



CENTER FOR ADVANCED PROTEOMICS RESEARCH

NEW JERSEY MEDICAL SCHOOL

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

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

UMDNJ Index No. _____ Non-UMDNJ PO No. _____
 PO Billing Address _____

Code	Service	Unit Price	Unit	Qty.	Total
S002	Low Level Protein Identification by MALDI-TOF/TOF	\$150	each		
S003	Protein Mixture Identification by LC/MS/MS(LTQ Orbitrap Velos)	\$275	each		
S003-B	Protein Mixture Identification by LC/MS/MS(LTQ Orbitrap Velos) (bulk rate for up to 10 samples)	\$2000	each		
S005	Extra Protein Identification Data Analysis Time (over the default 2 hours)	\$100	hour		
S006	Peptide Mass Determination by MALDI-TOF	\$50	each		
S007	Protein Mass Determination by LTQ Orbitrap Velos	\$150	each		
S012	BioRad Criterion 2D Gel (11cm)	\$160	gel		
S013	Sypro Ruby Staining and Typhoon Gel Imaging	\$50	gel		
S014	Extra Gel Data Analysis Time (over the default 1 hour/gel)	\$75	hour		
S015	Sample Clean Up	\$50	each		
S016	Custom Service	\$100	hour		
S017	Protein Identification by MALDI (bulk rate up to 100)	\$5000	each		
S018-4	iTRAQ (4 plex) Proteomics	\$4000	each		
S018-8	iTRAQ (8 plex) Proteomics	\$5000	each		
S019	DIGE Gel and Imaging (3 plex)	\$1500	each		
S021	User Operation of ABI 4800	\$200	hour		
S022	Instrument Training	\$100	hour		
S023	User Operation of ABI 4800 (bulk rate 100 off hour access)	\$10,000	each		
S025	User Operation of Typhoon Imager	\$40	hour		
S026-1	ICAT (One heavy/light pair)	\$1500	each		
S026-3	ICAT (Three heavy/light pair) with data analysis	\$4500	each		
S028-1	Protein Mixture Identification by 2D LC/MS/MS (MALDI)	\$3000	each		
S028-2	Protein Mixture Identification by 2D LC/MS/MS (LTQ Orbitrap Velos)	\$3000	each		
PI Signature*					
Print PI Name		Date		Total Charge	

* As per UMDNJ 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:

Sample #10:
