

Label	Value
<b>Core Facility Name</b>	Center for Translational Proteomics
<b>Last Name</b>	Pandey
<b>First Name</b>	Akhilesh
<b>Email</b>	<a href="mailto:pandey@jhmi.edu">pandey@jhmi.edu</a>
<b>Phone</b>	410-502-6662
<b>Amount of Funding Requested</b>	\$25,000
<b>Briefly describe the core services you offer:</b>	<p>We provide advanced mass spectrometry-based discovery services to the JHU community – this includes both qualitative analysis and quantitative proteomics analyses. Following are the key services that are offered:</p> <ol style="list-style-type: none"> <li>1. Comprehensive profiling of whole proteomes – Deep characterization of proteins in biological samples using the most sensitive mass spectrometry and sample preparation technologies.</li> <li>2. Quantitative analysis of whole proteome – Comparison of protein level expression in multiple samples using various labeling approaches. The labeling approaches include in vivo labeling methods such as SILAC and in vitro labeling methods such as TMT.</li> <li>3. Comprehensive profiling of post-translational modifications – Enrichment of proteins that are modified by post-translational modifications (e.g. phosphorylation, acetylation, ubiquitylation, methylation) followed by mass spectrometry analysis for global analysis of signaling pathways.</li> <li>4. Identification of protein cleavage sites – Identification of protein cleavage sites by proteolytic enzymes in the cells which are involved various cellular regulations and this processing is also involved in the disease. The identification of the cleavage sites are performed by enrichment of N-terminal peptides by TAILS or other related approaches.</li> <li>5. Top-down and middle-down proteomics – To provide services to identify intact proteins with their post-translational modifications.</li> <li>6. Protein turnover measurement – Classical proteomics technology just measure protein abundance. Pulse-chase SILAC measurements can provide information about protein dynamics.</li> <li>7. Proteogenomics analysis – The Center will provide various types of bioinformatics analysis including proteogenomics analysis and identification of unknown post-translational modifications.</li> </ol>
<b>What specific services do you plan to offer as part of this RFA?</b>	<ol style="list-style-type: none"> <li>1. Comprehensive profiling of post-translational modifications – Identification of post-translational modifications (e.g. phosphorylation, acetylation, ubiquitylation, methylation) in biological samples for global analysis of signaling pathways.</li> <li>2. Quantitative analysis of proteomes – Comparison of protein levels expression changes in multiple samples using various labeling approaches. The labeling approaches could include in vivo labeling methods such as SILAC or in vitro labeling methods such as TMT. This category could include pilot studies aimed at identifying potential biomarkers.</li> <li>3. Top-down and middle-down proteomics – To provide services to identify intact proteins with their post-translational modifications.</li> </ol>
<b>How do these services address the goals of the pilot program?</b>	<ol style="list-style-type: none"> <li>1. They will introduce investigators to the power of high end mass spectrometry so that they can incorporate this technology routinely into their scientific program.</li> <li>2. They will help generate pilot data for grants to be submitted.</li> <li>3. In some cases, they will lead to interdisciplinary collaborations and help form</li> </ol>

	<p>teams.</p> <p>4. In all cases, they will enhance the science.</p> <p>5. In some cases, they will lead to development of methods that could then be applied on a broader scale.</p> <p>6. They could help test a hypothesis being proposed for a larger project.</p> <p>7. We will be able to identify the investigators at JHU who require high end proteomics services.</p>
<p><b>How would you select recipients to receive core services? Please describe the process and criteria you might use.</b></p>	<p>Process: The most deserving projects will be selected by a small committee comprising of Dr. Akhilesh Pandey (Director), Dr. Chan-Hyun Na (Manager) and Dr. Gerald Hart (Director, Department of Biological Chemistry). This committee will choose the most deserving investigator/project combinations that are most likely to benefit from the offered services.</p> <p>Criteria:</p> <ol style="list-style-type: none"> <li>1. Novelty of the project.</li> <li>2. Whether the investigator is new to proteomics.</li> <li>3. Whether pilot data is required for submission of a grant.</li> <li>4. Whether the project will benefit from the instrumentation e.g. HCD or ETD fragmentation, high resolution, TMT labeling with MS3 level quantitation etc.</li> <li>5. Whether the investigator is truly in need of funds to support proteomics analysis</li> <li>6. Whether the project is interdisciplinary</li> <li>7. Likelihood of a grant submission if the pilot study is successful</li> </ol>
<p><b>How do you plan to allocate the amounts available to individual investigators?</b></p>	<p>We will subsidize the entire project if it costs under \$5,000 or provide a subsidy up to \$5,000 with the investigator covering the rest if the project is projected to cost more than \$5,000. We anticipate that we will be able to fund 7-10 investigators through this mechanism.</p>