Center for Molecular Analysis
Mass Spectrometry Sample Submission Form

Dr. Mark E. Bier, Director
Center for Molecular Analysis
Dept. of Chemistry
Mellon Institute Bldg
Carnegie Mellon University
4400 Fifth Avenue
Pittsburgh, PA 15213

http://www.chem.cmu.edu/cma/
mbier@andrew.cmu.edu
412-268-3540 (O)
412-268-6897 (FAX)

CMA use only
#Samples: _____
#48h Priority: _____   **#MS^n:** _____
#Protein ID: _____   **#Prep:** _____
Receive date: _____ **by** _____
Analysis date: _____ **by** _____
Notebook/Page #: _____

- Prepare samples according to the guidelines at http://www.chem.cmu.edu/cma/ms.html. *Additional sample prep will result in double service rate.*
- Fill out this form and submit it at the CMA (MI 860) 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 412-268-7548 with any questions, comments, or special requests.
- *See http://www.chem.cmu.edu/cma/rates.htm for current service rates.*

CHARGE NUMBER (Oracle (CMU) OR PO (non-CMU) #): _____

An oracle or PO # must be provided before sample analysis. Non-CMU submissions must include a hard copy of the PO.
        ***** *Please PRINT* *****

Name: _____   **Date:** _____   **Email:** _____

Phone: _____   **Faculty Advisor / PI:** _____

Department / Room: _____

Billing address (non-CMU): _____

SAMPLE INFORMATION:
** NO RADIOACTIVE ISOTOPES! **
Sample toxicity: [ ] Nontoxic   [ ] Unknown   [ ] Toxic (explain): _____

Concentration: _____   **Solvent system:** _____ **purity:** _____%

Compatible solvents: _____ **Previous analyses: [ ] MS [ ] NMR [ ] FTIR, [ ] UV-Vis**

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

Isotopic enrichment ?: _____   **Storage temp: [ ] 25°C, [ ] 2-8°C, [ ] -20°C**

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

Molecular Formula: _____   **MW** _____ **[ ] Avg. or [ ] Monoisotopic**

Brief description of the project: _____

Masses / mass range of interest: _____

Show structure here: *(Use the back of this form or attach additional pages if necessary.)*

Analysis priority: [ ] Standard (1 week)   [ ] Priority (48 hrs. – double rate)

Ionization type: [ ] ESI   [ ] MALDI

Scans required: [ ] MS   [ ] MS/MS of masses: _____ (double rate for MS^n)

Additional options: [ ] Polymeric analysis (M$_{n,w,z}$ and PDI)   [ ] Protein identification (double rate)

        [ ] Deconvolution   [ ] LC-MS

Results format: [ ] Paper (spectra)   [ ] Email (spectra in PowerPoint)   FREE