



**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			
Name		Billing Address	
Organisation/ Institution		Email	
		Telephone	
		Fax	
Purchase Order Number		Client Mascot Login	Username:
			Password:

**Note:** Credit Card details are required with Request Form (enter details on page 4).

Sample Information - Please complete details on all pages & sign page 4	
Source: (e.g. gel-band, freeze-dried or aqueous sample)	Buffer composition for liquid or freeze-dried sample:
Staining Method: (eg. Coomassie, silver*, other)	Amount of protein in sample(s):
Note: *Please request mass spectrometry silver stain protocol first.	Purity of sample(s):
	Volume of liquid sample(s):
Provide details at Section C for target database.	Chemicals used for reduction & alkylation, if any:
	No. of Samples (n):

**Proteomics Analysis price guide as of June 2020.** Consult our website for latest price information.

Service 001 - Protein identification by mass spectrometry (sequencing by MS/MS)	Price (USD)
<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) \$200 per sample Multiple samples (10-25) \$190 per sample Bulk quantity (>25) \$175 per sample
<input type="checkbox"/> Raw data	\$75 per sample
<input type="checkbox"/> MS Spectra	\$75 per sample
<input type="checkbox"/> Custom database analysis	\$75 per sample

#### 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			
	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?

.....

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.

.....

.....

**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.**

**Proteomics International**

**Credit Card Information**

Visa       MasterCard

Card Number \_\_\_\_\_

Expiry \_\_\_\_ / \_\_\_\_

Name on the Card: \_\_\_\_\_

Email address for invoice / receipt. \_\_\_\_\_

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