



Proteomics International

REQUEST FORM 005

Differential Expression – iTRAQ analysis

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Lab Use



Accreditation No: 16838
ISO 17025 certified

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

Sample Information - Please sign & complete details on page 2	
Is your target database one of the following: (Human, Rat, Mouse, Zebrafish, <i>E. coli</i> , Rice, Yeast) If not, please provide more details on section B of this form.	Buffer composition for liquid or freeze dried sample:
Amount of protein in sample: Method of assessment: Volume of liquid sample:	Any other treatments or chemicals present: (e.g. acetone precipitation, sucrose etc)

Consult 1st Base for latest price information (Feb 2012).

Service 005 - Differential Expression – iTRAQ analysis		Price
Sample labelling and analysis by 2D LC-MALDI mass spectrometry, with automatic database analysis 1 st experiment	Up to four samples	Enquire
Sample labelling and analysis by 2D LC-MALDI mass spectrometry, with automatic database analysis 2 nd experiment (replicate)	Up to four samples	Enquire

Lab use only:

Prep received:		MS received:	
Processed/Operator:		Plate No./Spot set:	
QC No:		MS data analysis/Operator:	
Batch:		Report reference:	
Special Considerations:		Checked:	

For each sample please provide identification information and whether there are biological

replicates: e.g. Wild type SN3a, Wild type SN3b, Mutant SN4a, Mutant SN4b (a= biological replicate 1, b=2 etc)

No.	Sample number /identification	Biological/ Technical replicate	(Lab use only)		
			PI number	iTRAQ Label	Lot No:
1					
2					
3					
4					
5					
6					
7					
8					

(Please append extra table if required)

Comments:

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/TermsAndConditions>).
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.

Authorised Signature _____ **Date:** _____

Lab use only

Protein per sample		SCX Peak Area		WAP/ UWA (Circle)
Probot	F1F2	F3F4	F5F6	F7F8
Injected/ Initial Volume e.g. 10/50				
Plate Nos				
Spotset				

Form B: Further details on the target 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 your target organism?

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2. What other organisms are likely to be present in the sample provided?

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3. What are the most taxonomically related species of your 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.

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Please Note

***Please consider *de novo* peptide sequencing if the target species is not available or not well represented in the NCBI or Swiss-Prot databases.**

***Where a client's specific database is provided, database set up will be required. Searches conducted against client databases will incur additional set up charges and the results can only be supplied to client in Html, Xml or Excel files (default = Html).**