2021 GRCF Core Symposium Agenda
Live Event Date: April 14, 9 am – 5 pm

9:00 - 9:55 am
Opening Plenary Session, 'A new method to spatially map large volumes of human tissues and tumors at single-cell resolution (CODA)'

Sponsor: Genetic Resources Core Facility

Denis Wirtz
Vice Provost for Research
Smoot Professor, Chemical and Biomolecular Engineering, Pathology, Oncology
Director Johns Hopkins Physical Sciences-Oncology Center
Johns Hopkins University and Johns Hopkins School of Medicine

Through research at the interface of physics, biology, and oncology, Wirtz has made seminal contributions in cancer cell migration, cytoskeleton biophysics, and the nascent field of mechanobiology. He has developed quantitative methods, which are widely used both in academia and industry. He has pioneered research in cell migration in 3D settings. Denis Wirtz has founded the Johns Hopkins Institute for NanoaBioTechnology (INBT). He is the Director of the NCI-funded postdoctoral training program in nanotechnology for oncology and Director of the NCI-funded Physical Sciences-Oncology Center. Wirtz is author and co-author of 240 peer-reviewed articles. Wirtz is the Theophilus H. Smoot Professor of Engineering and Science, Wirtz received a physics engineering degree from the Free University of Brussels in 1988, and MSc and PhD in Chemical Engineering from Stanford University in 1993. Wirtz has been the Vice Provost for Research of Johns Hopkins University since 2014.

10:00 - 10:55 am
‘Unveil the immune response to cancer and infectious disease with powerful immunoassays’

Sponsor: Thermo Fisher Scientific
Uncovering the interactions between the immune system and cancer cells or pathogens is key for understanding and controlling both cancer and infectious disease. The evolving research field of immuno-oncology focuses on an individual’s immune system as potential innovative treatment approaches to combat cancer. Immune checkpoint molecules have been identified as critical players in the regulation of NK cell- and T cell-mediated immune responses. Thus, the systematic analysis of crucial soluble immune stimulatory and inhibitory factors using multiplexing high-throughput immunoassays will help to shed light on the regulation of checkpoint pathways and to monitor response to immunotherapeutic treatment. Likewise, innovative assay formats to characterize the humoral response to infection are urgently needed as the novel human coronavirus SARS-CoV-2 and the associated respiratory disease COVID-19 continue to evolve worldwide. Simple, rapid and multiplex high-throughput assays will enable researchers to assess the prevalence of SARS-CoV-2 infection and to examine the immunological memory and potential protective immunity of previously infected or vaccinated individuals. Moreover, analyzing the level of a broader panel of immunomodulatory markers will allow researchers to decipher the complex interplay of soluble mediators accounting for the so-called cytokine storm or cytokine release syndrome (CRS), an overactive state of the immune system that is a common complication associated with SARS-CoV-2 infection.

Thus, it is of great interest to identify dynamic changes in the immune system in the context of both immuno-oncology research and SARS-CoV-2 infection research for a more holistic view of a subject’s immune status.

This webinar will provide an understanding of powerful immunoassay solutions (RUO) to explore major questions around the host immune response to cancer and SARS-CoV-2 infection, providing important insights for the development and monitoring of therapies and vaccines.

**Learning Objectives**

- Provide new insights into immunomonitoring approaches to characterize and understand key changes in the immune system associated with cancer and infectious disease
- Outline immunoassay solutions to advance immuno-oncology research
- Introduce novel serological assay platforms (RUO) to accurately detect SARS-CoV-2 specific antibodies and support SARS-CoV-2 research
The expanding range of RNA-seq applications and technologies increasingly face the challenge of extremes of low input amounts and degraded samples. RNA samples can include a large dynamic range of transcript expression, and highly expressed transcripts with minimal biological interest can dominate readouts, masking detection of more informative low-abundance transcripts. Our RNaseH-based method for depleting abundant RNAs is optimized for high performance with both FFPE samples and high-quality inputs. Probe sets developed for this method include rRNA from human, mouse, rat and bacteria, and also globin transcripts from blood. We also launched a customizable approach to enrich for RNAs of interest by eliminating any unwanted RNAs across different species. For samples composed of single cells or picogram amounts of total RNA, detection of low-abundance transcripts is challenging but can be achieved by full-length transcript sequencing using a robust method incorporating template switching and enzymatic fragmentation to provide uniform transcript coverage.

Digital PCR (dPCR) is a highly viable solution for copy number variation (CNV) detection, rare mutation detection and quantification, validation of NGS results, and applications alike. However, currently available solutions are either very complex to operate, or lack a scalability option for users with variable throughput and flexible workflow needs. Unlike current systems relying on droplet generation, QIAGEN’s offering of fully integrated walkaway instrument options and multiple plate configurations with increased partitions can potentially solve throughput, speed, and usability challenges. In this talk, we will first present the improvements that the QIAcuity offers over existing systems. Then reveal how the QuantiNova LNA PCR Assays provide highly sensitive and accurate locked nucleic acid (LNA)-enhanced digital PCR quantification for mRNA.
and lncRNA targets, detecting even the smallest expression changes at the lowest concentrations.

1:00 - 1:55 pm

**Keynote Address: Will have title by March 5th**

**Sponsor: Genetic Resources Core Facility**

Joshua W Modell
Assistant Professor
Johns Hopkins University School of Medicine, Molecular Biology and Genetics

Will have by March 5th

2:00 - 2:55 pm

**‘Genomics in 2021 and Beyond’**

**Sponsor: Illumina**

Dan Gheba
Executive Sequencing Specialist, Illumina, Inc.

Basic and translational research is the driving force behind Illumina’s mission to improve human health by unlocking the power of the genome. In collaboration with the resources at the JHU GRCF, advances in Illumina technology are creating simpler library preparation, more cost-effective sequencing, and easier to understand data analysis tools. Please join us for a webinar around 2021’s hottest topics in genomics and learn how the latest Illumina innovations can drive your research forward.
‘Advancing Immunotherapeutics Research with Immuno-oncology Cell Line Panels and Milliplex Multiplexing Assays’

Sponsor: MilliporeSigma

M. Zulfiker Hossain
PhD – Research Technology Specialist, Advanced Genomics and Cell Models and Amy

R. Johnson
PhD - Field Application Scientist, Immunoassay Platform Solutions

Over the past decade, immunotherapeutics have emerged as a promising approach for the treatment of a variety of diseases including cancer. In this webinar, we’ll discuss cutting-edge tools for immunotherapeutics research. Variable expression of tumor-associated antigens and MHC polymorphism in patient cell populations make it difficult to predict when and why a specific immunotherapy might fail. We utilized our advanced cell engineering workflow to generate cell lines with controlled levels of tumor-associated antigens or mono-allelic expression of specific MHC/HLA molecules. These genetically modified cell lines can be used as controls in validated assays or for the development of new assays to test candidate immunotherapies. Our immuno-oncology cell lines are thus designed to simplify evaluation of immunotherapeutic strategies through cell-based assays and immunoassays.

In these complex biological systems, multiple interconnected mechanisms are involved in simultaneously producing a cellular response to disease or therapeutic intervention. This response can be quantified by measuring biomarkers such as cytokines, hormones, and signaling proteins. Multiplexing enables researchers to more fully understand the complexities of their biological systems by assessing multiple biomarkers in a single sample, thus increasing throughput and saving precious sample. We will discuss how Milliplex multiplexing immunoassays can be easily integrated into any study to facilitate your immunotherapeutics research. Collectively, our innovative physiologically relevant tools can help provide deeper insight into the function and performance of novel immunotherapeutic approaches.
Next Generation Sequencing (NGS) excels as a discovery technique and is ideal for performing global analyses. By looking at all possible targets, NGS allows for the discovery of new molecules or pathways that were not known to have a specific biological function. However, once new targets have been identified they must be confirmed using an alternative testing mechanism. Droplet digital polymerase chain reaction (ddPCR™) was developed to provide high-precision, absolute quantification of nucleic acid target sequences with a wide range of applications. Compared to traditional real time PCR, ddPCR has an increased signal-to-noise ratio and allows for the removal of PCR efficiency biases. As a result, ddPCR can be used to analyze events that require a high level of sensitivity. The advantages of ddPCR make it an ideal platform for orthogonal validation of NGS data.