

Form Filling Guidelines for MS Service

Orbitrap Eclipse
and
tims-TOF Pro

Orbitrap Eclipse Service Request Form

Please use the correct form for Orbitrap Eclipse/ tims-TOF Pro/ MALDI-TOF/TOF.

A. User Information

User Name:	Click or tap here to enter text.	Email:	Click or tap here to enter text.
Tel. No.:	Click or tap here to enter text.	Department/ School:	Click or tap here to enter text.
Supervisor's Name:	Click or tap here to enter text.	Account to be charged:	Click or tap here to enter text.
Date:	Click or tap to enter a date.		

Click to fill in the corresponding information.

Please consult your supervisor for a chargeable research funding account

B. For Official Use Only

Sample Submission Date:	Click or tap to enter a date.	Sample Processing Date:	Click or tap to enter a date.
Sample Completion Date:	Click or tap to enter a date.	Reference No.:	Click or tap here to enter text.
Service Charge:	Click or tap here to enter text.	Remarks:	Click or tap here to enter text.

Skip this part (Official Use Only).

C. Project and Sample Information

Project Objectives and Expectations: (e.g. how samples should vary from control)

Click or tap here to enter text.

Please describe clearly the objective or expected results

- A particular type of modification?
- Detection of particular proteins?
- Grouping for quantification?
- etc.

Sample Origin: (e.g. human, mouse, etc.)

Click or tap here to enter text.

Sample species. Taxonomy ID may also be included.

Sample Storage Condition: Room Temperature 4 °C -20 °C

Biohazard Sample: No Yes

e.g., Infectious? Virus Containing? Special handling?

Potential Modifications: No Others: Click or tap here to enter text.

PTM or chemical modifications? (Please note that enrichment is highly recommended for PTM studies)

Quantitation: No Label-free TMT TMT Lot no.: Enter text.
Channel: Choose an item.
Quant MS order: Choose.

(For Orbitrap Eclipse only) For TMT quantification, please specify the Lot number of the TMT reagent and the channel used. Please refer to the FAQ on BioCRF website for the differences between MS2 and MS3 TMT Quantitation.

Mass Analyzer Ion Trap (Recommended for maximizing protein IDs)
 Orbitrap (Must be used for TMT quantitation)

(For Orbitrap Eclipse only) Please refer to the FAQ on BioCRF website for the differences between Ion Trap and Orbitrap detection.

Data/ Result Format: Raw data (.raw) Extracted data (.mzXML)
 Database search result using Proteome Discoverer (.xlsx)

Extracted data are normally not necessary unless you would like to perform database search by yourself and the search engine used does not support the raw data format.

(Please note that BioCRF does not responsible for long term storage of data. Users should always backup their own data.)

Protocol used for sample: (Details of cells used, lysis method, purification steps, wash & elution buffer conditions, protein precipitation method, protein digestion method, if applicable)

Please describe as detail as possible. The sample processing protocol and the data acquisition parameters may be adjusted based on the description to achieve optimal results.

Click or tap here to enter text.

MS_Sample Submission Form. xlsx

Sample	Sample Name/ Tube Label	Sample Type	Buffer	Concentration ($\mu\text{g}/\mu\text{l}$)	Volume (μl)	Total Amount (μg)	Remarks
1							
2							

e.g., cell lysate/
cell pellet/ IP
protein, etc.

Please measure the protein concentration with a reliable assay. Check also the compatibility of the assay and the sample buffer.

Sample identifier

e.g., dried/ PBS/
RIPA, etc.

Form Filling Guidelines for MS Service

MALDI-TOF/TOF

Please use the correct form for Orbitrap Eclipse/ tims-TOF Pro/ MALDI-TOF/TOF.

Mass Spectrometry Service (MALDI TOF/TOF) Request Form

Fill in the corresponding information.

User Information	
User name: _____	User E-mail: _____
Tel no: _____	User's signature: _____
Department or school: _____	
Supervisor's name: _____	Supervisor's signature*: _____

* Please seek your supervisor's approval and signature if 10 samples (or more) are submitted at once.

Sample Information	
Specify sample origin: <u>e.g., human</u>	
Sample storage:	<input type="checkbox"/> Room Temp <input type="checkbox"/> 4°C <input checked="" type="checkbox"/> -20°C
Biohazard sample:	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No
<input checked="" type="checkbox"/> 1. Protein Identification*	
Sample Type (Protein/ digested peptides): <u>e.g., Protein</u>	
Sample amount: <u>e.g., 50 ug for each sample</u>	
Database:	<input type="checkbox"/> NCBIInr <input checked="" type="checkbox"/> SwissProt <input type="checkbox"/> Others (pls specify): _____
Suspected modification: <u>e.g., phosphorylation</u>	
Taxonomy: <u>e.g., 9606 (for homo sapiens)</u>	
<i>*Only In solution digestion and desalting service are available</i>	
<input type="checkbox"/> 2. Mass Determination	
Sample Concentration (in solution): _____ pH: _____	
Solvent/buffer composition: _____	
Estimated MW: _____	

Select the service required and fill in the corresponding part.

e.g., Infectious? Virus Containing? Special handling?

In-gel digestion service is no longer provided. Users have to perform in-gel digestion by themselves and submit the resultant peptides for analysis. Please refer to the in-gel digestion protocol in the FAQ on the BioCRF website under the question “What samples can be submitted?”

Fill in as appropriate

No.	Sample Name (Estimated M.W.)	No.	Sample Name (Estimated M.W.)
1	e.g., Protein 1 (14k Da)	6	(Da)
2	e.g., Protein 2 (50k Da)	7	(Da)
3	(Da)	8	(Da)
4	(Da)	9	(Da)
5	(Da)	10	(Da)

Note: Please acknowledge Biosciences Central Research Facility HKUST in resulted publications

Skip this part (Official Use Only).

For office use only	
Ref. no.: _____	
Sample processing date: _____	Sample submission date: _____
Report delivery date: _____	Service charge: _____
Remark: _____	