

Proteomics and Metabolomics Facility – Sample Submission Form

Name: _____ Submission Date: _____

Affiliation/PI name: _____

Billing Address (for external users): _____

Cost number (for UN users): _____ E-Mail: _____

Analytical Requirements:

- A. Protein Identification from gel bands. *Indicate stain used and provide gel image:* _____
- B. Free Amino Acid Analysis (A, I, L, V, F, W, Y, D, N, E, Q, M, C, S, T, R, H, K, G, P, Tau, GABA).
- C. Hydrolyzed Amino Acid Analysis (A, I, L, V, F, Y, D, E, MetS, CyA, S, T, R, H, K, G, P).
- D. Free Sugar Analysis (Fructose, Sucrose, Glucose, Raffinose, Arabinose, Mannose, Xylose, Galactose, Lactose).
- E. Stress Hormone Assay including ABA, SA, JA, JA-Ile, OPDA.
- F. Growth Hormone Assay including IAA, IAA-Asp, t-Zeatin, c-Zeatin, t-ZRiboside.
- G. Gibberellins Assay (GA1, GA3 and GA4)
- ! The requests H-M must be discussed with PMF staff before submission!***
- H. Protein Identification from Solution or Bead samples (from IP, Co-IP or pull down).
- I. Quantitative Proteomic Analysis using Labeling approaches (TMT or iTRAQ) or Label-Free.
- J. Identification and Quantification of Post-translational modifications, including Phosphorylation.
- K. Targeted Quantification of Small Molecule or Peptide.
- L. Non-Targeted Profiling and Relative Quantification of Small Molecule
- M. Other _____

Number of Samples: _____

Please append a full list of sample names as a table form with any other relevant information if applicable. Send it as an electronic file as well as hard copy.

Contact information:

Sophie Alvarez, Ph.D., Director, salvarez@unl.edu
Mike Naldrett, Ph.D. Assistant Director, mnaldrett@unl.edu
Beadle Center – E-154
Phone: 402-475-4575

Drop samples off to Beadle Center – E-154 or
Ship samples to:
Sophie Alvarez/Mike Naldrett
UNL - Center for Biotechnology
1901 Vine St
E-119 Beadle Center
Lincoln, NE 68588

Further Information for Protein Identification:

- For protein identification, please indicate here which organism the proteins/sequences came from: _____
- If the protein is not a native sequence, i.e. contains a tag (such as GST / His / GFP etc), point mutations or any other changes to the sequence then you **MUST** supply an electronic copy of the sequence.
- Please indicate any known or suspected modifications of amino acids: _____

Additional Information:
