

# Analytical Services – Mass Spec. Analysis

## LC/MS and LC/MS/MS Sample Submission Form

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|                        |                          |
|------------------------|--------------------------|
| <u>AS use only</u>     |                          |
| #Samples: _____        |                          |
| Priority: _____        | #MS <sup>n</sup> : _____ |
| Sample ID: _____       | #Prep: _____             |
| Receive date: _____    | by _____                 |
| Analysis date: _____   | by _____                 |
| Notebook/Page #: _____ |                          |

- Prepare samples according to the guidelines at end of this form.
- Fill out this form and submit it at the HHS 1001 with samples. Incomplete forms will delay the analysis.
- Label all samples clearly with your name, date and the sample's ID.
- You are responsible to pick up your samples within 7 days after the analysis.
- Please call 540-231-8221 with any questions, comments, or special requests.

**ACCOUNT NUMBER # :** \_\_\_\_\_

Account # must be provided before sample analysis. Non-VT submissions must include a hard copy of the PO.

Name: \_\_\_\_\_ Faculty Advisor / PI: \_\_\_\_\_

Date: \_\_\_\_\_ Email: \_\_\_\_\_ Phone: \_\_\_\_\_ Department / Room: \_\_\_\_\_

### SAMPLE INFORMATION

**\*\* NO RADIOACTIVE ISOTOPES! \*\***

Sample toxicity: Nontoxic Unknown Toxic (explain): \_\_\_\_\_

Concentration: \_\_\_\_\_ Solvent system: \_\_\_\_\_ Estimated Purity: \_\_\_\_\_%

Compatible solvents: \_\_\_\_\_ Previous analyses: [ ] MS [ ] NMR [ ] FTIR, [ ] UV-Vis

Counter ions, salts, and buffers in solution (include conc.): \_\_\_\_\_

Desired Storage temperature: [ ] 25°C, [ ] 2-8°C, [ ] -20°C

LC Chromatogram to Determine Purity? [ ] Yes [ ] No Include Peak Areas? [ ] Yes [ ] No

Special handling: \_\_\_\_\_ Light sensitive? [ ] Yes [ ] No

Molecular Formula: \_\_\_\_\_ MW \_\_\_\_\_

Masses / mass range of interest: \_\_\_\_\_

Brief description of the project: \_\_\_\_\_

**PRINT possible structures and attach to this form!**

Desired Priority: [ ] Standard [ ] Rush Priority

Ionization type: [ ] ESI (+) [ ] ESI (-) [ ] APCI (+) [ ] APCI (-)

Injection Type: Direct Infusion [ ] MS [ ] MS/MS

Or [ ] LC-MS [ ] LC/MS/MS

If desired, list masses for fragmentation: \_\_\_\_\_

Additional options: [ ] Polymeric analysis [ ] Protein Analysis

Results format: [ ] Email (spectra in Word) [ ] AND Paper (spectra)

## Analytical Services – Mass Spec. Analysis

### System Overview:

- Optimum mass range 30-1500 m/z
- Resolution of 0.1-1 amu
- Positive / negative ion modes
- ESI and APCI sources
- MS<sup>n</sup> (i.e. MS-MS) mode for structural analysis
- LC-MS capability

**Instrument calibration can be provided upon request**

### Sample Preparation:

- **Solvent Systems**
  - ESI-friendly such as 50/50 Water/Acetonitrile, Water/Methanol, etc.
  - *If submitted in chlorinated or non-polar solvent, some polar organic solvent such Methanol or Acetonitrile will be added.*
  - **Positive Ionization:**
    - A small amount of formic acid (0.1% v/v) can be added to enhance the signal. TFA is not recommended.
- **Direct Injection**
  - Prepare at least 100µL of sample. For flow-injection analysis 100µL is typically sufficient.
- **Recommended sample concentrations:**
  - Small organics: 50-200µM
  - Small peptides: 5µM (pmol/µL)
  - Large proteins: 20-100µM (pmol/µL)
  - Polymers: 100-1000µM