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**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	Industry Price	Unit	Qty.	Total
S1	Protein Mixture Identification by LC/MS/MS	\$950	each		
S2	Protein Mixture Identification by LC/MS/MS (bulk rate for up to 10 samples submitted together)	\$6,600	each		
S3	Protein Mass Determination	\$600	each		
S4	Full SDS-PAGE Lane (mini-gel) Digestion	\$200	hour		
S5	Sample Clean Up	\$170	each		
S6-8	iTRAQ (8 plex) Proteomics	\$12,100	each		
S7-6	Iodo TMT (6 plex) Proteomics	\$9,000	each		
S8	TMT (16 plex) Proteomics	\$16,000	each		
S9	Data Sharing	\$1000	each		
S10	Custom Service	\$300	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:**

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**Instructions on remaining sample after analysis:**

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

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

**Sample Storage Condition:** \_\_\_\_\_

**Sample Post-translational modification:**

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**Sample Protein/Peptide known structure:**

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

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

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

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

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

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

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**Sample ID:**

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

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

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

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

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

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

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

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

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