

PROTEIN & PEPTIDE MASS SPECTROMETRY SAMPLE SUBMISSION FORM

NC STATE UNIVERSITY

Mass Spectrometry Facility
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Customer Identification

Submission Date	P.O. or Acct.#	P.I. (Authorizer)
Submitted by		Phone
Send Invoice to		FAX
Billing Address/Dept.		E-mail

Sample Identification*

Note: please submit one form for each sample in solution or for the bands from one SDS-gel

Label (as appears on vial)

Sample Format

Method of purification: _____

Purity: _____

Criteria for purity: gel image other: _____

Solution Buffer, salts in solution: _____

Approximate MW (Da) if known: _____

Reduction & alkylation chemicals: _____

Digestion enzyme: _____

from Gel Proteins for analysis: gel image with bands checked

Bands to be analyzed: _____

Concentration (µg/µL)

Suspected Modifications

Amino Acids Modified

Taxonomy (species)

Storage Requirement

Sequence (if known) & Comments

Analysis Instructions

- Stand alone HPLC run by MS facility
- Protein in solution – clean-up/desalting by Sep-Pak
- Protein in solution – clean-up/desalting by Zip Tip
- Mass determination of intact protein by ESI-MS
- Mass determination of intact protein by LC-MS
- Digestion of protein in solution
- Reduction/alkylation/digestion of protein in solution or gel band
- Sequencing: ESI-MS/MS
- Sequencing: LC-MS/MS
- Qualitative analysis
- Quantitative analysis
- Self-use (MALDI-TOF)

For Facility Use

Instrument	Ionization	Date
<input type="checkbox"/> Thermo LTQ-Orbitrap		
<input type="checkbox"/> Agilent LC-TOF		
<input type="checkbox"/> Agilent 5975 GC/MS		
<input type="checkbox"/> HP GCD GC-MS		
<input type="checkbox"/> Bruker Omnicflex MALDI-TOF		
<input type="checkbox"/> Thermo TSQ Quantum Discovery MAX LC-MS		

Additional Notes

Date Received:	Date Completed:	Analyst:	Time spent:
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*Local samples must be picked up after completion of analysis. Samples shipped as return requested without prior arrangement will not be returned.