

MASS SPECTRUM REQUEST FORM

Name:

Supervisor's name:

Date:

Speed code:

Your Email:

Supervisor Email:

Sample code:

Molecular weight: Daltons

The sample I am submitting was made by me: Yes

Sample solubilized in(specify as %):

No

Concentration:

Storage conditions: Shelf fridge freezer Air/moisture sensitivity: Air and Moisture Light sensitivity:

% Purity and unknown contaminants:

Sample boiling point:

Sample thermally stability: e

Ionization Technique

ESI (+/-) Nominal mass EI Exact mass

Inlet system

Infusion Probe

If this sample came from another group or lab, Name :

Email:

Contact # :

Chemical structure and empirical formula
(please use empty space on the next page)

eef

Tune parameters (for MS Specialist Only)

Capillary Exit :

Skimmer1:

Hexapole1:

Hexapole RF:

Skimmer2:

Lens1 Transfer:

Lens 1 Pre-pulse:

Source parameters (for MS Specialist Only)

Capillary:

Nebulizer:

Dry gas:

Dry Temperature:

Service provided	Internal sample rates	Service needed
ESI (+/-) with accurate mass	15.00	<input type="checkbox"/>
ESI(+/-) with nominal mass	13.50	<input type="checkbox"/>
EI with direct insertion probe/ GC-MS	13.50	<input type="checkbox"/>
EI with accurate mass	15.00	<input type="checkbox"/>

Any special conditions and/or precautions

I have read the information on page 2 and agree to abide by those conditions in my samples:

Yes No

Sample submission for ESI-MS analysis

- The concentration of analyte in the range 0.5-1 milligram per mL (non-protein or peptides) will be further diluted by operator. (Can only be diluted with MeOH or ACN)
- Mass spectrometers that use electrospray as the ionization source are only compatible with volatile organic solvents such as MeOH, ACN and water. (Samples must be cleaned of inorganic salts and in-soluble buffers) If your samples are incompatible with these solvents, please discuss alternatives other than ESI-MS that can be used for your samples.
- Please make sure that your sample is completely dissolved and there should not be any precipitation in your vial and the solution must not be cloudy.
- Please take precautions to filter your sample if precipitation is observed prior to sample submission. (We would like to avoid downtime and avoid blockages and contaminations inside the mass spectrometer)
- Please do not use low vapor pressure solvents, such as DMSO. Just dilute them into MeOH or ACN.
- Do not use *trifluoroacetic acid (TFA)* in your samples. If you need to acidify your samples use formic acid (FA)
- Concentration of protein should be 1-10 μM in either buffered solution with ammonium acetate/ ammonium formate or MeOH/H₂O, MeOH only with/without 0.1% formic acid.
- *Over concentrated samples* lead to increased chemical noise, poor mass resolution, blockage in the sample delivery lines and contamination of the mass spectrometer vacuum part.

Please note:

To safeguard and prolong the working state of the instrument please ensure to:

- Use only Optima, LC-MS Grade solvents with a purity of 99.9%
- These solvents must be contained in glass bottles (not plastic), transferred to glass beakers, prior to dissolution in your samples, and samples submitted must also be contained in glass vials.
- Mass spectrometers are vulnerable to PEG (polyethylene glycol) contamination most often and it masks away all molecular peaks from an ESI mass spectrum, due to its capability of ionizing very well. Contamination can only be avoided or minimized by refraining from the use of plasticware during sample prep or opting for most consumables that have less leach out profiles etc.
- Please also ensure to notify if your samples are PEGylated on the request form, so that we can decide about analysis.
- Ensure that there **is proof of a HPLC, TLC trace or some kind of preliminary purification step** followed to highlight the purity of the sample that is being submitted for analysis.
- If by chance it is noted that there is any idea of your samples undergoing polymerization at high temperature, high voltage settings please refrain from opting for sample analysis via ESI.

Please help me to get you decent mass spec. results by ensuring that you provide me with clean samples.

Thank you.