



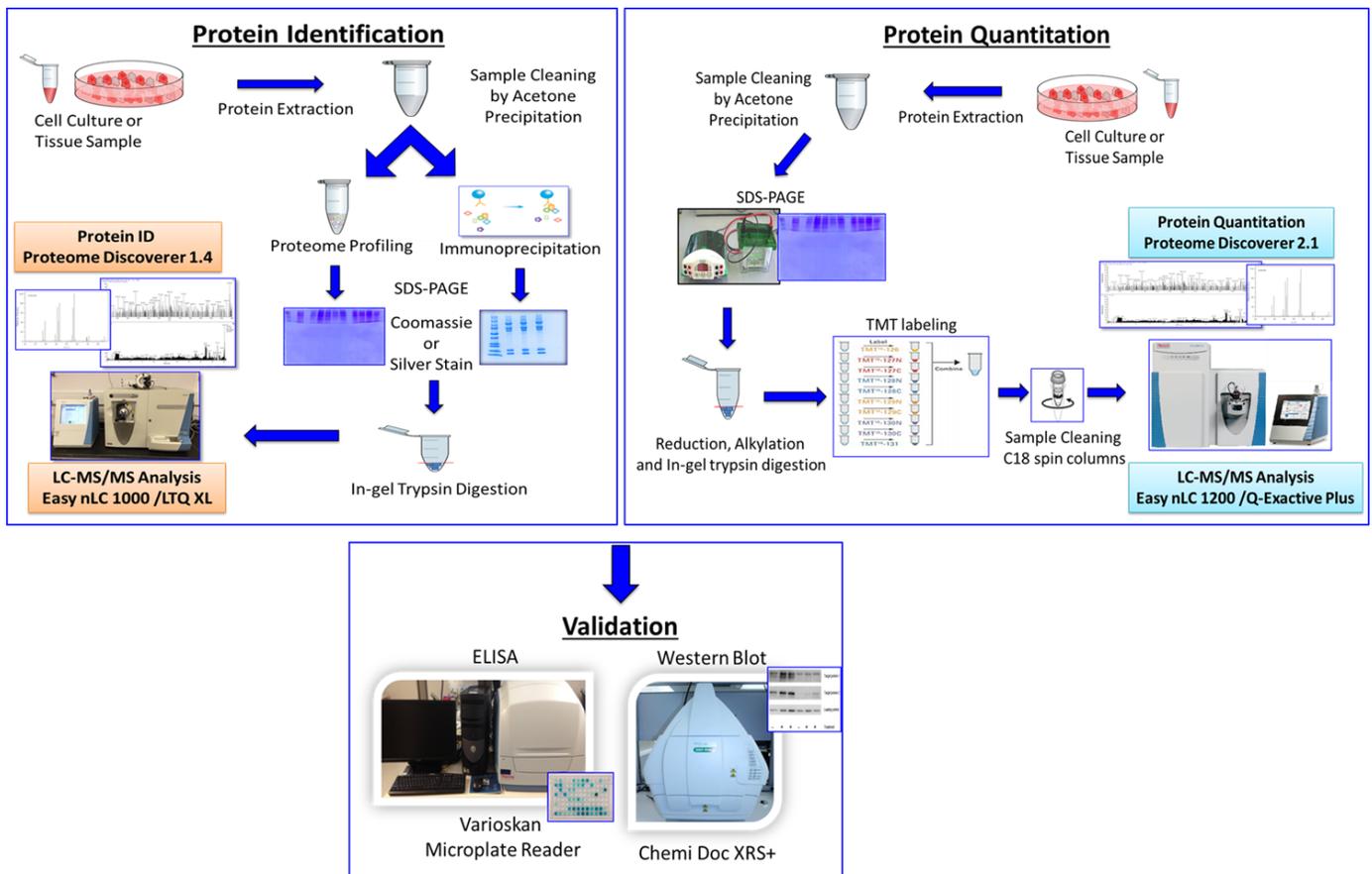
**University of Puerto Rico: Medical Sciences Campus
Comprehensive Cancer Center
Translational Proteomics Center**



FACILITY GUIDELINES:

1. **CONSULT:** Contact via email our director Dr. Loyda Meléndez for an initial consultation on the experimental approach for your project and to decide if our services suit your purposes.
2. **REGISTRATION:** **Your project must be properly registered and an RCMI account must be ready prior to scheduling your experiment.** Contact the staff to request a RCMI user account. Instructions will be provided to generate E-tickets for the services requested. Also, the staff will send the official Registration Form.
3. **SAMPLE SUBMISSION:** Once we have all the samples in our facility, we can schedule your experiment. Include the following requirements:
 - Registration form: Filled and signed by the investigator. This form includes relevant information on abstract and biosafety; please bring the required documentation included in the form.
 - Sample Inventory: a written document that lists all the samples to be submitted, with the names as they are labelled in the vials, group category and protein concentration.
 - Samples: Coordinate with the staff the amount of total protein needed as it varies depending on the experiment requested. We suggest that they be normalized with lysis buffer.
 - Relevant Previous Data: when applicable, include in the documentation the relevant preliminary data, such as total protein concentrations.
 - Procedures and reagents: provide all the protocols performed prior to submission and include every reagent used in your samples as some may interfere with mass spectrometry or peptide labeling. Is important to specify the recipe of your lysis buffer and in special cases deliver an additional volume of 10 mL of the buffer.
 - Labeled Gel Image: only when delivering samples in a gel format.
4. **SAMPLE PROCESSING:** Samples are scheduled in our calendar according to the **order of arrival** to our laboratory. Below there is the general workflow we use, but you can contact the staff for more details about experimentations. The time estimated for generating results is approximately 2-4 weeks including the mass spectrometry analysis but will depend greatly on the number of samples delivered. Technical setbacks with mass spectrometry instrumentation may occur which also take time

and will be notified when occurring. The staff will communicate when decisions are required to proceed and for more updates.



5. **MASS SPECTROMETRY ANALYSIS:** The instrumentation to be used and the time needed for analysis will depend on the services requested. Details on instrument methods are provided in the final report. The raw data generated is further analysed with the Proteome Discoverer software for either Protein ID or Protein Quantitation by TMT. These results are then exported to Excel and sent to the user or the Bioinformatics Core Facility.
6. **FINAL REPORT:** When finished, the staff will send to the investigator a Final Report in a PDF format describing all the procedures performed with the samples for inclusion in presentations and manuscripts. An Excel file is generated after the database search with high level of confidence and will also be sent to the user if no further analysis is required by the Bioinformatics facility (as is the case for TMT Labelling). Raw data will be provided upon request.
7. **INVOICE:** The staff will provide an Invoice of the Fees for the Services requested per sample, as specified in our official list of fees on the website. The Invoice will be handed to the investigator after the services have been performed, if needed a quote can be provided before.

CONTACT PEOPLE:

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Thank You for choosing our proteomics facility, we are always at your service!

