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### Center for Advanced Proteomics Research (CAPR) Service Order Form (F003) (We do not have service for radioactive samples at present time)

Group: _____	Name: _____
Address: _____	Date: _____
_____	Tel: _____
	Fax: _____
	E-mail: _____

Rutgers project No. \_\_\_\_\_ Rutgers UDO String \_\_\_\_\_

Non-Rutgers PO No. \_\_\_\_\_ PO Billing Address \_\_\_\_\_

Code	Service	External price	Unit	Qty.	Total
S001-A	Protein Mixture Identification by LC/MS/MS(long gradient)	\$480.00	each		
S001-B	Protein Mixture Identification by LC/MS/MS(long gradient) (bulk rate for up to 10 samples)	\$3600.00	each		
S002-A	Protein Mixture Identification by LC/MS/MS(short gradient)	\$300.00	each		
S002-B	Protein Mixture Identification by LC/MS/MS(short gradient) (bulk rate for up to 10 samples)	\$2250.00	each		
S003	Protein Mass Determination by LTQ Orbitrap Velos	\$225.00	each		
S004	Extra Protein Identification Data Analysis Time(over the default 2 hours)	\$150.00	hour		
S005	Extra Gel Data Analysis Time (over the default 1 hour/gel )	\$150.00	hour		
S006	Sample Clean Up	\$75.00	each		
S007-4	iTRAQ (4 plex) Proteomics	\$7800.00	each		
S007-8	iTRAQ (8 plex) Proteomics	\$8550.00	each		
S008-6	Iodo TMT(6 plex) Proteomics	\$3750.00	each		
S008-10	TMT(10 plex) Proteomics	\$9000.00	each		
S009-1	ICAT (One heavy/light pair)	\$2250.00	each		
S009-3	ICAT (Three heavy/light pair) with data analysis	\$6750.00	each		
S0010	Sypro Ruby Staining and Typhoon Gel Imaging	\$75.00	gel		
S0011	BioRad Criterion 2D Gel western blot	\$600.00	each		
S0012	Biotin Switch for SNO peptides	\$450.00	each		
S0013	Generate publication quality spectrum figure	\$300.00	each		
S0014	PTM enrichment	\$300.00	each		
S0015	Data analysis of each PTM site quantitation	\$75.00	each		
S0016	Consultation with CAPR staff	\$150.00	hour		
S0017	Custom Service	\$150.00	hour		

<b>PI Signature*</b>	<b>Date</b>	<b>Total Charge</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:** \_\_\_\_\_

**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.):**

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**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:** \_\_\_\_\_