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Title: [Advanced microfluidic model of lung cancer for precision drug therapy](#)

PIs: Ian Papautsky, PhD, Professor, Department of Biomedical Engineering, UIC

Takeshi Shimamura, PhD, Associate Professor, Department of Surgery, UIC

Anindita Basu, PhD, Assistant Professor, Department of Genetic Medicine, UChicago

This project is on developing new tools for lung cancer diagnosis. They aim to develop a platform that can evaluate the effectiveness of drug therapies using small samples of patient-derived cancer cells. Specifically, their goal is to create a microfluidic platform that can assess the response of patient-specific lung cancer treatments using 3D patient-derived tissues and factors that influence drug response. They plan to utilize patient-derived organoids along with oncogenic inhibitors to understand the interaction between the tumor and its microenvironment, and evaluate drug response using a microfluidic platform.

The investigators are excellent. Papautsky directs CADMIM which is a NSF supported Industry-Academic consortium, is on the Lab on a Chip Advisory board, and has pioneered many microfluidic innovations. Shimamura is a cancer researcher and has previously published an aspect of this proposal with Papautsky. Basu developed dop-seq and brings single cell transcriptomics expertise to study TME. The team is excellent and combines a microfluidics researcher, cancer cell biology, and epi-genetics and transcriptomic profiling.

The project involves developing a simple microfluidic trap array that can be scaled to clinically relevant samples. This approach would allow rapid screening of PDOs which is currently labor intensive. Their aims will provide preliminary data to pursue other NIH proposals.

Targeted patient therapies based on PDOs would help with clinical outcomes of lung cancer.

The interesting aspect of their proposal is to develop dynamic drug treatment profiles and not just one constant one and hopefully develop an individual therapy plan for each cancer sample. They will analyze the patient derived organoids with transcriptomics and comparative gene expression analysis.