Lab Use



Contact details

REQUEST FORM 003

Proteome Mapping - MuDPIT analysis

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SECTION A

Corganisation/ Institution Email Telephone	Name				Billing Address				
Telephone Fax									
Purchase Order Number Fax	Organisation/				Email				
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, E. coli, Rice, Yeast If not, please provide more details in Section C of this form. No. of Samples (n): Proteomics Analysis price guide as of June 2020. Consult our website for latest price information. Service 003 - Proteome Mapping – MuDPIT analysis Did LC-MS/MS. Protein sample is run through an extended LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS) Did LC-MS/MS. Protein sample is run through a sophisticated 2D LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS) Lab use only: Prep Received: Plate No./Spot set: Processed/Operator: MS data analysis/Operator: QC No: Report Reference: Enzyme Lot No: Checked Workflow:	Institution				Telephone				
Buffer composition for liquid or freeze-dried sample:						Fax			
Is your target database one of the following: Human, Rat, Mouse, Zebrafish, E. coli, Rice, Yeast Method of assessment: If not, please provide more details in Section C of this form. No. of Samples (n): Proteomics Analysis price guide as of June 2020. Consult our website for latest price information. Service 003 - Proteome Mapping – MuDPIT analysis If 10 LC-MSMS, Protein sample is run through an extended LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS) If 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) Fingle sample; >1000 protein IDs sq. 2000 per experiment shadows a single sample; >2000 protein IDs sq. 2000 per experiment shadows a single sample; >2000 protein IDs sq. 2000 per experiment shadows a single sample; >2000 protein IDs sq. 2000 per experiment shadows a sample; >2000 protein IDs sq. 2000 protei	Sample Informat	ion - Ple	ase complete details on a	II pages	& sign page	e 3			
Human, Rat, Mouse, Zebrafish, <i>E. coli</i> , Rice, Yeast If not, please provide more details in Section C of this form. No. of Samples (n): Proteomics Analysis price guide as of June 2020. Consult our website for latest price information. Service 003 - Proteome Mapping – MuDPIT analysis In Lo-MSMMS. Protein sample is run through an extended LC gradient, and the eluent is analysed by electrospray mass spectrometry (MSMS) In Lo-MSMMS. Protein sample is run through a sophisticated 2D LC gradient, and the eluent is analysed by electrospray mass spectrometry (MSMS) Price (USD) \$2,200 per experiment by electrospray mass spectrometry (MSMS) Price (USD) \$2,200 per experiment by electrospray mass spectrometry (MSMS) Processed/Operator: MS data analysis/Operator: Plate No./Spot set: Processed/Operator: Report Reference: Enzyme Lot No: Checked Workflow:	· · · · · · · · · · · · · · · · · · ·								
If not, please provide more details in Section C of this form. 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 If In LC-MS/MS. Protein sample is run through an extended LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS) If In LC-MS/MS. Protein sample is run through a sophisticated 2D LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS) If In 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 Stab use only: Prope Received: Processed/Operator: MS data analysis/Operator: QC No: Report Reference: Enzyme Lot No: Checked Workflow:	Is your target data	Is your target database one of the following:			Amount of protein in 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	Human, Rat, Mouse, Zebrafish, E. coli, Rice, Yeast				Method of assessment:				
Proteomics Analysis price guide as of June 2020. Consult our website for latest price information. Service 003 - Proteome Mapping – MuDPIT analysis Price (USD) □ 1D LC-MS/MS. Protein sample is run through an extended LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS) □ 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) Lab use only: Prep Received: Plate No./Spot set: Processed/Operator: MS data analysis/Operator: QC No: Report Reference: Enzyme Lot No: Checked Workflow:	If not, please prov	ide more	details in Section C of this fo	rm.	Volume of liquid sample(s):				
Service 003 - Proteome Mapping - MuDPIT analysis 1D LC-MS/MS. Protein sample is run through an extended LC gradient, and the eluent is analysed by electrospray mass spectrometry (MS/MS) 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) 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	No. of Samples (n):								
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Lab use only: Prep Received: Processed/Operator: QC No: Enzyme Lot No: Plate No./Spot set: Report Reference: Checked Workflow:	☐ 1D LC-MS/MS. Protein sample is run through an extended LC gradient, and the eluent is ana by electrospray mass spectrometry (MS/MS)			ysed	Single sample;	>1000 protein IDs	\$2,200 per experiment		
Prep Received: Processed/Operator: MS data analysis/Operator: QC No: Report Reference: Checked Workflow:				is analysed	Single sample;	>2000 protein IDs	\$4,400 per experiment		
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Processed/Operator: QC No: Report Reference: Checked Workflow:	Lab use only:								
QC No: Report Reference: Checked Workflow:	Prep Received:			Pla	te No./Spot se	et:			
Enzyme Lot No: Checked Workflow:	Processed/Operato	r:		MS	data analysis	s/Operator:			
	QC No:			Rep	oort Referenc	e:			
Special Considerations: Checked Report:	Enzyme Lot No:			Che	ecked Workflo	ow:			
	Special Consideration	ons:		Che	ecked Report:				

SECTION B

For each sample please provide the following information if known:

	Sample Det	ails	Lab use only				
No.	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.

• 41	rised Signature
No	ote: Please be aware that samples are destroyed by analysis and cannot be returned.
4.	For students, please ensure supervisor signs this form.
3.	I have completed both pages of this submission form with details for each sample submitted for analysis.
2.	Hazards: I declare that the sample(s) are non-harmful, non-infectious and non-radioactive.
1.	I have read and understood the Proteomics Analysis Price List and agree to the charges and to Proteomics Internationa standard Terms and Conditions (available at: http://www.proteomics.com.au/analytical-services/terms-and-conditions/).
riease	e sign here below:
Dloose	o cian hara balaw:
	presented in the NCBI or Swiss-Prot databases.
	<u>ote</u> ease consider <i>De novo</i> peptide sequencing (Service 002) if the target species is not available or not we
NI.	
	databases, otherwise where can they be downloaded? Please provide details.
4.	Is the database for the target organism or its related species available in the NCBI or Swiss-Products have been extended. Please provide database
3.	What are the most taxonomically related species of the target organism?
2	. What other contaminating organisms are likely to be present in the sample provided?
1.	What is the target organism?