

Dr. Hong Li, Director. Office Phone: (973) 972-8396 Lab Phone: (973) 972-5340 Fax: (973) 972-1865 E-mail: [liho2@njms.rutgers.edu](mailto:liho2@njms.rutgers.edu)  
 Cancer Center Building Rm F1226 (Office); Rm F1105 (Lab); 205 South Orange Avenue, Newark, NJ 07103  
 Web: <http://njms.rutgers.edu/proweb>

**Center for Advanced Proteomics Research (CAPR)  
 Service Order Form (F004)**  
*(We do not have service for radioactive samples at present time)*

Group: \_\_\_\_\_ Name: \_\_\_\_\_  
 Address: \_\_\_\_\_ Date: \_\_\_\_\_  
 \_\_\_\_\_ Tel: \_\_\_\_\_  
 \_\_\_\_\_ Fax: \_\_\_\_\_  
 \_\_\_\_\_ E-mail: \_\_\_\_\_

PO No: \_\_\_\_\_

PO Billing Address: \_\_\_\_\_

Code	Service	External Academic price	Unit	Qty.	Total
S1	Protein Mixture Identification by LC/MS/MS	\$685	each		
S2	Protein Mixture Identification by LC/MS/MS (bulk rate for up to 10 samples submitted together)	\$4,822	each		
S3	Protein Mass Determination	\$631	each		
S4	Full SDS-PAGE Lane (mini-gel) Digestion	\$185	hour		
S5	Sample Clean Up	\$129	each		
S6-8	iTRAQ (8 plex) Proteomics	\$8,776	each		
S7-6	Iodo TMT (6 plex) Proteomics	\$7,058	each		
S8	TMT (16 plex) Proteomics	\$11,605	each		
S9	Data Sharing	\$737	each		
S10	Custom Service	\$234	hour		
<b>PI Signature*</b>		<b>Date</b>			
<b>Print PI Name</b>					

\*As per Rutgers guidelines, PI must sign the service order form.

**Additional Information:**  
**Specific objectives of the analysis:**

---

---

**Instructions on remaining sample after analysis:**

---

---

**Sample buffer composition attached: Yes / No If  
No, please specify:**

---

**Sample species (e.g. *Homo sapiens*):** \_\_\_\_\_  
**Sample Storage Condition:** \_\_\_\_\_

**Sample Post-translational modification:**

---

**Sample Protein/Peptide known structure:**

---

**Sample Protein/Peptide Quantity:** \_\_\_\_\_  
**Sample Protein/Peptide Concentration:** \_\_\_\_\_

**Method used to measure Protein/Peptide Concentration (e.g. BCA, Bradford etc.):**

---

**Interested in molecular weight (MW) range:**

**Interested in pH range:** \_\_\_\_\_

**Expected sequence (for MS sequencing only):**

---

**Sample ID:**

**Sample #1:** \_\_\_\_\_

**Sample #2:** \_\_\_\_\_

**Sample #3:** \_\_\_\_\_

**Sample #4:** \_\_\_\_\_

**Sample #5:** \_\_\_\_\_

**Sample #6:** \_\_\_\_\_

**Sample #7:** \_\_\_\_\_

**Sample #8:** \_\_\_\_\_

**Sample #9:** \_\_\_\_\_