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

Proteomics International

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NATA
ISO/IEC 17025

SECTION A

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

Note: **For Credit Cards/other online payments refer to last page**

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: (e.g. Coomassie, silver*, other) **Note**: *Please request mass spectrometry silver stain protocol first.	**Amount of protein in sample(s):** **Purity of sample(s):** **Volume of liquid sample(s):**
Storage condition of sample: (-80°C, -20°C, 2 – 8°C, Room temperature)	**Chemicals used for reduction & alkylation, if any:**
Provide details at Section C for target database.	**No. of Samples (n):**

Proteomics Analysis price guide as of January 2024: **Price (Ex. GST)**

Service 001 - Protein identification by mass spectrometry (sequencing by MS/MS)		☐**USD**	☐**AUD**
☐ 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 (10-25) Bulk quantity (>25)	$200 per sample $190 per sample $175 per sample	$300 per sample $285 per sample $265 per sample
☐ Raw data ☐ MS Spectra ☐ Custom database analysis		$75 per sample $75 per sample $75 per sample	$115 per sample $115 per sample $115 per sample

Lab use only:			
Date Received + Initial:		Spot set:	
Sample Second Checked by:		MS data analysis + Operator:	
Storage Location:		Client login:	Username:
Date Processed + Operator:			Password:
Instrument use:		Report Reference:	
Special Considerations:		Report Checked by:	

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	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.

   ………

   ………..

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.

For online credit card payment, please tick here:

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: _____**