



**Proteomics International**

# REQUEST FORM 005

Lab Use

## Differential Expression – iTRAQ analysis

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ISO/IEC 17025

### SECTION A

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

**Sample Information – Please complete details on all pages & sign page 4**

**Proteomics Analysis price guide as of July 2016.** Consult our website for latest price information

Service 005 – Differential Expression – iTRAQ Analysis & Proteome Mapping			Price (USD)
<input type="checkbox"/>	<b>1D-LC map</b> – Confirmation of sample viability (part discounted)		Please enquire
<input type="checkbox"/>	<b>4-plex iTRAQ</b> - Sample labelling and analysis by 2D LC-MS/MS with automatic database analysis	Up to four samples	Please enquire
<input type="checkbox"/>	<b>4-plex iTRAQ</b> ; duplicate experiment (2 x 4-plex)		Please enquire
<input type="checkbox"/>	<b>4-plex iTRAQ</b> ; triplicate experiment (3 x 4-plex)		Please enquire
<input type="checkbox"/>	<b>8-plex iTRAQ</b> - Sample labelling and analysis by 2D LC-MS/MS with automatic database analysis	Up to eight samples	Please enquire
<input type="checkbox"/>	<b>8-plex iTRAQ</b> ; duplicate experiment (2 x 8-plex)		Please enquire
<input type="checkbox"/>	<b>8-plex iTRAQ</b> ; triplicate experiment (3 x 8-plex)		Please enquire
<input type="checkbox"/>	<b>Data and result files</b> for publication purposes		Please enquire

### Lab Use Only:

	1D experiment	iTRAQ rep1	iTRAQ rep2	iTRAQ rep3
Sample Received:				
Processed/Operator:				
Spot set:				
MS analysis/Operator:				
Report Reference:				
Checked Workflow:				
Checked Report:				
Storage:				

## SECTION B

### NOTE:

- 40  $\mu\text{L}$  plasma is required for a single iTRAQ experiment and 80  $\mu\text{L}$  plasma is required for duplicate iTRAQ experiments
- Liquid samples should be in a volume of 100  $\mu\text{L}$  - 200  $\mu\text{L}$  and have a concentration of 2 mg/mL – 5 mg/mL
- Acetone precipitated sample pellets should contain a minimum of 100  $\mu\text{g}$  of protein but not exceed 200  $\mu\text{g}$  per tube.  
Excess of 200  $\mu\text{g}$  will not be processed.
- Samples should contain equivalent amounts of protein per tube.

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

### Comments:

## SECTION C

### iTRAQ experimental Design

Please i. Circle appropriate response

**Is this a single experiment?**

**Yes                      No**

**Is this experiment?**

**4 plex                      8 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)**

#### **4-plex**

<b>Label</b>	114	115	116	117
<b>Sample name</b>				
<b>Amount of protein</b>				
<b>PI Ref</b>				

**Control Sample** (please circle)

**114    115    116    117**

#### **8-plex**

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

**Control Sample** (please circle)

**113    114    115    116    117    118    119    121**

## 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:** \_\_\_\_\_