The Breast Cancer Clinical Research Unit (BCCRU) focuses on the translational interface of therapeutic development. Breast cancer is a heterogeneous disease and, thus, there are large inter-patient variations in terms of disease course, prognosis, relapse, and resistance to conventional or targeted therapeutics. Our activities are directed towards personalised treatment and range from preclinical models to correlative studies and clinical trials.

Our current research areas aim to:

- Study the implications of hypoxia for immunotherapies.
- Understand the individual factors regulating the response to immunotherapy in breast cancer, taking advantage of an advanced, personalised “tumouroid” platform.
- Tackle the mechanisms of resistance against novel therapies in advanced breast cancer.
- Incorporate our findings into concept-driven clinical trials.

“At the Breast Cancer Clinical Research Unit, we are focused on individualising therapy for advanced breast cancer.”

OVERVIEW
RESEARCH HIGHLIGHTS

We have established a collection of 35 patient-derived tumours from breast cancer patients. We call a tumour a mix of a patient-derived organoid (a well-established model for cancer research, which perpetuates the tumour material from a given patient, preserving its mutations and general features, and is highly reliable for drug screening and predictive purposes) and the patient’s cells derived from the immune system. This sophisticated model allows us not only to screen conventional drugs, but also to understand their impact on the ability of the immune system to reject the tumour, a feature that is absent in common patient-derived mouse models of cancer. Tumours enable us to improve our understanding of immunotherapy and to better understand the impact of other drugs on the immune system, allowing for personalised synergetic treatment combinations. This collection is expanding, and we plan to this be the core of our research in the coming years.

A critical problem in hormone-positive breast cancer is the development of clonal heterogeneity. Tumours, after progression on aromatase plus CDK4/6 inhibitors, develop many different mutations to circumvent drug exposure, impacting the duration of response to subsequent treatment lines. Our preliminary data suggest that different tumour sub-compartments harbour different sets of mutations, and even selecting a “right” therapeutic choice is insufficient for eradicating a whole tumour. We are now undertaking an approach based on mutational signatures that are pervasive across different clones and that may allow for selecting therapies that kill broader tumour compartments than therapies selected according to traditional point mutations. This is being tested in patient tumours.

We finalised our work regarding predictive factors of sensitivity to paclitaxel in early breast cancer from the perspective of phosphoproteomics. A CDK4-Filamin A axis that converges in the regulatory machinery of tubulin acetylation is responsible for turning cancer cells sensitive to this drug. This pair of markers is highly accurate in predicting sensitivity in the clinical setting.

*PUBLICATIONS*

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*PATENT*

**PCT/EP2022/051700.** LUMICA V. 1.0. Algorithm – a compatible drug-screening platform for microorganism generation and for cancer research, which perpetuates the tumour material from a given patient, preserving its mutations and general features, and is highly reliable for drug screening and predictive purposes.

**INTELLECTUAL PROPERTY REGISTRATION**


**AWARDS AND RECOGNITION**

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