**Proteomics Service Inquiry**

**Instructions:**

Please fill out all fields and submit completed form to Tenny Lao (ying.lao@umanitoba.ca). We will provide you with a customized project plan to meet your research requests. It is highly recommended to discuss before sample preparation to avoid possible incompatibilities.

**Customer Information:**

PI Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ FOAP: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Phone: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Email address: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Project Description (Please briefly explain objectives, experimental design and approach):**

Click or tap here to enter text.

**Services** (check required service(s))**:**

* [ ] Identification of protein interaction partners (provide Uniprot number of target proteins in Table below)
	+ [ ] Co-immunoprecipitation (co-IP)
	+ [ ] BioID
	+ [ ] Crosslinking protein interaction
	+ [ ] Other approach. Please describe: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
* [ ] Identification of proteins in a complex mixture (such as serum, urine, and cell lysates)

Indicate dynamic range for low abundant proteins \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

* [ ] Protein Quantification
	+ [ ] Isobaric labeling-based relative quantification
	+ [ ] SILAC-based relative quantification
	+ [ ] Absolute quantification
	+ [ ] Label-free quantification
	+ [ ] Parallel reaction monitoring
* [ ] Protein Post-translational modification (PTM) analysis (purified proteins are preferred)
	+ list all expected PTMs \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Sample Information:**

**Indicate sample type:** [ ] Tissue [ ] Cells [ ] Biological fluids [ ] Lysates [ ] Purified Proteins [ ] Peptides [ ] Others

Others: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

For cell samples, please indicate cell counts (if known) \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Additional Sample Information:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|   | Name  | Species | Name and Uniprot # of target protein (s) | Sample state (gel piece, liquid, beads, etc) | Protein quantity (ug) | Volume (ul) | Buffer Composition (detergents or salts) | Biohazard (yes/no) |
| 1 |   |   |   |   |   |   |   |   |
| 2 |   |   |   |   |   |   |   |   |
| 3 |   |   |   |   |   |   |   |   |
| 4 |   |   |   |   |   |   |   |   |
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| 16 |   |   |   |   |   |   |   |   |

Please describe sample preparation for every sample in a separate page.

Additional comments: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_