

Mass Spectrometry and Protein Analysis Request Form

(Form must be filled out completely)

User Information:

User Name:	P.I. Name:	Date:
e-mail:	Phone No:	Shortcode/P.O. #
Fax No:	Department/Company:	<input type="checkbox"/> Rheumatic Disease Core Center
Address:		<input type="checkbox"/> MDRTC

Sample Information:

Name:	<input type="checkbox"/> PVDF Blot	Transfer Buffer:	Stain:
Concentration:	<input type="checkbox"/> Liquid	Buffer components:	
Molecular Weight:	<input type="checkbox"/> Gel	Stain Type:	
Radioactivity: <input type="checkbox"/> YES <input type="checkbox"/> NO	<input type="checkbox"/> Solid	Solubility:	Quantity:
Storage Temp: <input type="checkbox"/> 4°C <input type="checkbox"/> -20°C <input type="checkbox"/> -80°C	Notes:		
Easily Replaced? <input type="checkbox"/> YES <input type="checkbox"/> NO			

Services: (please check services requested)

<input type="checkbox"/> Electrophoresis:			
<input type="checkbox"/> SDS PAGE	Gel Type: <input type="checkbox"/> Bis-Tris <input type="checkbox"/> Tris-HCl		
<input type="checkbox"/> 2-D PAGE	pH Range: <input type="checkbox"/> 4-7 L <input type="checkbox"/> 3-10 L <input type="checkbox"/> 3-11 NL <input type="checkbox"/> 6-11L <input type="checkbox"/> other		
	<u>Sample Contains:</u>		
	Lipids, DNA, Carbs, etc: <input type="checkbox"/> YES <input type="checkbox"/> NO	Protease Inhibitor: <input type="checkbox"/> YES <input type="checkbox"/> NO	_____
	Ionic Detergents: <input type="checkbox"/> YES <input type="checkbox"/> NO	Salts: <input type="checkbox"/> YES <input type="checkbox"/> NO	
<input type="checkbox"/> PVDF blot			
<input type="checkbox"/> Protein Digestion	<input type="checkbox"/> in-gel <input type="checkbox"/> in-solution	<input type="checkbox"/> Trypsin <input type="checkbox"/> Chymotrypsin <input type="checkbox"/> other	
<input type="checkbox"/> Mass Spectrometry - Electrospray	<input type="checkbox"/> Mass Spectrometry - MALDI-TOF	<input type="checkbox"/> Database Search	
<input type="checkbox"/> Protein Identification	<input type="checkbox"/> Peptide Mass Fingerprinting	Species: _____	
<input type="checkbox"/> LC-MS Analysis	<input type="checkbox"/> Intact Molecular Weight Analysis	Tissue: _____	
<input type="checkbox"/> Intact Molecular Weight Analysis	<input type="checkbox"/> Data Interpretation	pI (Method of Determination): _____	
<input type="checkbox"/> Data Interpretation	<input type="checkbox"/> Data in Electronic Format		
<input type="checkbox"/> Data in Electronic Format	<input type="checkbox"/> Microdesalting (zip tip)	MW (Method of Determination): _____	
Buffers/Solvents	Water ♦ Trifluoroacetic acid ♦ Acetonitrile ♦ Ethanol ♦ Methanol ♦ Urea <50mM ♦ Salts and non-phosphate buffers <100mM		
MALDI-TOF MS	♦ HEPES ~5mM ♦ Acetic or Formic acid ♦ Guanidine/HCl <4M ♦ Hexafluoroisopropanol less than 40% ♦ Octyl- glucoside less than 0.05%		
Acceptable Buffers/Solvents	Water ♦ Acetic Acid ♦ Formic Acid ♦ Aqueous ammonium hydroxide ♦ Acetonitrile		
ESI-MS	♦ Methanol ♦ Ethanol ♦ Isopropanol ♦ max. 100 mM Ammonium acetate		

Outsourcing Services:

<input type="checkbox"/> N- Terminal Sequencing	Number of Residues: _____	<input type="checkbox"/> Liquid <input type="checkbox"/> Blot	Transfer Buffer: _____
<input type="checkbox"/> Amino Acid Analysis	<input type="checkbox"/> Qualitative <input type="checkbox"/> Quantitative	<input type="checkbox"/> Cys <input type="checkbox"/> Trp	

Comments:

NOTE: Cancellations are not to be accepted after analysis has been started. In case the desired sequencing result can not 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 Protein Structure Facility policy.

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