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type	Protein identification on HRMS for simple/purified samples		(III IINK)	
	(Orbitrap fusion Lumos direct injection) - (purified, Digested & desalted Samples)			
□В	Protein identification on HRMS for complex samples			
□ C	(Orbitrap fusion Lumos with neoUHPLC) - (Digested & desalted Samples) Quantitative proteome analysis on HRMS for complex samples (excluding Labelling) (Orbitrap		1	
L	fusion Lumos with neoUHPLC) - (Digested & desalted Samples)			
□ D	PTM identification by MS/MS on HRMS			
	(Orbitrap fusion Lumos with neoUHPLC) - (PTM Enriched, Digested & desalted Samples)		1	
□ E	Un-targeted metabolomics/lipidomics on HRMS (Orbitrap fusion Lumos with UHPLC) - (purified samples)			
□F	Targeted proteome analysis on LC-MS/MS per 60 min run	1		
	(Triple Quadrupole with UHPLC) - (for Digested & desalted samples)			
□ G	Additional charges for enzyme digestion and desalting for protein mixture sample if required.	Ī	1	
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^{*}If the sample is a gel, please supply a gel image. **If samples are submitted dry, please name the solvent that the compound is soluble in.

***If custom sequence, please e-mail us the sequence in FASTA format. #Report will be sent by email only.

For official use only:		
DBT-ILS Mass Spectrometry facility, Bhubaneswar	Request ID	Date of request

For official use only:

Sample Details:

- 1. Request ID:
- 2. Date of submission:
- 3. Remark:

Signature of operator / Proteomics Facility Manager

Report Details:

- 4. Result/ Report File name:
- 5. Date of report send /email:
- 6. Remark:

Signature of operator / Proteomics Facility Manager

Remarks for each job: (If Necessary):

Details information for users:

*Inst	*Instrument user charges (per sample/ run) for ILS Mass Spectrometry Facility (Excluding GST charges)							
Job type	Jobs Requested	BRIC-AI / ILS Users (In INR/ sample)	Academic (In INR/ sample)	Non- Academic/ Industry (In INR / sample)				
Α	Protein identification on HRMS for simple/purified samples (Orbitrap fusion Lumos direct injection) - (purified, Digested & desalted Samples)	2,500/-	5,000/-	8,000/-				
В	Protein identification on HRMS for complex samples (Orbitrap fusion Lumos with neoUHPLC) - (Digested & desalted Samples)	3,000/-	6,000/-	10,000/-				
С	Quantitative proteome analysis on HRMS for complex samples (excluding Labelling) (Orbitrap fusion Lumos with neoUHPLC) - (Digested & desalted Samples)	3,500/-	7,000/-	12,000/-				
D	PTM identification by MS/MS on HRMS (Orbitrap fusion Lumos with neoUHPLC) - (PTM Enriched, Digested & desalted Samples)	7,500/-	15,000/-	20,000/-				
E	Un-targeted metabolomics/lipidomics on HRMS (Orbitrap fusion Lumos with UHPLC) - (purified samples)	3,000/-	6,000/-	10,000/-				
F	Targeted proteome analysis on LC-MS/MS per 60 min run (Triple Quadrupole with UHPLC) - (for Digested & desalted samples)	1,000/-	2,000/-	5,000/-				
G	Additional charges for enzyme digestion and desalting for protein mixture sample if required.	2,000/-	4,000/-	8,000/-				

Please contact for sample preparation guidelines and more details-

Mass spectrometry facility Manager: Mr. R. Rajendra K. Reddy

Phone- 91-674- 2304233(D), 2300137 Ext: 233

Webpage: www.ils.res.in

E-mail- msfacility@ils.res.in