**Proteomics & Metabolomics Core (PMC) Facility**

TSRB, Room 110, 71 S. Manassas St., Memphis, TN 38163

[www.uthsc.edu/proteomics/](http://www.uthsc.edu/proteomics/) Tel: 901-448-3077 **d**kakhnia@uthsc.edu

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# Sample Submission/Service Request Form

**Customer/Payment (**UTHSC Investigators)

|  |
| --- |
| Principal Investigator: Contact Person:  |
| Department: Phone:  |
| Account #: Email: |
| PI Signature Date: |

**Requested Services - Proteomics**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Service Type | Service Codes | Number of Units | Unit Price,$ | Full Price,$ |
| **Sample Preparation**Service Codes 101-120 |  |  |  |  |
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| **Direct Infusion**Service Codes 202, 203 |  |  |  |  |
|  |  |  |  |
| **Protein Identification**Service Codes 300-312 |  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| **Protein Identification &****Mapping of Specified PTMs\***Service Codes 401-404 |  |  |  |  |
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|  |  |  |  |
| **Differential Protein Expression Profiling**Service Codes 501-533  |  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| **Other -** Service Code 534 |  |  |  |  |
| **Total Cost**  | **Internal Users** |  |
| **External Users rate surcharge, per service 50%** |  |

**\*PTMs and Modified Residues of Interest**

|  |  |
| --- | --- |
| PTM | Modified Residue(s) |
|  |  |
|  |  |
|  |  |

**SAMPLE INFORMATION:**

**Please specify materials and procedures you have used for sample preparation**.

 Proteins have been extracted from:

 Cultured Cells Cells Body Fluid Tissue

 Target proteins have been fractionated (separated, isolated) into:

 Gel Band(s)

 Stain: Coomassie Sypro Ruby Other:

 IP complex (Antibody:\_\_\_\_\_\_\_\_\_\_; Elution Method:\_\_\_\_\_\_\_\_\_)

 Other:

 Protein samples have been tested for quality control (QC) using:

 Agilent QC test SDS PAGE

 Protein concentration have been determined or estimated

 g/l g/band

 Cysteine residues have been reduced

Reducing agent TCEP DTT βME

 Cysteine residues have been alkylated

Alkylating agent: IAA MMTS Other:

 Proteins have been processed for ‘clean-up’ using:

 Acetone precipitation FASP Column Other:

 Proteins have been digested:

Enzyme (specificity): Trypsin (K, R) Lys-C Other:

 Digested proteins have been processed for ‘clean-up’ or fractionation:

 Digested samples have been “desalted” using ZipTips or equivalent

 8 fractions sample have been collected using high pH RP (C18) fractionation

 Proteins/peptides have been labeled for differential expression analysis

 SILAC: 2-plex 3-plex

 TMT: 6-plex 10-plex

 iTRAQ: 4-plex 8-plex

 Other:

**Sample buffer:**

**Comments:**

**SAMPLE INFORMATION (continued):**

Please specify: The organism (human, bovine, mouse, *E.coli*, yeast, etc.) and tissue

 Total amount of protein (g) in the sample/band

 Concentration (g/l). The MW of target proteins (when known)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| ## | **Sample Name** | **Organism** | **Tissue Type** | **Amount** **(g)** | **Concentration****(g/l)** | **MW****(kDa)** |
| 1 |  |  |  |  |  |  |
| 2 |  |  |  |  |  |  |
| 3 |  |  |  |  |  |  |
| 4 |  |  |  |  |  |  |
| 5 |  |  |  |  |  |  |
| 6 |  |  |  |  |  |  |
| 7 |  |  |  |  |  |  |
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| 11 |  |  |  |  |  |  |
| 12 |  |  |  |  |  |  |
| 13 |  |  |  |  |  |  |
| 14 |  |  |  |  |  |  |
| 15 |  |  |  |  |  |  |
| 16 |  |  |  |  |  |  |
| 17 |  |  |  |  |  |  |
| 18 |  |  |  |  |  |  |

Use additional page when necessary

**Analysis:**

\_\_\_\_Drop to sever \_\_\_\_

Pass to mBIO Core (initials\_\_\_ )

Data Pick Up: