

Proteomics Sample Submission Form
University of Utah
Mass Spectrometry and Proteomics Core Facility

User Information

Name: _____ Submission Date: _____
Department: _____ Telephone: _____
Principal Investigator: _____ Email address: _____
Account # _____ Do you want results sent to you by Email? yes (additional \$5 charge)

Fill in all applicable information as completely as possible

Sample Information

Sample ID / Description on vial or gel _____
MW / Formula _____ Approx Amount _____ Approx Purity _____ HPLC purified: yes no
Did you send sequence information by email to the MS Core? yes no Storage conditions: 4⁰C -20⁰C -80⁰C
Hazardous Material? _____ If YES, please describe (toxic, radioactive, carcinogen, etc.) _____

Gel bands or 2D spots:

Stain used: coomassie _____ colloidal blue _____ sypro ruby _____ silver (which kit?) _____
Pre-cast gel _____ Fresh cast gel _____ Was the gel made at least 24 hrs prior to use? yes no Polyacrylamide % _____

Proteins in Solution:

Concentration _____ Describe the solution in detail (buffer, salts, pH, etc.) _____
Does the solution contain (or was the protein exposed to) any of the following and at what concentration (even trace levels):
Detergents (e.g. SDS, Triton) _____ Did you use glassware previously exposed to detergents? _____
PEG _____ Polymers _____ Sephadex _____ DTT _____ BME _____ HEPES (or other non-volatile buffer) _____
EDTA _____ Phosphate salts _____ Flag tag elution _____ Elution reagents _____
Protease inhibitors (e.g. AEBSF; Roche Mini Complete, aprotinin, leupeptin) _____ Phosphatase inhibitors _____
Any enzymes _____ Reduction and alkylation _____ Denaturants (e.g. urea) _____
Has the protein sample been derivatized in any way or exposed to potential derivatizing reagents (e.g. alkylation, NEM)? _____

Desired Information:

Protein ID _____ Protein ID (complex isolate, IP pull-down) _____ Target proteins (name or access. #) _____
ID disulfide linkages _____ Peptide denovo sequencing (what ions) _____ Fragmentation: CID ECD IRMPD
Intact MW _____ Identify truncation, cut sites, or degradation products _____ "Top-down" intact protein analysis (FTMS with ECD) _____
ID peptides w/ sulfur (cys, met) or selenium _____ Accurate mass measurement (<2ppm _____) (<1ppm _____) (full scan _____)
Method of Analysis: LC/MS/MS _____ LC/MS/MS (FTMS) _____ MALDI/FTMS _____ MALDI/ToF _____ ESI/MS _____ ESI/FTMS _____

Database Search Information: (what you want searched)

Select one of the following databases: MSDB _____ NCBI _____ Custom database _____ Mascot "Decoy" (search for false positives) _____
Taxonomy: Specific (e.g. human, mouse) _____ or All Taxonomies _____ or Both (\$22 extra) _____
If desired, select up to three modifications below (normally include oxidation (M)). Do you have a custom modification request? _____
(Searches for additional modifications are extra, see prices on web site).

acetyl (K) acetyl (N-term) AEBSF (KYH) amide (C-term) BEMAD (ST) Biotin (K) biotin (N-term) carbamidomethyl (C) carbamyl (K) carboxymethyl (C) deamide(NQ)
 GlcNAc (ST) homoserine (C-term M) homoserine lactone (C-term M) methyl ester (C-term) methyl ester (DE) MMTS (C) NEM (C) oxidation (M) oxidation (PHW)
 phosphorylation (STY) pyro Glu (N-term E) pyro Glu (N-term Q) sumoylation (K) sumoylation (N-term) sulfation (STY) sulfation (M) ubiquitination (K) Other (custom)

Location and Staff

Room 470 BPRB
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581-5018 or 585-9865

www.cores.utah.edu

Director: Chad C. Nelson, Ph.D. (chad.nelson@genetics.utah.edu)
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Analyst: Mike Hanson, Ph.D. (mike.hanson@genetics.utah.edu)

MS file names:

Cost for analyses:

Notified user of completed analysis: email phone Date: