



Liquid Chromatography- Mass Spectrometry (LC-MS)

LC-MS is a versatile and highly sensitive analytical technique for the measurement of small molecular weight compounds in a diverse range of sample types. It uses a series of mass detection systems to provide both quantitative and qualitative analyses. Situated in the Centre for Analytical Bioscience within the School of Pharmacy, our MS facilities are ideal for small molecule analysis (<2000m/z) and are complemented by a suite of UHPLC or specialised surface analysis interfaces (DESI, LESA) and software for data interpretation.

Capabilities

- Ultra-high-performance liquid chromatography (UHPLC) coupled to either high resolution-MS or QTrap MS.
- Accurate mass measurement (<5 ppm) for untargeted metabolomics and high resolution targeted quantitative analysis.
- Multiple reaction monitoring (MRM) and parallel reaction monitoring (PRM) for high sensitivity or specific quantitative analysis.
- Multi-stage MS and data-dependant MS fragmentation for structural elucidation and MS/MS identification.
- Ambient analysis of chemical compounds on biological/material surfaces using LESA-MS.
- Direct infusion high throughput analysis with NanoMate (no LC separation).
- Spot analysis or imaging with AP-MALDI (5 μ m resolution).

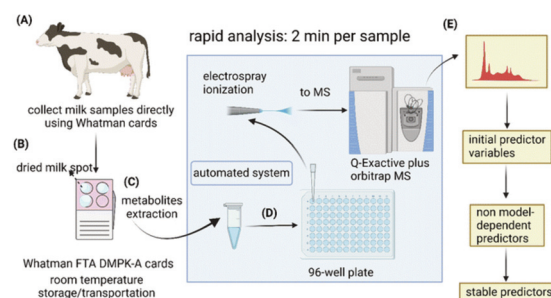
Typical applications

- Quantification of drug/drug metabolites, endogenous metabolites/lipids and contaminants in cells, microorganisms, plants, biofluids, tissues and environmental samples.
- Global metabolite profiling, metabolomics, biomarker discovery and surface analysis.
- Understanding the metabolic effects of biotic and/or abiotic perturbations on a biological system, for example drug-induced changes to intracellular metabolite pathways.
- Absolute quantification of a wide range of intra and extracellular metabolites using isotope dilution mass spectrometry.
- Isotope-assisted metabolic pathway profiling.

Metabolic alterations in dairy cattle with lameness revealed by untargeted metabolomics of dried milk spots using direct infusion-tandem mass spectrometry

To determine whether metabolic signatures associated with lameness could be discovered with untargeted metabolomics, we developed a novel workflow using direct infusion-tandem mass spectrometry to rapidly analyse (2 min per sample) dried milk spots (DMS) that were stored on commercially available Whatman® FTA® DMPK cards for a prolonged period (8 and 16 days). An orthogonal partial least squares-discriminant analysis (OPLS-DA) method validated by triangulation of multiple machine learning (ML) models and stability selection was employed to reliably identify important discriminative metabolites. With this approach, we were able to differentiate between lame and healthy cows based on a set of lipid molecules and several small metabolites.

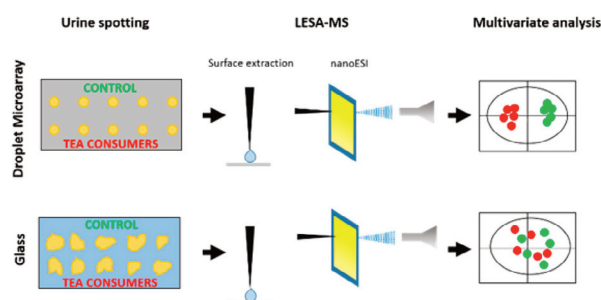
Wenshi He, Ana S. Cardoso, Robert M. Hyde, Martin J. Green, David J. Scurr, Rian L. Griffiths, Laura V. Randall and Dong-Hyun Kim, *Analyst*, 2022, 147, 5537



Size analysis of a mixture of polystyrene nanoparticles

The use of the Droplet Microarray (DMA) provides a surface-assisted LESA-MS method delivering significant improvement of the surface extraction repeatability leading to the acquisition of more robust and higher quality data. Such a method shows potential to be used for LESA-MS for controlled and reproducible surface extraction and for acquisition of high quality, qualitative data in a high-throughput manner.

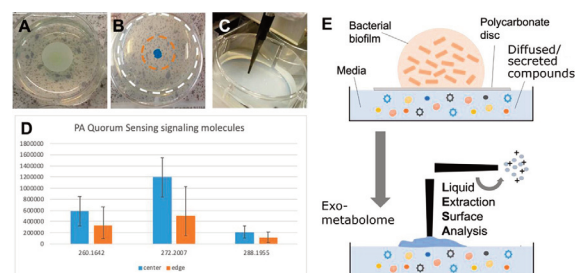
Meurs J, Alexander MR, Levkin PA, Widmaier S, Bunch J, Barrett DA and Kim D-H, *Anal. Chem.* 2018, 90, 10, 6001-6005



Probing interkingdom signalling molecules via Liquid Extraction Surface Analysis–Mass Spectrometry

Here, we present a model system for growing biofilms on discs before utilizing rapid and direct surface sampling MS, namely, liquid extraction surface analysis, to study the microbial exometabolome. One of the benefits of this approach is its surface-specific nature, enabling mimicking biofilm formation in a way that the study of planktonic liquid cultures cannot imitate. Our model system provides a route to investigate changes in the exometabolome, such as metabolites that become circulatory in the presence of multiple pathogens, and provides a rapid analytical approach to gaining a mechanistic understanding of bacterial signalling.

Shaun N. Robertson, Fadi Soukariéh, Thomas M. White, Miguel Camara, Manuel Romero, and Rian L. Griffiths, *Anal. Chem.* 2023, 95, 11, 5079–5086



Our facilities

QTRAP 6500+ and QTrap 4000 Quadrupole Linear Ion Trap LC-MS/MS

- Equipped with HPLC and UHPLC.
- Quantitative and qualitative targeted metabolite profiling, and for ID confirmation. Used where sensitivity is required.
- Advanced MS scanning options and information dependant acquisition offer unique approaches to metabolite profiling and identification.

Thermo Fisher QExactive (Hybrid quadrupole Orbitrap) high resolution mass spectrometer

- Equipped with NanoLC, UHPLC and TriVersa NanoMate.
- Small molecules profiling and identification.
- Quantitative and qualitative measurements.
- Metabolomics and lipidomics with high resolution measurements.

Thermo Orbitrap FusionTM LumosTM TribridTM Mass Spectrometer

- Resolution > 500,000 FWHM.
- MSn capabilities.

TriVersa NanoMate, Liquid Extraction Surface Analysis-Mass Spectrometry (LESA-MS)

- Surface extraction and analysis under ambient conditions.
- Direct infusion high throughput analysis.
- Advantages where UHV analysis may not be suitable; alternative to ToF-SIMS and MALDI.
- Coupled to QExactive MS to achieve a high resolution and confidence in identification using data dependant MS/MS.
- The new LESAPLUS allows for automated LESA experiments plus additional nano-LC separation.

Ambient Pressure Matrix Assisted Laser Desorption Ionisation (AP-MALDI)

- Surface analysis/imaging under ambient conditions.
- Unlike regular MALDI, it does not require a vacuum chamber, which means the analysis is faster and the samples can be kept in their native status.

Data Analysis

- We perform data analysis for untargeted metabolomics with Compound Discoverer 3.3 (Thermo Scientific) and multivariate analysis with SIMCAP.
- For quantitative analysis we use TraceFinder (Thermo Fisher Scientific), Analyst (Sciex) and MultiQuant.

Find out how LCMS could help with your applications, designs or solutions:

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