

# MASS SPECTROMETRY RESEARCH FACILITY

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## Proteomics Service Submission Form

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### Contact Information

Name: \_\_\_\_\_ Department: \_\_\_\_\_

Research Group: \_\_\_\_\_ Email: \_\_\_\_\_ Telephone: \_\_\_\_\_

Project Code/Charge Account number/ \_\_\_\_\_ Date: \_\_\_\_\_

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### Sample Information

Number of samples being submitted: \_\_\_\_\_

Sample IDs (multiple samples can be submitted here)  
\_\_\_\_\_

Sample type: Tryptic digest\*  Intact Protein  Peptide

Sample Volume supplied: \_\_\_\_\_ Sample concentration: \_\_\_\_\_

Sample molecular weight: \_\_\_\_\_

Sample buffer/solvents: \_\_\_\_\_

Sample buffer concentration: \_\_\_\_\_

Sample Purification: ZipTip  C18 spin Columns  SepPak

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### MS Proteomic Service required

Intact protein molecular weight measurement

Protein Identification

Protein Post-Translational Modification Analysis:

• Common modification

• Glycosylation (please provide details)

Comments: \_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

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## *Guidelines for sample submission*

1. Provide 10-20ul of samples in no recovery vials\* for LC-MS/MS analysis

### **\*Autosampler vials appropriate for analysis**

Waters ([Total Recovery \(part number: 186000385C.\)](#))



**Figure 1: Waters Total Recovery Vial**

2. Provide samples in 1.5 ml eppendorf tube for MADI-TOF/TOF analysis.

3. Label your tube with the sample ID.

3. Fill in online sample submission form to provide us with more information about your sample

**Please note:** We plan to return raw data files for the analysis requested within 2 weeks of submission but please be aware the Proteomics Service currently relies on a single instrument and delays can occur for technical reasons.