



**Proteomics International**

# REQUEST FORM 003

## Proteome Mapping – MuDPIT analysis

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Lab Use



Accreditation No: 16838  
 ISO 17025 certified

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>

Sample Information - Please sign & complete details on page 2	
<b>Is your target database one of the following:</b> (Human, Rat, Mouse, Zebrafish, E. coli, Rice, Yeast )  If not, please provide more details on section <b>B</b> of this form.	<b>Buffer composition for liquid or freeze dried sample:</b>
<b>Amount of protein in sample:</b>  <b>Method of assessment:</b>  <b>Volume of liquid sample:</b>	<b>Any other treatments or chemicals present:</b> (e.g. acetone precipitation, sucrose etc)

Consult 1st Base for latest price information (Feb 2012).

Service 003 - Proteome Mapping – MuDPIT analysis		Price
<input type="checkbox"/> 1D LC-MALDI. Simple protein sample is run through an extended LC gradient, and the eluent spotted for MALDI-TOF/TOF analysis	Single (simple sample)	Enquire
<input type="checkbox"/> 2D LC-MALDI. Complex protein sample is run through a sophisticated 2D LC gradient, and the eluent spotted for MALDI-TOF/TOF analysis	Single (complex sample)	Enquire

**Lab use only:**

Prep received:		MS received:	
Processed/Operator:		Plate No./Spot set:	
QC No:		MS data analysis/Operator:	
Batch:		Report reference:	
Special Considerations:		Checked:	

For each sample please provide the following information if known:

No.	Sample Details		Lab use only			
	Sample number/ Identification	Molecular mass (kDa)	PI number	Sprot	Spec-Q	S-Dbase
1						
2						
3						
4						
5						
6						
7						
8						
9						
10						
11						
12						
13						
14						
15						
16						
17						

(Please append extra table if required)

**Comments:**

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/TermsAndConditions>).
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.

Authorised Signature \_\_\_\_\_ Date: \_\_\_\_\_

## SECTION B

### 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.**

**\*Where a client's specific database is provided, database set up will be required. Searches conducted against client databases will incur additional set up charges and the results can only be supplied to client in Html, Xml or Excel files (default = Html).**