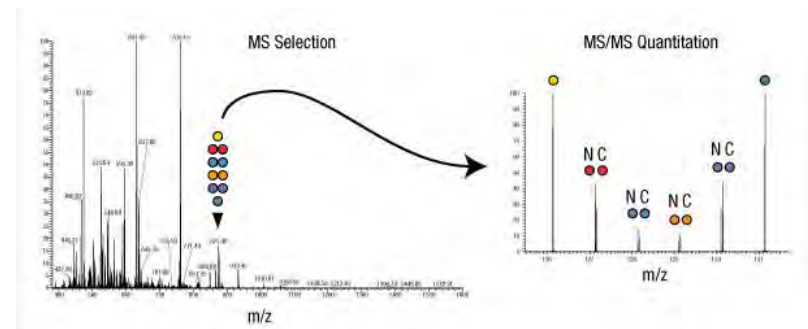
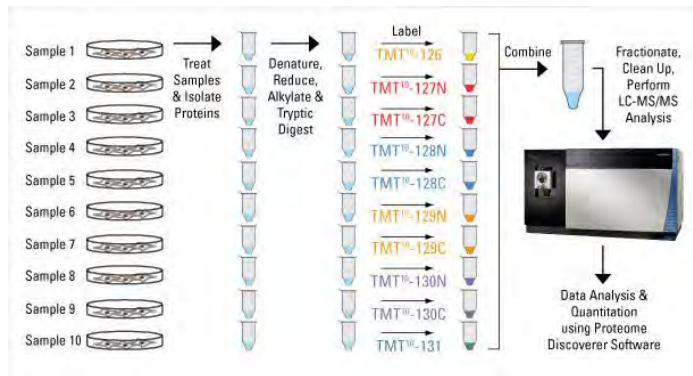


Two components

- Academic Component
 - Undergraduate level
 - Students interested in clinical research.
 - Graduate
 - Working on specific objectives of doctoral thesis
 - We offer conferences and courses
- Research Component
 - Facilitators and collaborate with **Clinical Faculty** in:
 - » Experimental design
 - » Biostatistics
 - » Repository of clinical samples
 - » Sample conditioning for MS / MS
 - » Protein labeling
 - » Proteomic data analysis

Methodologies applied:

- ELISA test
- Protein Identification by MS / MS
Protein Chemistry
Mass Spectrometry and
Bioinformatics
- Quantification of Proteins by MS / MS
TMT



Some of the most relevant research conducted with our collaboration include:

Research	PI and Co-PI
Biomarkers of Kidney Damage / Diabetes T2	Ileana Ocasio, MD Horacio Serrano, PhD
Biomarkers of Lung Cancer	Carlos Cortijio, PhD Horacio Serrano, PhD
Pharmacoproteomics (Rheumatoid arthritis)	Luis Vilá, MD Horacio Serrano, PhD

Other collaborations in progress include proteomics studies of the following diseases:

Research	PI and Co-PI
Hypospadias	Juan C. Jorge, PhD
Biomarkers of Alzheimer's (No traditional Sample)	Ivonne Z. Jiménez, MD
Parkinson	Sherly Pardo, MD
HIV	Loyda Meléndez, MD
Thyroid Cancer	William Mendez, MD
Pancreatic Cancer	Texel Longoria, MD
Preeclampsia and premature delivery	Jossie Romaguera, MD

HIV and Drug abuse

Proteomics Clin. Appl. 2015, 00, 1–11

DOI 10.1002/prca.201400204

1

RESEARCH ARTICLE

^{18}O proteomics reveal increased human apolipoprotein CIII in Hispanic HIV-1+ women with HAART that use cocaine

Frances Zenón¹, Inmaculada Jorge², Ailed Cruz³, Erick Suárez⁴, Annabell C. Segarra⁵, Jesús Vázquez², Loyda M. Meléndez^{1} and Horacio Serrano⁶*

¹ Department of Microbiology, University of Puerto Rico Medical Sciences Campus, San Juan, Puerto Rico

² Laboratorio de Proteómica Cardiovascular, Centro Nacional de Investigaciones Cardiovasculares (CNIC), Madrid, Spain

³ Department of Biochemistry, University of Puerto Rico Medical Sciences Campus, San Juan, Puerto Rico

⁴ Department of Biostatistics and Epidemiology, Graduate School of Public Health, University of Puerto Rico Medical Sciences Campus, San Juan, Puerto Rico

⁵ Department of Physiology, University of Puerto Rico Medical Sciences Campus, San Juan, Puerto Rico

⁶ Department of Internal Medicine, University of Puerto Rico Medical Sciences Campus, San Juan, Puerto Rico

Purpose: Drug abuse is a major risk factor in the development and progression of HIV-1. This study defines the alterations in the plasma proteome of HIV-1-infected women that use cocaine.


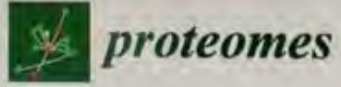
Experimental design: Plasma samples from 12 HIV-seropositive Hispanic women under antiretroviral therapy were selected for this study. Six sample pairs were matched between nondrug users and cocaine users. After IgG and albumin depletion, SDS-PAGE, and in-gel digestion, peptides from nondrug users and cocaine users were labeled with ^{16}O and ^{18}O , respectively, and subjected to LC-MS/MS and quantitation using Proteome Discover and QuiXoT softwares and validated by ELISA.

Received: December 17, 2014

Revised: May 26, 2015

Accepted: July 27, 2015

And we work on this panoramic article regarding the possibilities of making clinical proteomics with non-traditional samples



Article

A Quantitative Proteomics Approach to Clinical Research with Non-Traditional Samples

Rígel Licier ^{1,2,*}, Eric Miranda ^{2,3} and Horacio Serrano ^{2,3,*}

¹ Department of Medicine, San Juan Bautista School of Medicine, Caguas 00727, Puerto Rico
² Quantitative Proteomics Laboratory, Comprehensive Cancer Center of Puerto Rico, San Juan 00936, Puerto Rico; eric.miranda@upr.edu
³ Department of Internal Medicine, University of Puerto Rico, Medical Sciences Campus, San Juan 00936, Puerto Rico
* Correspondence: rigello@sanjuanbautista.edu (R.L.); horacio.serrano@upr.edu (H.S.); Tel.: +787-454-3192 (R.L.); +787-643-8071 (H.S.)

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Abstract: The proper handling of samples to be analyzed by mass spectrometry (MS) can guarantee excellent results and a greater depth of analysis when working in quantitative proteomics. This is critical when trying to assess non-traditional sources such as ear wax, saliva, vitreous humor, aqueous humor, tears, nipple aspirate fluid, breast milk/colostrum, cervical-vaginal fluid, nasal secretions, bronco-alveolar lavage fluid, and stools. We intend to provide the investigator with relevant aspects of quantitative proteomics and to recognize the most recent clinical research work conducted with atypical samples and analyzed by quantitative proteomics. Having as reference the most recent and different approaches used with non-traditional sources allows us to compare new strategies in the development of novel experimental models. On the other hand, these references help us to contribute significantly to the understanding of the proportions of proteins in different proteomes of clinical interest and may lead to potential advances in the emerging field of precision medicine.

Keywords: quantitative proteomics; MS/MS; clinical samples; precision medicine; screening

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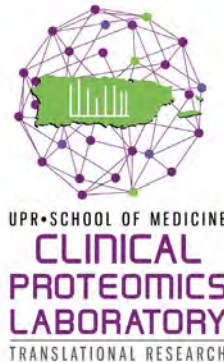
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