



**Proteomics International**

# REQUEST FORM 001

Lab Use

## Protein Identification by Mass Spectrometry (Sequencing by MS/MS)

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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>Fax</b>	
<b>Purchase Order Number</b>		<b>Client Mascot Login</b>	<b>Username:</b>
			<b>Password:</b>

Sample Information - Please complete details on all pages & sign page 3	
<b>Source:</b> (e.g. gel-band, freeze-dried or aqueous sample)	<b>Buffer composition for liquid or freeze-dried sample:</b>
<b>Staining Method:</b> (eg. Coomassie, silver*, other)  <b>Note:</b> *Please request mass spectrometry silver stain protocol first.	<b>Amount of protein in sample(s):</b>
	<b>Purity of sample(s):</b>
<b>Provide details at Section C for target database.</b>	<b>Volume of liquid sample(s):</b>
	<b>Chemicals used for reduction &amp; alkylation, if any:</b>
	<b>No. of Samples (n):</b>

**Please consult APICAL for latest price information.**

Service 001 - Protein identification by mass spectrometry (sequencing by MS/MS)	Price (USD)
<input type="checkbox"/> by MALDI-TOF/TOF (PMF+MS/MS) mass spectrometry, with automatic database analysis (Optimal for Coomassie stained gels and 2D gel spots)	Single (pure sample) Multiple samples (>10) Bulk quantity (>50) No result fee
<input type="checkbox"/> by electrospray (LC-MS/MS) mass spectrometry, with automatic database analysis (Optimal for gel bands containing 2 or more proteins, or low abundant samples (e.g. silver stained))	Single (pure sample) Multiple samples (>10) Bulk quantity (>50) No result fee
	<i>Enquire</i>

**Lab use only:**

Prep Received:		Plate No./Spot set:	
Processed/Operator:		MS data analysis/Operator:	
QC No:		Client login:	Username:
			Password:
Enzyme Lot No:		Report Reference:	
Special Considerations:		Checked Workflow:	
		Checked Report:	

## SECTION B

**For each sample please provide the following information if known:**

No.	Sample Details				Lab use only			
No.	Sample Identification	Amount of protein (mg or uL)	Purity %	Molecular mass (kDa)	PI number	Spot No.	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.**

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