

Lab no:  
 Date received:  
 Total number of samples received:  
 Received by:

## MASS SPECTROMETRY SAMPLE SUBMISSION FORM (Proteomics II – Intact Protein)

Kindly refer to Terms and Conditions on page 2

Name : \_\_\_\_\_  
 Company/ School/ Department : \_\_\_\_\_  
 Project supervisor : \_\_\_\_\_  
 Email : \_\_\_\_\_  
 Contact number : 

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 Payment method : \_\_\_\_\_ Research grant code : \_\_\_\_\_

### SAMPLE INFORMATION

1. Kindly provide as much information as possible
2. Attach HPLC result, if possible

Sample name : *Please kindly fill in the table in page 3*  
 Sample origin : \_\_\_\_\_  
 Expression host : \_\_\_\_\_

All samples **will be filtered** to remove any particulate matter. Please tick appropriate syringe filter to use for your sample(s).

Type of syringe filter (non-sterile, 13mm) : 
  Polypropylene 
  Nylon 
  Polyether sulfone  
 Cellulose acetate 
  Hydrophobic PTFE  
 Pore size (µm) : 
  0.22 
  0.45

<sup>a</sup> Counter ions, salts & buffers available in solution : \_\_\_\_\_

<sup>a</sup> Sample should be desalted and dissolved in water with 0.1% formic acid. Salt and buffer concentration should be as low as possible.

Storage temperature : 
  Room temp 
  2-8°C 
  -20°C 
  -80°C

### For known sample

Protein of interest (eg: Myoglobin) : \_\_\_\_\_  
 Molecular weight (monoisotopic/exact mass) : \_\_\_\_\_ kDa

### For unknown sample

Proposed protein name/ related protein : \_\_\_\_\_  
 Proposed molecular weight (monoisotopic/exact mass) : \_\_\_\_\_ kDa  
 Additional sample information : \_\_\_\_\_

### Analysis method (please ✓ respective box(es))

Feel free to contact Technical Officer in-charge in LCMS Lab (ext 44405) if you are not sure which method to use for your sample analysis

Agilent 6520 Accurate Mass Q-TOF LC/MS Ionization source: ESI or Nano ESI (ChipCube) 
  Agilent 6520 Accurate Mass Q-TOF LC/MS Ionization source: MALDI Q-TOF

Additional option :  Deconvolution

### Special requirement

- Return extra sample(s) *Note: Please provide full address for courier purpose*
- Other (please state): \_\_\_\_\_

### **SAMPLE PREPARATION GUIDELINES**

1. All samples should be dissolved in an ESI-friendly solvent system. Suitable solvents include: water, methanol and acetonitrile (no THF and TFA as they promote ion suppression).
2. Sample should be **desalted and dissolved in water with 0.1% formic acid**. Salt and buffer concentration should be as low as possible.
3. Please note that solution samples containing non-ionic detergents or high alkali salt will not be accepted (eg: Tween-any, Triton-any, NP-40, EDTA, Glycerol). Detergents and salts may destroy/ suppress the ionization process.
4. All samples **MUST** be filtered to remove any particulate matter.
5. Recommended sample concentrations:

Ionization source	Recommended sample concentration
ESI	~ 10-100pmol/uL or 0.1-5mg/mL
Nano-ESI	~ 1-40pmol/uL or 0.1-4mg/mL ( <i>available for Q-TOF LC/MS only</i> )
MALDI	~ 1-50pmol/uL or 0.1-5mg/mL

6. Submission tube(s) should be either an eppendorf tube or a HPLC vial. Vial insert can be used.
7. Vial insert should be used for sample volume <200uL. The minimum sample volume is 15uL with the use of a microvolume vial insert.

### **SAMPLE SUBMISSION GUIDELINES**

1. Prepare samples according to the guidelines above.
2. All samples should be submitted in solution form. Solids are only accepted when compound is unstable in solution.
3. No radioactive sample will be accepted.
4. Label all samples clearly with **your name, date and sample's ID**.
5. Fill out this form and submit it to LCMS Laboratory (refer to address below).

### **TERMS & CONDITIONS**

#### **Charges for common analysis**

Analysis method	Charge (per run)
Agilent 6550 Accurate Mass Q-TOF LC/MS Ionization source: Nano ESI (ChipCube)	RM 275

#### **Sample and data storage policy**

1. Extra samples will only be returned if such request is made in the sample submission form.
2. The LCMS laboratory will not store sample(s) for client after completion of the sample analysis.
3. All data files (processed data files & report) will be given in a CD-R or DVD upon completion of the sample analysis. It will be the sole responsibility of the client to keep these files.
4. The LCMS laboratory is not obligated to keep the data files for future analysis.
5. Should there is a need to re-process/ re-analyse sample data file by the laboratory in future, client has to provide the material and the data files to the laboratory.
6. Raw data will only be given upon request.

I have read, understood and agreed with the terms and conditions above.

Signature \_\_\_\_\_

Name \_\_\_\_\_

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#### Contact details

LCMS Laboratory Room  
Room 3-2-46, Level 2, Building 3,  
Jeffrey Cheah School of Medicine and Health Sciences,  
Monash University Malaysia,  
Jalan Lagoon Selatan,  
47500 Bandar Sunway,  
Selangor Darul Ehsan, Malaysia.  
Tel: +603 5514 4405      Fax: +603 5514 6323

**Sample information (you may add extra sheet if needed)**

<sup>b</sup> NO crude sample will be accepted as the presence of complex matrices might clog the HPLC/Chip columns

No	Sample name/ID	Physical form S – solid L – liquid	Sample weight/ volume/ concentration	Toxicity (please ✓ where applicable)			<sup>b</sup> Purity (please ✓ where applicable)			Enzyme(s) used to digest protein sample	Known/ Possible modification(s)
				1 - Non-toxic	2 - Toxic	3 - Unknown	4 - Pure	5 - Fractionated	6 - Others (please state)		
				1	2	3	4	5	6		