



**Proteomics International**

# REQUEST FORM 003

Lab Use

## Proteome Mapping – MuDPIT analysis

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ISO/IEC 17025

### SECTION A

Contact details	
<b>Name</b>	<b>Billing Address</b>
<b>Organisation/ Institution</b>	<b>Email</b>
	<b>Telephone</b>
<b>Purchase Order Number</b>	<b>Fax</b>

**Note:** For Credit Cards/other online payments refer to last page

Sample Information - Please complete details on all pages & sign the last page	
<b>Source:</b> (e.g. freeze-dried or aqueous sample)	<b>Buffer composition for liquid or freeze-dried sample:</b>
<b>Is your target database one of the following:</b> Human, Rat, Mouse, Zebrafish, <i>E. coli</i> , Rice, Yeast <b>If not, please provide more details in Section C of this form.</b>	<b>Amount of protein in sample(s):</b>  <b>Method of assessment:</b>  <b>Volume of liquid sample(s):</b>
<b>Storage condition of sample:</b> (-80°C, -20°C, 2 – 8°C, Room temperature)	
<b>No. of Samples (n):</b>	<b>Any other treatments or chemicals present:</b> (e.g. acetone precipitation, sucrose etc.)

### Proteomics Analysis price guide as of January 2024

Price (Ex. GST)

Service 003 - Proteome Mapping – MuDPIT analysis		<input type="checkbox"/> USD	<input type="checkbox"/> AUD
<input type="checkbox"/> 1D LC-MS/MS. Protein sample is run through an extended LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS)	Single sample; >1000 protein IDs	\$2,200 per experiment	\$3,300 per experiment
<input type="checkbox"/> 2D LC-MS/MS. Protein sample is run through a sophisticated 2D LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS)	Single sample; >2000 protein IDs	\$4,400 per experiment	\$6,600 per experiment

Lab use only:			
Date Received + Initial:		Instrument use:	
Sample Second Checked by:		Spot set:	
Storage Location:		MS data analysis + Operator:	
Date Processed + Operator:		Report Reference:	
Special Considerations:		Report Checked by:	
		Workflow Checked by:	

## SECTION B

For each sample please provide the following information if known:

No.	Sample Details				Lab use only		
	Sample Identification	Amount of protein (mg or uL)	Purity %	Molecular mass (kDa)	PI number	Checked by	Comments
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15							

(Please append extra table if required)

**Comments:**

## SECTION C

### Further details on database for protein identification

**Effective protein identification by mass spectrometry is highly dependent on access to an appropriate database. Answers to the following questions will guide the data analysis pipeline.**

1. What is the target organism?

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2. What other contaminating organisms are likely to be present in the sample provided?

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3. What are the most taxonomically related species of the target organism?

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4. Is the database for the target organism or its related species available in the NCBI or Swiss-Prot databases, otherwise where can they be downloaded? Please provide details.

.....

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#### **Note**

**Please consider *De novo* peptide sequencing (Service 002) if the target species is not available or not well represented in the NCBI or Swiss-Prot databases.**

For online credit card payment, please tick here:



Please sign here below:

1. I have read and understood the Proteomics Analysis Price List and agree to the charges and to Proteomics International's standard Terms and Conditions (available at: <http://www.proteomics.com.au/analytical-services/terms-and-conditions/>).
2. **Hazards:** I declare that the sample(s) are non-harmful, non-infectious and non-radioactive.
3. I have completed both pages of this submission form with details for each sample submitted for analysis.
4. For students, please ensure supervisor signs this form.

Note: Please be aware that samples are destroyed by analysis and cannot be returned.

**Authorised Signature** \_\_\_\_\_

**Date:** \_\_\_\_\_