



## Mass Spectrometry and Protein Analysis Request Form

(Please fill out form completely)

Client Information	Sample Information	Sample Type
Name: _____	Sample Name: _____	<input type="checkbox"/> Gel Stain Type: _____
Email: _____	Concentration: _____	<input type="checkbox"/> Liquid Amount: _____ Buffer Components: _____
Phone #: _____	Molecular Weight: _____	<input type="checkbox"/> Solid Amount: _____ Solubility: _____
P.I. Name: _____	Species: _____	<input type="checkbox"/> PVDF Blot Stain: _____
Department: _____	Tissue: _____	Transfer Buffer: _____
Address: _____	Radioactivity: <input type="checkbox"/> Yes <input type="checkbox"/> No	
Date: _____	Storage Temp: <input type="checkbox"/> 4°C <input type="checkbox"/> -20°C <input type="checkbox"/> -80°C	
Shortcode/PO: _____	Easily Replaced?: <input type="checkbox"/> Yes <input type="checkbox"/> No	

Requested Services	<b>Qualitative Proteomics Services</b> <input type="checkbox"/> Protein Identification <input type="checkbox"/> Protein Profiling (GeLCMS) <input type="checkbox"/> Maximum Sequence Coverage <input type="checkbox"/> Phospho- or Glyco- Site Mapping <input type="checkbox"/> Localization of Other Modifications	<b>Quantitative Proteomics Services</b> <input type="checkbox"/> Label-Free Quantitation (Spectral Count) <input type="checkbox"/> TMT/iTRAQ (Isotope Labeling) <input type="checkbox"/> SILAC (Metabolic Labeling) <input type="checkbox"/> PRM (Most Accurate) <input type="checkbox"/> Extensive/Manual Data Interpretation	<b>Pathway Analysis</b> Project Number: _____ Data File Name: _____ Desired Comparisons: _____
	<b>N-terminal Sequencing (Edman)</b> Number of Residues: _____ <input type="checkbox"/> Liquid <input type="checkbox"/> Blot	<b>N/C Term. Sequencing (MALDI-TOF)</b> Protein Amount: _____ Schedule a consultation appointment	<b>Electrophoresis</b> <input type="checkbox"/> SDS PAGE <input type="checkbox"/> 2-D PAGE
	<b>Intact Molecular Weight Analysis</b> <input type="checkbox"/> MALDI-TOF MS <input type="checkbox"/> ESI MS	<b>Quantitative Amino Acid Analysis</b> <input type="checkbox"/> Duplicate <input type="checkbox"/> Triplicate Cysteine and Tryptophan are not included in Analysis	
	<b>Acceptable Buffers/Solvents:</b> Water ♦ Trifluoroacetic acid ♦ Acetonitrile ♦ Ethanol ♦ Methanol ♦ Urea <50mM ♦ HEPES ~5mM ♦ Guanadine/HCl <4M ♦ Salts and non-phosphate buffers <100mM ♦ Acetic or Formic Acid ♦ Hexafluoroisopropanol <40% ♦ octyl-glycoside <0.05% <b>Acceptable Buffers/Solvents:</b> Water ♦ Acetonitrile ♦ Ethanol ♦ Methanol ♦ Aqueous ammonium hydroxide ♦ Isopropanol ♦ max. 100mM Ammonium acetate ♦ Formic Acid ♦ Acetic acid		
	<b>Comments:</b>           		

**NOTE:** Cancellations are not to be accepted after analysis has been started. In case the desired sequencing result cannot be obtained due to N-terminal blockage, interfering buffer components, or low amount of the submitted sample, charges still apply. **Submission of this request confirms acceptance of the Proteomics & Peptide Synthesis Core policy.**

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