



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
Purchase Order Number		Fax

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

Please consult 1st BASE 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	<i>Enquire</i>
<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	

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	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: _____