



Bruker Technology Spotlight

Cutting-Edge Solutions for Quantitative Spatial Biology & Single-Cell Omics

Tuesday, June 7 — 5:15-6:15PM | Nassau Suite
Symposium and Reception

Bruker Technology Spotlight

Cutting-Edge Solutions for Quantitative Spatial Biology & Single-Cell Omics

Engage in illuminating discussion and delectable finger food as we delve into the latest technologies and research in spatial and single cell biology. Wine and light fare will be served. Please register for the event so that we may plan food and beverage accordingly.

Guest Speakers:

Lixin Zhang, MD Ph.D. | Research Scientist, Magee-Womens Research Institute and Department of Obstetrics, Gynecology, and Reproductive Sciences, University of Pittsburgh School of Medicine

Nikolai Slavov, Ph.D. | Allen Distinguished Investigator and Associate Professor, Bioengineering Department and Barnett Institute, Northeastern University

[RSVP](#)

[EVENT WEBSITE](#)

Tuesday, June 7 — 5:15-6:15PM

Symposium Agenda

5:15PM	Welcome and Introduction (Mark Munch, Ph.D.)
5:25PM	ChipCytometry Basics & CellScape Introduction (Kevin Gamber, Ph.D.)
5:35PM	Ovarian cancer: from tissue spatial identity to individual cellular activity (Lixin Zhang, Ph.D.)
5:50PM	Exploring functional protein covariation across single cells (Nikolai Slavov, Ph.D.)
6:05PM	Introducing Spatial 3D Genomics (Suvarna Gandlur, Ph.D.)
6:15PM	Open to talk with Bruker representatives



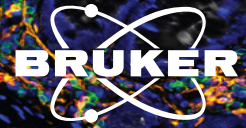
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Bruker Technology Spotlight: Presentation Abstracts

Ovarian cancer: from tissue spatial identity to individual cellular activity

Ovarian cancer is one of the five leading causes of cancer death in women. More than 75% of cases are diagnosed at advanced stages with a high recurrence rate. We are currently testing chemotherapy in combination with immune therapy to improve the survival rate of ovarian cancer patients. To further optimize the therapeutic regimens, it is imperative to have a more precise understanding of protein biomarker changes in the microenvironment surrounding the cancer tissues before, during, and after treatment. Our newly established ovarian cancer cell lines generated from human and mouse tissues can provide information on molecular changes in reaction to certain treatments, at single cell level. In addition to anti-tumor cytotoxic immune cells, antibody-secreting tumor infiltrating B cells have become a potential key factor in tumor microenvironment regulation. Here I report our recent progress on these topics and the use of Canopy ZellScanner One to address some of our research questions.

Presenter: Lixin Zhang, MD Ph.D.

Research Scientist, Magee-Womens Research Institute and Department of Obstetrics, Gynecology, and Reproductive Sciences, University of Pittsburgh School of Medicine

Exploring functional protein covariation across single cells

Biological functions are reflected in the natural variation of proteome configurations across individual cells. Emerging single-cell proteomics methods may decode this variation and empower inference of biological mechanisms with minimal assumptions. I will describe both established and emerging single-cell mass-spectrometry methods, and how these methods have allowed us to interpret protein covariation in different biological systems, including primary macrophages and melanoma cells primed for drug resistance. The focus of my talk will be on conceptual innovations and strategies for data acquisition and interpretation that make single-cell protein analysis accessible, robust and highly quantitative.

Presenter: Nikolai Slavov, Ph.D.

Allen Distinguished Investigator and Associate Professor, Bioengineering Department and Barnett Institute, Northeastern University



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