



Proteomics Core Facility Service Request Form

Please remit form and samples to:
The Ottawa Hospital General Campus · Room W5256
501 Smyth Road, Ottawa, Ontario K1H 8L6
613 737-8899 x73455 · proteomics@ohri.ca

This area for facility use only

Submission ID

Date Received

Date Completed

PI First Name _____ Department _____

PI Last Name _____ Institution _____

Submitted By _____ E-mail _____

P.O. # _____

University of Ottawa clients please provide PO number. First time customers please attach complete mailing and billing address. Hazardous samples (biohazards, radioactive, etc.) are not permitted.

Proteomics Samples List			
#	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	
...	Please attach additional sheet(s) if required		

Sample Details
Sample format:
<input type="checkbox"/> protein in gel
<input type="checkbox"/> protein in solution
<input type="checkbox"/> peptides (protein digest)
Stain:
<input type="checkbox"/> none
<input type="checkbox"/> blue
<input type="checkbox"/> silver
<input type="checkbox"/> sypro
Protein was treated with:
<input type="checkbox"/> iodoacetamide
<input type="checkbox"/> iodoacetic acid
<input type="checkbox"/> urea
<input type="checkbox"/> MMTS
<input type="checkbox"/> iTRAQ/ TMT
<input type="checkbox"/> cross-linker (specify)
<input type="checkbox"/> enzyme (specify)
<input type="checkbox"/> _____

Species (taxonomy) for protein matching (please list all, including any antibodies, blocking proteins, etc.)

Post-translational modifications expected (including isotopic labels, tags, etc.)

Service Requested
<input type="checkbox"/> Standard Protein Identification Service
<input type="checkbox"/> Custom Service (specify on back of form)



Please supply any further information or special instructions.

Pre-submission Checklist

Part A – All Samples

- I understand that all Core Facility services are for *research purposes only*.
- I have read and understood the sample preparation guidelines (www.ohri.ca/proteomics).
- I understand that LC-MS/MS analysis does not provide 100% protein sequence coverage.
- 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) in the sample will affect the results.
- I understand that limitations apply to the detection of post-translational modifications (PTMs), and I have indicated on this form all modifications that are relevant to this analysis.

Part B - If submitting samples in gel:

- The stain used is compatible with mass spectrometry.
- Optional (recommended): I have e-mailed or attached a photo of the stained gel.

Part C – If submitting proteins or peptides in solution:

- The samples are free of particles or debris.
- The samples are free of detergents or other chemical interferences.
- Please indicate composition of solution (including any salts, etc.) in the comments section, above.
- High-abundance background proteins, such as albumin or antibody, have been depleted.
- If submitting proteins for trypsin digestion, the pH of the solution should be 6.8 – 8.0
- Please write the amount/concentration of sample (if known).
- I understand that in-solution samples may require additional purification and/or a pre-screening analysis in addition to the main analysis and that a fee will be charged for this work.