REQUEST FORM 001

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

Proteomics International

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Accreditation No: 16838
ISO 17025 certified

SECTION A

Contact details			
Name		**Billing Address**	
Organisation/ Institution		**Email**	
		Telephone	
Purchase Order Number		**Fax**	

Sample Information – Please sign & complete details on page 2	
Source: (e.g. gel-band, freeze-dried or aqueous sample)	**Buffer composition for liquid or freeze dried sample:**
Is the target database one of the following: (Human, Rat, Mouse, Yeast, *E. coli*, Zebrafish) If not, please provide more details on section **B** of this form	**Amount of protein in sample:** **Purity of sample:** **Volume of liquid sample:**
Staining method: (e.g. Coomassie, silver*, other) **Note**: Please request mass spectrometry silver stain protocol first.	**Chemicals used for reduction & alkylation, if any:**
	No. of Samples (n): / **Duplicates:**

Consult 1st BASE for latest price information (September 2013).

Service 001 - Protein identification by mass spectrometry (sequencing by MS/MS)		Price
☐ by MALDI-TOF/TOF (PMF+MS/MS) mass spectrometry, with automatic database analysis	Single (pure sample)	Enquire
(Optimal for Coomassie stained gels and 2D gel spots)	Multiple samples (>10)	
	Bulk quantity (>50)	
	No result fee	
☐ by electrospray (LC/MS/MS) mass spectrometry, with automatic database analysis	Single (pure sample)	Enquire
(Optimal for gel bands containing 2 or more proteins, or low abundant samples (e.g. silver stained))	Multiple samples (>10)	
	Bulk quantity (>50)	
	No result fee	
Client specific database set up	For 1 database	

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:	

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?

    ……

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.

    ………

    ……...

<u>Note</u>

*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).