



Proteomics International

REQUEST FORM 001

Lab Use

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

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ABN 78 096 013 455



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 July 2021. 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:		Date completed:	
		Date filed (operator):	

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?

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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.

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: _____