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Registration form for Matrix Assisted Laser Desorption Ionisation -Time of Flight Facility

(maldi.bios@iitb.ac.in)

Date:____________

Internal Registration Number (Office use only): ____

Name of User: ____

Name of Institution/Organization:______________________________________

Name of the Dept/Div/Sec:____

Email and Tel.No.: ____

Nature of samples involved:____

____

Number of Samples to be tested:____

Type of Analysis required: ____________________________________

Any other details to be shared: ___________________________________

____

Kindly mention details (and bring along for discussion) from literature search performed on similar studies: ____

____

Note:

- Kindly fill separate sample submission forms for different sample type with complete information as requested in the form (pg-2).
- Also please fill the check list for the tolerance for common buffer compounds / solvents used during sample preparation / processing attached with this form (pg-3).
- SDS-PAGE image for proteins is mandatory and for other sample types mass information of any other suitable data will be accepted.
- Zip-tipping of samples is must for all peptide analysis and also for proteins wherever required (will be confirmed by the MALDI staff in charge).

SAMPLE INFORMATION:

A) MOLECULAR WEIGHT DETERMINATION:
FOR PROTEINS/PEPTIDES / OLIGOS (DNA/ RNA) / GLYCANS / Others:

Sr. No.	Key points	Remarks
1	Type of Analysis M. wt / Other objective depending on Mol. Wt	
2	Sample Name	
3	Nature of the Sample (Known/Unknown, Single/Mixture)	
4	Conc. of protein /Oligos/Glycans in the sample (in pmoles or µg)	
5	Range of Mol. wt. of the sample protein	
6	Solvents / Buffers etc used during purification & Processing of the sample	
7.	Mass obtained on SDS-PAGE (proteins)/ other suitable technique (other samples)	

B) PROTEIN IDENTIFICATION
FOR PEPTIDES:

Sr. No.	Key points	Remarks
1	PMF or MS/MS	
2	Sample Name	
3	Nature of the Sample (Known/Unknown, Single/Mixture)	
4	Conc. of sample (prior digestion)	
5	Source (Taxonomy)	
6	Sample processing method (In-gel digestion/In-solution digestion)	
7	Protease used for digestion	
8	If samples are in gel digests approximate MW and pI	
9	A brief description on the desalting methods employed	
10	Chemicals used for reduction, alkylation, if any	
11	Please specify known/possible protein modifications	
12	SDS-PAGE observation	

Check List For MALDI Samples : Chemical Tolerance For Common Buffer Compounds

Sr. No.	Buffer component [a]	Maximum concentration [b]	Please tick the appropriate (mention the conc. if YES)	
			YES	**NO**
1	Sodium chloride	50 mM		
2	Phosphate	10 mM		
3	Tris base	50 mM		
4	Urea	1 M		
5	Guanidine	1 M		
6	Azide	0.1% (v/v)		
7	Glycerol	1% (v/v)		
8	PEG 2000	0.1% (w/v)		
9	SDS	0.01% (w/v)		
10	Triton X-100, RTX-100, or NP-40	0.1% (v/v)		
11	Tween	0.1% (v/v)		
12	CHAPS	0.01% (w/v)		
13	*n*-Octyl-β-glucopyranoside	1% (v/v)		
14	Zwittergent	0.1% (v/v)		
15	Lauryldimethylamine oxide (LDAO)	1% (w/v)		

Abbreviations:

a: CHAPS, 3-[(3-cholamidopropyl)-dimethylammonio]-1-propane sulfonate; PEG, polyethylene glycol; SDS, sodium dodecyl sulfate; Tris, tris(hydroxymethyl) aminomethane.

b: It is recommended to have conc. of the compounds mentioned in the checklist (if any) at a conc. lower than maximum tolerance.

INSTRUCTIONS FOR SAMPLE PREPARATION

- Experiments should be discussed with the facility in-charge before appointment.
- Purity of samples is extremely important for generating good data.
- Protein concentrations should be measured accurately before starting the experiment.
- The molecular weight (SDS IMAGE copy mandatory)as well as the pI of the proteins should be known before analysis.
- Zip-tipping of samples must for all peptide analysis and also for proteins wherever required (will be confirmed by the MALDI staff in charge).
- Appointments will be provided as per que and the user will be informed about the same.
- Kindly perform literature review on similar work and accumulate as much information as
- possible for good quality data.
- Any query regarding your MALDI experiment can be emailed on maldi.bios@iitb.ac.in

Whenever the prepared samples are used in the publications appropriate acknowledgement of usage of IIT Bombay MALDI facility must be mentioned. The details should be forwarded to maldi.bios@iitb.ac.in

GIVEN MATERIAL IS NOT POISONOUS OR TOXIC IN ANY WAY: ___________

We agree to acknowledge the Matrix Assisted Laser Desorption Ionisation (MALDI) Central Facility of IIT BOMBAY in our Publications/Reports/Thesis in which the data is used with due feedback through email.

Name & Signature of User:____

Sample received (date): ____

Sample analysis completion (date): ________________________________

Name & Signature of concerned Staff-in-charge/TA: ___________________________________

Remarks (If any)____