OHRI Proteomics Core Facility

Service Request Form

Steps to submit samples:

1) Complete this form and electronically submit to Andrew Macklin at proteomics@ohri.ca . Paper copies are no longer necessary.

2) Coordinate a sample drop-off time or put them in the freezer in room W5155 (TOH General Campus).
If you need access to the 5th floor, please text Andrew's cell at 613-304-1687

This section is for facility use only

Submission ID

Date Received

Date Completed

Fee ($) to be charged for Service

Facility Manager Signature

P.I. First Name_____ Institution _____

P.I. Last Name _____ Department _____

Name of Lab Member Submitting Samples _____

Lab Member E-mail _____

OHRI Cost Centre _____

---OR---

University of Ottawa P.O. # _____

First-time non-OHRI and non-uOttawa clients please attach complete mailing and billing addresses.

Sample Names			
#	**Sample Name**	**#**	**Sample Name**
1		**17**	
2		**18**	
3		**19**	
4		**20**	
5		**21**	
6		**22**	
7		**23**	
8		**24**	
9		**25**	
10		**26**	
11		**27**	
12		**28**	
13		**29**	
14		**30**	
15		**31**	
16		**32**	

**If more than 32 samples are being submitted, please attach additional sample lists to email*

Sample Details

Submitted Sample format:

☐ **Digested peptides in solution** (Recommended: reconstitute in 10-15uL of water containing 0.1-0.5% formic acid)
Which protease was used for digestion into peptides: ☐ Trypsin ☐ Other: _____
Proteins were treated with:
☐ Dithiothreitol (DTT) ☐ Iodoacetamide ☐ iodoacetic acid ☐ MMTS ☐ Urea
☐ Cross-linker (specify): _____
If not 10-15uL of water containing 0.1-0.5% formic acid, what are the buffer components and volume:
_____

☐ **Gel Bands** (Recommended: please attach a photo of the stained gel to this document or email)
If so, the gel was stained with: ☐ Coomassie Blue ☐ Silver ☐ Other: _____

☐ **Proteins in-solution (lysates)**
Sample volume: _____ µL Protein Concentration: _____
Lysis/Binding/Elution buffer components: _____

☐ **Protein pre-bound to magnetic beads** (don't freeze, submit by 2pm Mon-Thurs with 2 days advanced notice)
Sample volume: _____ µL
Binding/Elution Sample buffer components: _____

Has a chemical or metabolic label been incorporated for protein quantitation?
☐ SILAC (specify label): _____
☐ TMT / iTRAQ (specify kit): _____
☐ Other: _____

Protein Detection

What is the research priority with this batch of samples:

☐ Protein identification and quantification (typical)
☐ Maximize sequence coverage of a specific protein/construct of interest to detect a PTM or mutation. If so, specify the specific region or amino acids positions:
_____
_____

Species (taxonomy) of the proteins of interest:
☐ Human ☐ Mus musculus ☐ Other: _____

Which proteins do you expect to be detected that may serve as positive controls (Pulldown baits, known interactors etc.). Specify: _____

Are there any contaminant proteins to be expected (antibodies, blocking agents? Etc.)? Specify:
_____

Is there protein of interest is a custom construct, please provide the amino acid sequence when submitting this form. Are there any tags in your custom construct (Flag, myc, BirA, GFP etc.). If so, specify:
_____

LC-MS Services Requested

LC-MS analysis method to be used:

☐ I trust the Core will choose the most suitable method based on the project goals.

*Unless otherwise instructed, legacied methods will be used to match previous batches of sample submissions for the same project. It is recommended to switch to the newly optimized default HCD methods for new projects. If unsure about anything in this box, please contact the Core to discuss the most suitable options

-------OR the client selects the LC-MS Method below--------

- New default methods, Higher collision dissociation (HCD): ☐ 45min ☐ 60min ☐ 90min ☐ 180min
- Legacy Methods (to match pre-2024 experiments): ☐ 40min CID ☐ 45min HCD ☐ 55min CID ☐ 85min CID
- Other: _____

☐ I want to run a technical LC-MS duplicate injection of these samples. This generally leads to 20% more proteins detected but incurs additional fees.

☐ I want to analyze the samples by additional fragmentation methods (CID, ETD) for higher chances of achieving sequence coverage and PTM detection (incurs additional fees)

Additional Data Analysis Services Requested

☐ Maxquant Analysis requested (additional fees apply)
False-Discovery Rate (FDR) set to: ☐ 1% ☐100%

☐ I want to receive the MS Raw files so I can do my own database searching (upon request, complimentary)

☐ Custom service (specify): _____

Are there any other special instructions or notes on sample preparation that the Core Facility should be aware of?

_____

_____

Pre-submission Checklist

☐ I confirm the submitted samples are non-hazardous (no biohazard, no radioactivity). All Core Facility services are for research purposes only. I have read the sample preparation guidelines (www.ohri.ca/proteomics) and understand that failure to meet the sample submission guidelines may require additional work for the Core Facility and that a fee will be charged for this work. The facility cannot guarantee a specific turnaround time for results.

☐ I understand that this service will only identify sequences that are present in the reference proteome for the species specified on this form. Please contact the Core Facility if a custom reference sequence is required. I understand that the presence of high-abundance proteins (*e.g.* serum) and/or protein reagents (*e.g.* antibody, protein A/G) will affect the results unless they are depleted before submission. I understand that limitations apply to the detection of post-translational modifications (PTMs), and I have indicated all modifications that are relevant to this analysis. I understand that LC-MS/MS analysis does not provide 100% protein sequence coverage.

☐ If the client already digested the proteins into peptides, I confirm the samples are free of particulates (beads), detergents or other chemical interferences. The peptides are stored with 0.1-0.5% formic acid in water.