



Proteomics International

REQUEST FORM 003

Proteome Mapping – MuDPIT analysis

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Lab Use



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. freeze-dried or aqueous sample)	Buffer composition for liquid or freeze-dried sample:
Is your target database one of the following: Human, Rat, Mouse, Zebrafish, <i>E. coli</i> , Rice, Yeast If not, please provide more details in Section C of this form.	Amount of protein in sample(s): Method of assessment: Volume of liquid sample(s):
No. of Samples (n):	Any other treatments or chemicals present: (e.g. acetone precipitation, sucrose etc.)

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

Service 003 - Proteome Mapping – MuDPIT analysis	Price (USD)
<input type="checkbox"/> 1D LC-MS/MS. Protein sample is run through an extended LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS)	Single sample; >1000 protein IDs \$2,200 per experiment
<input type="checkbox"/> 2D LC-MS/MS. Protein sample is run through a sophisticated 2D LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS)	Single sample; >2000 protein IDs \$4,400 per experiment

Lab use only:

Prep Received:		Plate No./Spot set:	
Processed/Operator:		MS data analysis/Operator:	
QC No:		Report Reference:	
Enzyme Lot No:		Checked Workflow:	
Special Considerations:		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: _____