



REQUEST FORM 005A

Lab Use

Labelled Relative Quantitation Analysis

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SECTION A

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

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

Sample Information – Please complete details on all pages & sign the last page

Proteomics Analysis price guide as of January 2024:

		Price (Ex. GST)	
Service 005A – Labelled Relative Quantitation Analysis & Proteome Mapping		□ USD	□ AUD
<input checked="" type="checkbox"/>	1D-LC map (Proteome Mapping) – Mandatory sample viability check for all iTRAQ/TMT experiments	\$330 per experiment	\$495 per experiment
<input type="checkbox"/>	4-plex iTRAQ - Sample labelling and analysis by 2D LC-MS/MS with automatic database analysis	Up to four samples \$6,600 per experiment	\$9,900 per experiment
<input type="checkbox"/>	4-plex iTRAQ; duplicate experiment (2 x 4-plex)	\$9,900	\$14,850
<input type="checkbox"/>	4-plex iTRAQ; triplicate experiment (3 x 4-plex)	\$13,200	\$19,800
<input type="checkbox"/>	8-plex iTRAQ - Sample labelling and analysis by 2D LC-MS/MS with automatic database analysis	Up to eight samples \$8,250 per experiment	\$12,375 per experiment
<input type="checkbox"/>	8-plex iTRAQ; duplicate experiment (2 x 8-plex)	\$12,375	\$18,565
<input type="checkbox"/>	8-plex iTRAQ; triplicate experiment (3 x 8-plex)	\$16,500	\$24,750
<input type="checkbox"/>	6-plex TMT; Sample labelling and analysis by 2D LC-MS/MS with automatic database analysis	Up to six samples \$7,500 per experiment	\$11,250 per experiment
<input type="checkbox"/>	6-plex TMT; duplicate experiment (2 x 6-plex)	\$11,250	\$16,875
<input type="checkbox"/>	6-plex TMT; triplicate experiment (3 x 6-plex)	\$15,000	\$22,500
<input type="checkbox"/>	10-plex TMT; Sample labelling and analysis by 2D LC-MS/MS with automatic database analysis	Up to ten samples \$11,000 per experiment	\$16,500 per experiment
<input type="checkbox"/>	10-plex TMT; duplicate experiment (2 x 10-plex)	\$16,500	\$24,750
<input type="checkbox"/>	10-plex TMT; triplicate experiment (3 x 10-plex)	\$22,000	\$33,000
<input type="checkbox"/>	Data and result files for publication purposes	\$275	\$415

Lab use only:		
Date Received + Initial:		
Sample Second Checked by:		
Storage Location:		
Experiment	1D experiment	Labelled Quantitation experiment
Date Processed + Operator:		
Instrument use:		
Spot set:		
MS data analysis + Operator:		
Report Reference:		
Report Checked by:		
Workflow Checked by:		
Special Considerations:		

SECTION B

NOTE:

- 40 µL plasma is required for a single experiment and 80 µL plasma is required for duplicate 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 **will not** be processed.
- Samples should contain equivalent amounts of protein per tube.

Description of sample: (Liquid, Pellet, Lyophilised)	
Storage condition of sample: (-80°C, -20°C, 2 – 8°C, Room temperature)	
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 6-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 number				

Control Sample (please circle)

114 115 116 117

iTRAQ 8-plex

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

Control Sample (please circle)

113 114 115 116 117 118 119 121

TMT 6-plex

Label	126	127	128
Sample name			
Amount of protein			
PI number			
Label	129	130	131
Sample name			
Amount of protein			
PI number			

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

TMT 10-plex

Label	126	127N	127C	128N	128C
Sample name					
Amount of protein					
PI number					
Label	129N	129C	130N	130C	131
Sample name					
Amount of protein					
PI number					

Control Sample (please circle) **126** **127N** **127C** **128N** **128C** **129N** **129C** **130N** **130C** **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?

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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.

.....

.....

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: _____