

Mass Spectrometry



The mass spectrometry (MS) laboratory is a Core Service at Barts Cancer Institute and is currently managed by the Centre for Haemato-Oncology. MS has a variety of applications in cell and molecular biology and cancer research, including the analysis of:

- Pharmacokinetics and pharmacodynamics of drugs
- Samples' protein composition
- Protein structures
- Post-translational modifications of proteins
- Enzymatic activity

The MS Laboratory supports BCI researchers through collaborations in a variety of high quality MS-based analyses. This support covers both planning and carrying out proteomics, metabolomics and drug analyses.

Equipment

The lab is equipped with three LC-MS/MS systems based on different types of mass spectrometers serving different analytical purposes.

- **LHQ-Orbitrap connected to nano Acquity LC** - untargeted proteomics analysis
- **Q-tof connected to micro Acquity LC** - untargeted metabolomics analysis
- **TSQ Vantage connected to normal LC or nano acquity LC** - targeted analysis of drugs, metabolites and polypeptides

Proteomics, Metabolomics and Drug analytics

Offering metabolite and protein identification/characterisation, untargeted analysis of metabolites and proteins, metabolic profiling and targeted analysis of metabolites and drugs by LC-MS/MS.

Mass Spectrometry

Proteomics

- Protein identification
- Determination of protein post-translational modifications of proteins such as phosphorylation, acetylation, and more
- Relative quantification of proteins and their modifications
- Absolute protein quantification in targeted mode
- Molecular weight determination of intact proteins (top-down proteomics)

Data Analysis

Quantitative proteomics data are analysed using label-based or label-free appropriate software. Results are provided in electronic format, including protein hits, sequences of corresponding peptides and locations of modification sites & relative quantities where applicable.

Metabolomics experiments are tailored to the type of analytes of interest (polar/unpolar/both) and data is analysed using Waters software.

Targeted analysis of small molecules or proteins often requires optimisation of parent and fragment masses and chromatography conditions.

Publications

- Allen *et al.* Prognostic and therapeutic impact of ASS-1 control in bladder cancer as monitored longitudinally by PET imaging. *J Cancer Res.* 2014.
- Ghazaly *et al.* ProGem1: Phase I first-in-human study of the novel nucleotide, NUC-1031, in adult patients with advanced solid tumors. *J Clin Oncol.* 2013. 31(15): 2576.
- Rajeeve *et al.* Polyamine production is downstream and upstream of oncogenic PI3K signalling and contributes to tumour cell growth. *Biochem J.* 2013. 450, 619-628.
- Beltran *et al.* Calpain interacts with class IA phosphoinositide 3-kinases regulating their stability and signaling activity. *PNAS USA.* 2011. 108, 16217-16222.

