Lab Use

REQUEST FORM 005A

Labelled Relative Quantitation Analysis

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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 4

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

Service 005A – Labelled Relative Quantitation Analysis & Proteome Mapping		**Price (USD)**
☑ **1D-LC map (Proteome Mapping)** – Mandatory sample viability check for all iTRAQ/TMT experiments		$330 per experiment
☐ **4-plex iTRAQ** - Sample labelling and analysis by 2D LC-MS/MS with automatic database analysis	Up to four samples	$6,600 per experiment
☐ **4-plex iTRAQ;** duplicate experiment (2 x 4-plex)		$9,900
☐ **4-plex iTRAQ;** triplicate experiment (3 x 4-plex)		$13,200
☐ **8-plex iTRAQ** - Sample labelling and analysis by 2D LC-MS/MS with automatic database analysis	Up to eight samples	$8,250 per experiment
☐ **8-plex iTRAQ;** duplicate experiment (2 x 8-plex)		$12,375
☐ **8-plex iTRAQ;** triplicate experiment (3 x 8-plex)		$16,500
☐ **10-plex TMT;** Sample labelling and analysis by 2D LC-MS/MS with automatic database analysis	Up to ten samples	$11,000 per experiment
☐ **Data and result files** for publication purposes		$275

Lab Use Only:

	1D experiment	**Replicate 1**	**Replicate 2**	**Replicate 3**
Sample Received:				
Processed/Operator:				
Spot set:				
MS analysis/Operator:				
Report Reference:				
Checked Workflow:				
Checked Report:				
Storage:				

SECTION B

NOTE:

- **40 µL plasma is required for a single iTRAQ experiment and 80 µL plasma is required for duplicate iTRAQ experiments**
- **Liquid samples should be in a volume of 100 µL - 200 µL and have a concentration of 2 mg/mL – 5 mg/mL**
- **Acetone precipitated sample pellets should contain a minimum of 100 µg of protein but not exceed 200 µg per tube.**
  Excess of 200 µg <u>will not</u> be processed.
- **Samples should contain equivalent amounts of protein per tube.**

Description of sample: (Liquid, Pellet, Lyophilised)	
Amount of starting material: (eg. 100 mg Leaf, 1 mg muscle, no. of cells, etc.)	
Method used for protein estimation:	
Buffer composition: Note; please state buffer composition before drying, extraction buffer.	
Any other treatments or chemicals present including volume and final concentration: (eg. Acetone precipitation, sucrose, reduction reagents, etc.)	

Comments:

SECTION C

Experimental Design

Please i. Circle appropriate response

Is this a single experiment? **Yes** **No**

Is this experiment? **iTRAQ 4-plex** **iTRAQ 8-plex** **TMT 10-plex**

No. of replicates **1** **2** **3**

If more than 1 replicate **Repeat experimental design for each replicate** (Please print another copy of this page and fill in the details)

iTRAQ 4-plex

Label	114	115	116	117
Sample name				
Amount of protein				
PI Ref				

Control Sample (please circle) **114** **115** **116** **117**

iTRAQ 8-plex

Label	113	114	115	116
Sample name				
Amount of protein				
PI Ref				
Label	117	118	119	121
Sample name				
Amount of protein				
PI Ref				

Control Sample (please circle) **113** **114** **115** **116** **117** **118** **119** **121**

TMT 10-plex

Label	126	127a	127b	128a	128b
Sample name					
Amount of protein					
PI Ref					
Label	129a	129b	130a	130b	131
Sample name					
Amount of protein					
PI Ref					

Control Sample (please circle) **126** **127a** **127b** **128a** **128b** **129a** **129b** **130a** **130b** **131**

SECTION D

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?

   .....

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.

   ……

   ……

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:** _____