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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 | Internal Price | Unit | Qty. | Total |
|----------------------|-----------------------------------------------------------------------------------------------|----------------|---------------------|------|-------|
| S0 | Consultation with CAPR staff (1 st hr free/year/PI) | \$240 | hour | | |
| S1-A | Protein Mixture Identification by LC/MS/MS(3 hr gradient) | \$700 | each | | |
| S1-B | Protein Mixture Identification by LC/MS/MS(3 hr gradient) (bulk rate for up to 10 samples) | \$5,400 | each | | |
| S2-A | Protein Mixture Identification by LC/MS/MS(1 hr gradient) | \$480 | each | | |
| S2-B | Protein Mixture Identification by LC/MS/MS(1 hr gradient) (bulk rate for up to 10 samples) | \$3,600 | each | | |
| S3 | Protein Mass Determination via Fusion Lumos | \$360 | each | | |
| S4 | Full SDS-PAGE Lane (mini-gel) Digestion of Proteins | \$100 | each | | |
| S5 | Sample Clean Up | \$120 | each | | |
| S6-4 | iTRAQ (4 plex) Proteomics | \$10,800 | each | | |
| S6-8 | iTRAQ (8 plex) Proteomics | \$11,800 | each | | |
| S7-6 | Iodo TMT(6 plex) Proteomics | \$6,000 | each | | |
| S8-10 | TMT(10 plex) Proteomics | \$12,000 | each | | |
| S8-11 | TMT(11 plex) Proteomics | \$12,200 | each | | |
| S8-16 | TMT(16 plex) Proteomics | \$13,000 | each | | |
| S9 | Sypro Ruby Staining and Typhoon Gel Imaging | \$120 | gel | | |
| S10 | Biotin Switch for SNO peptide Mapping | \$700 | each | | |
| S11 | PRIDE Data Sharing and Submission | \$1,000 | each | | |
| S12 | Generate Publication-Quality Spectral Figure | \$400 | each | | |
| S13 | PTM enrichment | \$500 | each | | |
| S14 | Data Analysis of Each PTM Site Quantitation | \$120 | each | | |
| S15 | Custom Service | \$240 | 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: _____