

Mass Spec. Analysis

Accurate Mass & Purity

Dr. Mehdi Ashraf-Khorassani
Dept. of Chemistry
Hahn Hall South, Room 1001
Virginia Tech
Blacksburg, VA 24061

mashraf@vt.edu
540-231-8221 (O)

AS use only
#Samples: _____
Receive date: _____ by _____
Analysis date: _____ by _____
of repeats: _____
Total Time Billed: _____

- Prepare samples in solution according to the guidelines at end of this form.
- Fill out this form ELECTRONICALLY and submit with your samples. Incomplete forms will delay the analysis.
- Label all samples CLEARLY the sample's ID. Use an abbreviated ID if long.
- 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 NAME

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

Sample toxicity: Nontoxic Unknown Toxic (explain): _____

What solvent is the sample dissolved in? _____ Amt. in solution (mg) _____

Estimated Purity: _____ % Compatible solvents: _____

Previous analyses: [] MS [] NMR [] FTIR, [] UV-Vis

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

Special handling: _____ Light sensitive? [] Yes [] No

Molecular Formula: _____ MW _____

Masses / mass range of interest: _____

Additional Notes: _____

Use clean HPLC grade solvents when preparing samples.

Using Chemdraw PRINT possible structures and attach to this form!

Accurate Mass Sample Purity Both

Desired Priority: [] Standard [] Rush Priority

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

If desired, list masses for fragmentation: _____

Additional options: [] Polymeric analysis [] Protein Analysis

Analytical Services – Mass Spec. Analysis

System Overview:

- Optimum mass range 30-1500 m/z
- Resolution of <3ppm
- Positive / negative ion modes
- ESI and APCI sources
- MSⁿ (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