**Harvard Center for Mass Spectrometry**

**URL:** <http://massspec.fas.harvard.edu/>

**Facility Director:** Sunia Trauger

**Description:**

*Square Footage:* 2,000 square feet

*Facility Location:* Northwest Lab, B2 core laboratory space

The Harvard Center for Mass Spectrometry (HCMS) was launched on October 1, 2019 to serve as a single unified mass spectrometry resource facility. It combines the mass spectrometry-based resources previously available through two separate facilities, the Small Molecule Mass Spectrometry Facility (SMMS) and the Mass Spectrometry and Proteomics Resource (MSPRL). Our objective is to provide a better overall experience to the research community through a fully integrated mass spectrometry resource. HCMS offers high quality quantitative metabolomics, [proteomics](https://proteomics.fas.harvard.edu/) and lipidomics services, as well as customized molecular measurements using mass spectrometry. We also offer access and training to some equipment for routine mass spectrometry measurements. Contact us at (617) 384-9585 or check out our website for more information.

**Major Equipment:**

* Thermo Fusion IDX Orbitrap mass spectrometer for metabolomics
* Thermo q-Exactive Plus mass spectrometers (2x) for lipidomics and metabolomics
* Thermo Fusion Lumos with nano-LC for Proteomics
* Thermo q-Exactive HFX with nano-LC for Proteomics
* Thermo Orbitrap Elite with nano-LC for Proteomics
* Agilent 6460 Triple Quadruple Mass Spectrometer with Agilent 1290 uHPLC (2x)
* Bruker Impact q-TOF Mass Spectrometer (2x)
* Bruker Ultrflextreme MALDI-TOF/TOF with Biotools and FlexAnalysis
* Thermo GC-q-Exactive high resolution GC-FTMS with headspace, SPME, EI and CI

**Services:**

* Quantitative proteomics using TMT tagging
* Phospho-proteomics and other post-translational modifications characterization
* Protein identification, out of solution or gel
* Proteomics analysis which is customized based on complexity of sample, and coverage needed with fractionation of peptides, or digestion with multiple enzymes
* High Resolution LC-MS: Samples will be analyzed using high-resolution mass spectrometry. Interpreted data report will be provided to the user ~24 hours after sample submission.
* Lipidomics and metabolomics profiling of systems, global profiling.
* Data analysis for proteomics, metabolomics and lipidomics data, with curation by our expert staff. A full interpreted report and assistance in manuscript preparation.
* Intact molecular weight determination by LC-MS Analysis. Molecular weight determination using Max-Ent algorithm for various macromolecules. Interpreted report providing MW information (typically within 1 Da) will be provided to the investigator. This technique is ideal for studying covalent attachments to proteins of interest. MALDI-TOF of proteins, oligonucleotides and polymers
* Quantitative Analysis of Small Molecules: Using standard compounds, an optimum HPLC-MS/MS method will be developed for the molecule/molecules of interest. After this samples will be quantified using a standard curve based on internal or external standards on a triple quadrupole mass spectrometer.
* MALDI-TOF and TOF/TOF analysis of peptides, proteins and polymers, data analysis.
* Customized GC/MS based quantitative analysis with derivatization when needed
* LC-MS based impurity analysis for compounds using high resolution MS and MS/MS
* Customized mass spectrometry analysis

**Access and Training:**

We provide access and training to Harvard and affiliated researchers on some open access equipment including a Bruker Impact II high resolution q-TOF mass spectrometer, and a Bruker Ultraflextreme MALDI-TOF/TOF mass spectrometer.