

METABOLOMICS



Head
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Scientific Officers
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Metabolism is a centrepiece of cancer biology from its initiation, through its progression, to its response to treatment. The facility supports the Institute's research exploring the multiple roles of metabolism in cancer biology. We offer tailored support for the Institute's research projects, from experimental design to data analysis. Our well-established metabolomics platform uses state-of-the-art liquid-chromatography mass-spectrometry (LC-MS). Two Thermo Scientific Q Exactives instruments with high-resolution and accurate-mass are central for the targeted and untargeted analysis of the metabolome and lipidome of cells, tissues, and biological fluids. This platform is complemented by a Thermo Scientific Altis triple quad that broadens the sensitivity and specificity of the detection for specific metabolites of interest. In addition, an Agilent gas-chromatography mass spectrometry (GC-MS) triple quad instrument provides complementary coverage to our LC-MS systems.

We work closely with many groups within the Institute who have interests in cancer metabolism and during 2022, we have continued to contribute to their research (see publications). Our close collaboration with Saverio Tardito's group through Rachel's ongoing PhD project, continues to investigate the therapeutic gain of inhibiting both BRAF and glutaminase in the treatment of BRAF mutant melanoma.

The facility's core aim is to provide access to state-of-the-art LC-MS technology that is optimised for the detection of metabolites and lipids. We maintain and operate the instrumentation, providing both standard metabolite profiling and custom analysis when needed. Through the course of the year, we have continued to develop and add new methods to the facility's portfolio. This year, these included the measurement of polyamines, acyl carnitines and fatty acids (both free and total), complementing our existing untargeted lipidomics platform.

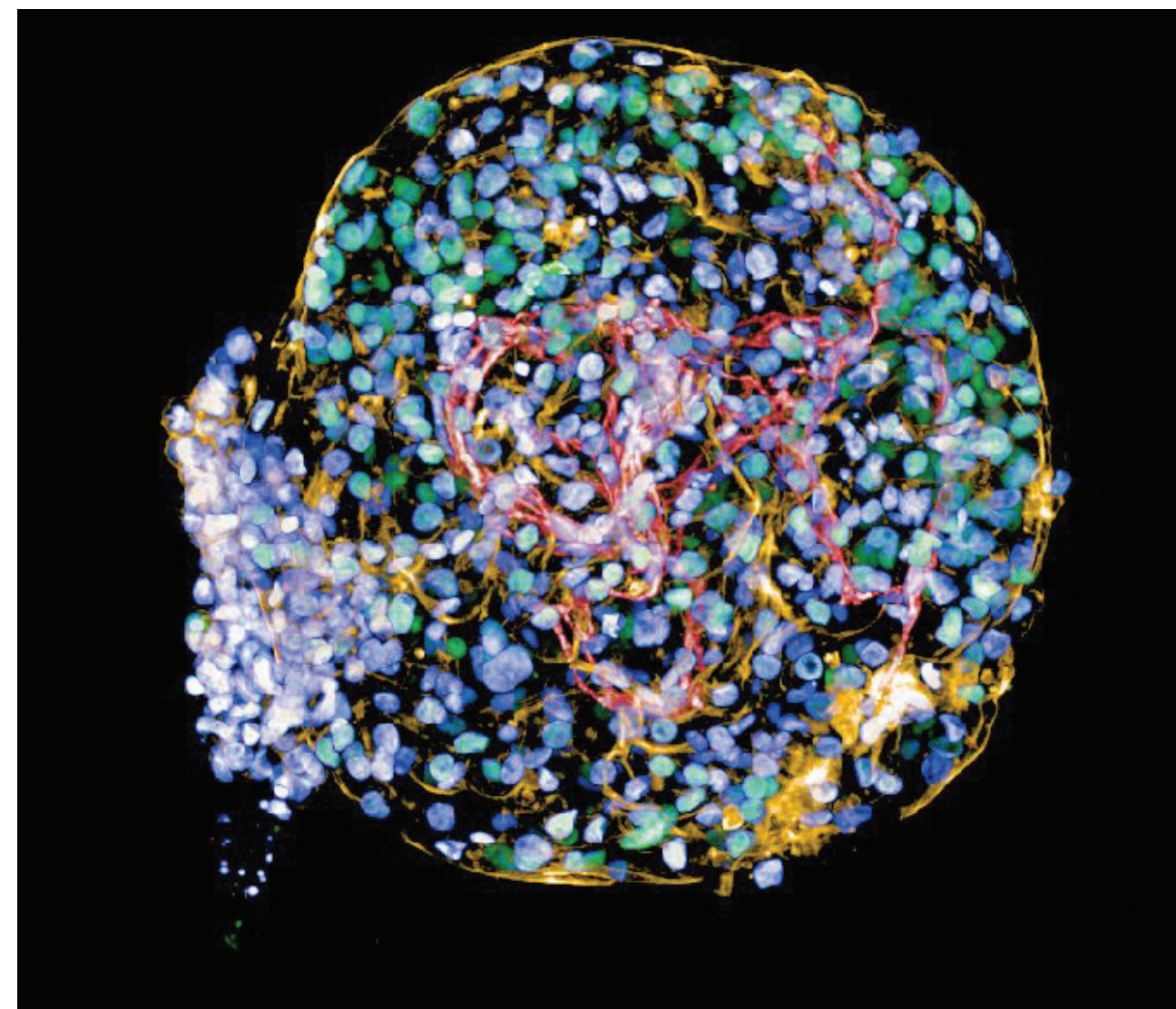
We also offer expertise and assistance in data analysis, data interpretation and experimental design. This year, we have updated our data

analysis pipeline, moving to modern analysis packages for targeted experiments and will soon offer updated in-house training for these approaches. To learn as much as possible from the data generated, we also collaborate with users to make use of more complex untargeted analysis.

In May, Alejandro Huerta Uribe joined the facility from the School of Cancer Sciences at the University of Glasgow. During his time in Oliver Maddocks' lab, Alejandro gained experience in cancer metabolism and high-resolution MS-based metabolomics which he is now employing in his role as a scientific officer in the facility.

During the summer, both David and Engy continued the long-standing association with Cold Spring Harbor labs, assisting in the organisation and practical instruction of the metabolomics course. The course runs for a period of two weeks, during which the students learn both the theory and application of different GC/LC-MS methodologies to answer fundamental biological questions.

Publications listed on page 117



Visualisation of human induced pluripotent stem cell derived liver organoids (maximum projection). Organoids were stained with HNF4-alpha (hepatocyte marker), CD31 (endothelial marker), DAPI (nuclear stain) and phalloidin (F-actin marker), prior to imaging with Opera Pheonix at 20x objective.

Image was taken by Sonam Ansel (Jim Norman's Lab, R20) with assistance from Lynn McGarry.