

TRANSLATION TECHNOLOGY

The UCLA-CTSI provides many state of the art technology cores and specialized service cores available to investigators (<http://people.ctsi.ucla.edu/institution/core-display>). The technology core described below is available at Lundquist/Harbor-UCLA. Applications for utilization of these resources are reviewed by the Scientific Advisory Committee of the UCLA-CTSI at Lundquist/Harbor-UCLA. Support for investigators using this core is provided through a voucher system. Please contact the UCLA-CTSI office at 310-222-2503.

BIOMEDICAL MASS SPECTROMETRY FACILITY (STABLE ISOTOPE TRACING)

Description

The Biomedical Mass Spectrometry Facility (BMSF) supports clinical research projects both from within UCLA and from outside institutions in clinical nutrition and metabolic research. The BMSF specializes in experimental design using stable isotopes and analytical methods (^{13}C carbon tracing) for physiological or metabolic investigations. It provides unique services in isotopomer distribution analysis of metabolites (tracer-based metabolomics) using GC/MS. In addition, the BMSF offers collaborations in the area of metabolite profiling and modeling of metabolic systems with tracers.

- Sample preparation: Samples are first partially purified for substrate classes such as amino acids, sugars, ribose and deoxyribose as well as lipids and fatty acids are extracted using established methods. Partially purified samples are derivatized (converting to non-ionic species) using published methods. A service fee will be charged for the labor and material in sample handling (\$50 per sample).
- Quantitative and qualitative analysis by GC/MS: Quantitative analysis will be carried out with isotope recovery standards. These isotope standards are purchased by the individual investigators. The charge for mass spectrometry analysis has a standard charge of \$80/hour of instrument use and the technician's hourly charge of \$25/hour. List of tests available:
 - Carbohydrates – glucose, fructose, galactose, ribose, deoxyribose and sugar alcohols
 - Amino acid profile – quantitative analysis of essential and non-essential amino acids
 - Fatty acid profile – saturated and unsaturated fatty acids including essential fatty acids
 - Mass isotopomer analysis – distribution of labeled metabolites from stable isotope labeling experiments
- Consultation: Consultation on technical problem or with method development will be charge on a flat rate of \$10,000 per project.
- Collaboration in metabolite profiling and tracer-based metabolomics: Since metabolic profiling or tracer-based metabolomics require our input from experimental design to the analysis of a large number of samples. Such services are available on a collaboration basis, i.e. the BMSF will be part of the research grant with a proper subcontract agreement.
- Training: Training is provided to CTSI supported fellows or junior faculty on CTSI approved projects.

Mass Spectrometer Resources

- Four gas-liquid chromatograph/mass spectrometer (GC/MS) systems (one Agilent Model 5971A, two Agilent Model 5973A and one Agilent Model 5975 Mass Selective Detector (MSD) Systems)
- An Agilent Model 5975C Mass Selective Detector (MSD) System which is dedicated for breath CO₂ analysis and analysis of other volatile compounds for clinical investigations.

Contact Information

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Location: 1124 W. Carson Street, Torrance, CA 90502. Walter Martin Research Building at Lundquist/Harbor-UCLA.

The Biomedical Mass Spectrometry Facility is currently located in E6 Building (room 148).
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