CENTER FOR ADVANCED PROTEOMICS RESEARCH

NEW JERSEY MEDICAL SCHOOL

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(QTOF)	$275	each		
S005	Extra Protein Identification Data Analysis Time (over the default 2 hours)	$75	hour		
S006	Peptide Mass Determination by MALDI-TOF	$50	each		
S007	Protein Mass Determination by Q-TOF	$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 (QTOF)	$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:_____