

Dr. Hong Li, Director. Office Phone: (973) 972-8396 Lab Phone: (973) 972-5340 Fax: (973) 972-1865 E-mail: 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 (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	Internal Price	Unit	Qty.	Total
S0	Consultation with CAPR staff (1 st hr free/year/PI)	\$180	hour		
S1-A	Protein Mixture Identification by LC/MS/MS(3 hr gradient)	\$500	each		
S1-B	Protein Mixture Identification by LC/MS/MS(3 hr gradient) (bulk rate for up to 10 samples)	\$4,000	each		
S2-A	Protein Mixture Identification by LC/MS/MS(1 hr gradient)	\$360	each		
S2-B	Protein Mixture Identification by LC/MS/MS(1 hr gradient) (bulk rate for up to 10 samples)	\$2,700	each		
S3	Protein Mass Determination via Fusion Lumos	\$270	each		
S4	Full SDS-PAGE Lane (mini-gel) Digestion of Proteins	\$75	each		
S5	Sample Clean Up	\$80	each		
S6-4	iTRAQ (4 plex) Proteomics	\$8,100	each		
S6-8	iTRAQ (8 plex) Proteomics	\$8,800	each		
S7-6	Iodo TMT(6 plex) Proteomics	\$4,500	each		
S8-10	TMT(10 plex) Proteomics	\$9,000	each		
S8-11	TMT(11 plex) Proteomics	\$9,200	each		
S8-16	TMT(16 plex) Proteomics	\$9,800	each		
S9	Sypro Ruby Staining and Typhoon Gel Imaging	\$80	gel		
S10	Biotin Switch for SNO peptide Mapping	\$500	each		
S11	PRIDE Data Sharing and Submission	\$750	each		
S12	Generate Publication-Quality Spectral Figure	\$300	each		
S13	PTM enrichment	\$350	each		
S14	Data Analysis of Each PTM Site Quantitation	\$80	each		
S15	Custom Service	\$180	hour		
PI Signature*		Date	Total Charge		
Print PI Name					

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

Additional Information:

Specific objectives of the analysis (describe what the ideal results/report format you'd like to see):

Instructions on the remaining samples after the analysis:

Sample buffer composition attached: Yes / No

If No, please specify: _____

Sample species (e.g. *Homo sapiens*): _____

Sample storage conditions: _____

Known/expected post-translational modifications:

For Proteins/Peptides, provide known structure, accession # or sequence:

Sample Protein/Peptide quantity and method of measurement: _____

Sample Protein/Peptide concentrations: _____

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

Interested in molecular weight (MW) range: _____

Interested in pH range: _____

Expected sequence (for MS sequencing only): _____

Sample ID, names and descriptions:

Sample #1: _____

Sample #2: _____

Sample #3: _____

Sample #4: _____

Sample #5: _____

Sample #6: _____

Sample #7: _____

Sample #8: _____

Sample #9: _____