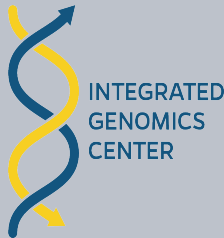




2026 Inaugural Johns Hopkins Integrated Genomics Center (JHIGC) Symposium

Keynote Address: "From Germline Discovery to Risk Management: Modern Genetic Epidemiology of Pancreatic Cancer"



Alison Klein, MHS, Ph.D.,

Professor of Oncology, Pathology and Epidemiology,
Johns Hopkins School of Medicine, Co-Leader, Cancer
Prevention and Control Program (CPC)

Come to Learn, Engage, and Network

April 22, 2026, 9 am - 2 pm, Turner Concourse

Featuring nine talks, exhibit concourse, luncheon, and GRCF Flair!

Welcome to the 2026 Inaugural Johns Hopkins Intergrated Genomics Center Symposium!

Welcome to the inaugural Johns Hopkins Integrated Genomics Center (JHIGC) Symposium.

This year marks an important milestone for our community as we formally introduce the Johns Hopkins Integrated Genomics Center: a unified, School of Medicine–level genomics enterprise designed to bring together complementary technologies, scientific expertise, and research support infrastructure under one cohesive vision.

Built on the strong foundation of the Genetic Resources Core Facility and our partnering genomics programs, this integration represents a strategic step forward. By aligning sequencing, single-cell and functional genomics, bioprocessing, and computational capabilities within a coordinated framework, we are strengthening our ability to serve investigators, scale innovation, and accelerate discovery.

Today's symposium reflects both continuity and transformation. We remain committed to showcasing emerging technologies, supporting impactful research, and fostering meaningful collaborations. At the same time, we celebrate a new chapter, one focused on institutional alignment, operational excellence, and a shared commitment to advancing genomics research at Johns Hopkins.

We are grateful for your partnership and participation in this pivotal moment. We look forward to a day of discovery, dialogue, and forward momentum.

Register Today
You must register in advance
to be eligible for all prizes!
Scan the QR Code



AGENDA



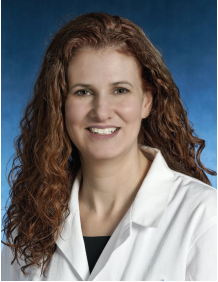
2026 Integrated Genomics Center Symposium Agenda

Turner Concourse, April 22, 2026, 9 am - 2 pm

Featuring - Exhibitors, Seminars, Keynote Address, Lunch & Prizes!

| Start Time | End Time | Event | Room | Featuring | Title |
|------------|----------|-----------------------------|---------------------|------------------------------|---|
| 9:00 AM | 2:00 PM | Exhibit Floor Open | Turner Concourse | IGC Services & IGC Suppliers | Come explore the many genomic services and products the IGC offers. And visit the suppliers to the GRFC! |
| 9:00 AM | 9:50 AM | Breakout Session I | MRB G-01 | Cell Signaling | CST solutions for transcriptomics and spatial biology |
| | | | MRB G-03 | Singular Genomics | Delivering Spatial Pathology at Scale on G4x |
| | | | West Room | TWIST Biosciences | Advancing Cancer Research with Twist Bioscience |
| 10:00 AM | 10:50 AM | Breakout Session II | MRB G-01 | Stellaromics | "The Next Dimension of Discovery: Pyxa 3D Spatial Multi-Omics" |
| | | | MRB G-03 | PacBio | PacBio HiFi sequencing for a more complete view of biology |
| | | | West Room | MilliporeSigma | From Genotype to Phenotype: Recent Advances in Genome & Epigenome Editing and Phenotypic Characterization |
| 11:00 AM | 11:50 AM | Breakout Session III | MRB G-01 | 10X Genomics | Mapping the Continuum: Advancing Biological Discovery with Integrated Single-Cell and Spatial Multiomics |
| | | | MRB G-03 | New England BioLabs | Breaking Through Bias to Redefine Precision in Small RNA Library Prep |
| | | | West Room | Takara | "From Slide to Insights: Spatial Transcriptomics Without Bioinformatics Barriers" |
| 12:00 PM | 12:50 PM | LUNCH | Turner Concourse | Rosina Gourmet | Catered Boxed Lunch |
| 1:00 PM | 1:50 PM | Keynote Address | Tilghman Auditorium | Alison Klein | "From Germline Discovery to Risk Management: Modern Genetic Epidemiology of Pancreatic Cancer" |

Keynote Address



TITLE: "From Germline Discovery to Risk Management: Modern Genetic Epidemiology of Pancreatic Cancer"

PRESENTER: Alison Klein, MHS, Ph.D., Professor of Oncology, Pathology and Epidemiology, Johns Hopkins School of Medicine, Co-Leader, Cancer Prevention and Control Program (CPC)

ROOM: Tilghman Auditorium

TIME: 1:00 pm - 1:50 pm

ABSTRACT:

Pancreatic cancer remains leading cause of cancer death world-wide. Over the past two decades we have made strides in identifying the underlying substantial heritable component of pancreatic cancer, but considerable challenges remain. This talk will provide an overview of how our germline discovery efforts have led to actionable risk management, integrating evidence from sequencing studies leveraging family-based cohorts, as well as GWAS to define the genetic architecture of susceptibility across rare, high-penetrance variants and common polygenic risk. We will focus on how technological advances have enabled the discovery and translation of genetic risk into clinical pathways, highlighting how modern genetic epidemiology can refine stratified prevention and improve outcomes in pancreatic cancer.

Breakout Session I

CST solutions for transcriptomics and spatial biology, Vicki McColloch, Field Application Scientist 9 am - 9:50 am, MRB G-01.

Abstract: Single-cell RNA sequencing has revolutionized cell biology by enabling the profiling of transcriptomes at a single cell resolution. However, it provides a partial view of cellular function. We will present an overview of InTraSeq technology, which allows for the simultaneous measurement of RNA and protein expression. InTraSeq enables the concurrent measurement of mRNA, surface markers, cytoplasmic proteins, and nuclear proteins within individual cells. This offers a comprehensive approach to studying cellular function, by combining RNA and protein profiling from the same sample while utilizing a relatively simple protocol. We will also discuss our SignalStar technology, which enables the detection of multiple phenotypic and functional markers while preserving spatial context and tissue architecture. It provides customizable, flexible, and highly-validated antibody panels for your spatial biology research. Amplify multiple targets simultaneously in FFPE tissue with high sensitivity and specificity, and generate results on ~8 targets in just 2 days.

Delivering Spatial Pathology at Scale on G4x, John Manuel, PA (ASCP), Spatial Science & Technology Advisor, 9 am - 9:50 am, MRB G-03.

Abstract: Imaging RNA and proteins in tissue with sub-cellular resolution brings new molecular-level insights to pathology. The G4X Spatial Sequencer uses NGS with 4-color, high-speed, sub-micron-resolution imaging to analyze gene transcripts and proteins in FFPE tissue sections. Processing up to 40 samples/run (1 cm² each), the G4X enables large-scale clinical studies for next generation pathology.

Advancing Cancer Research with Twist Bioscience, 9:00 am -9:50 am, West Room.

Abstract: Next-generation sequencing (NGS) has transformed cancer research and clinical oncology by enabling detailed molecular profiling of tumors. This presentation highlights three high-impact NGS applications shaping modern cancer diagnostics and monitoring: custom panels for targeted, cost-effective mutation analysis; liquid biopsy approaches using cell-free DNA to enable non-invasive detection and real-time disease monitoring; and methylation profiling to improve tumor classification, identify tissue of origin, and detect cancers earlier. Together, these technologies are advancing precision oncology, improving patient outcomes, and expanding our understanding of cancer biology.

Breakout Session II

The Next Dimension of Discovery: Pyxa 3D Spatial Multi-Omics, Matt Kane, M.A.,
Area Sales Manager - East Coast, Stellaromics, 10:00 am -10:50 am, MRB G-01.

Abstract: A significant limitation of traditional transcriptomic analysis methods is their reliance on dissociated single-cell samples or thin 2D tissue sections, which inevitably strip away crucial spatial context about how layers of diverse cells interact in three dimensions. Understanding cellular function, therefore, critically depends on preserving this 3D context; cell positioning and the surrounding microenvironmental cues profoundly influence disease progression, therapeutic response, and overall tissue function. The transition from 2D to 3D spatial omics is transformative to further advances in drug discovery. This shift represents a move from observing isolated components to understanding the systemic architecture of disease, profoundly changing the types of questions researchers can ask and answer. In this presentation we present Pyxa, a new 3D instrument and chemistry based on STARmap to do single cell transcriptomics in 20um – 100um thick tissue.

PacBio HiFi sequencing for a more complete view of biology, Jonas Korlach,
Co-Founder and Scientific Advisor, 10:00 am -10:50 am, MRB G-03.

Abstract: Accurate long-read HiFi DNA sequencing provides best-in-class performance for genome assembly, variant detection, RNA isoform discovery/expression, epigenomics, microbial community resolution, and more. The impact of more complete resolution and the resulting clarity to biological understanding that is unlocked with HiFi sequencing will be illustrated. Discussion will include recent updates in numerous multi-omic applications to show how HiFi sequencing is within reach for every lab and with the ability to scale.

From Genotype to Phenotype: Recent Advances in Genome & Epigenome Editing and Phenotypic Characterization, M. Zulfiqer Hossain, Ph.D.,
10:00 am -10:50 am, West Room.

Abstract: Genome editing has enabled the investigation of gene function and target identification and is helping researchers develop potential therapies against a wide range of diseases. Recent advances in CRISPR technology include promising approaches like base editing and epigenome editing. Genome or epigenome editing can have profound effects on cellular protein levels as well as viability and overall phenotype of the targeted cells. Therefore, the downstream effects of any genetic manipulation must be thoroughly assessed. The MILLIPLEX® multiplex assays and the Single Molecule Counting (SMC®) technology, which enhance the accuracy and precision of protein quantification can be effectively integrated into genome or epigenome editing workflows to achieve phenotyping goals.

Breakout Session III

Mapping the Continuum: Advancing Biological Discovery with Integrated Single-Cell and Spatial Multiomics, Brad Toms, Sr. Science & Technology Advisor, 11:00 am -11:50 am, MRB G-01.

Abstract: Understanding complex biological systems requires more than a list of cellular components; it requires a map of their interactions within a functional architecture. While single-cell sequencing has redefined our understanding of cellular heterogeneity, the loss of spatial context often obscures the mechanisms of disease. This presentation explores the synergy between single-cell and spatial multiomics, demonstrating how their integration enables a high-resolution view of biology in situ. We will discuss the transition from characterizing discrete cell states to mapping their precise locations and molecular interactions within the tissue microenvironment. By highlighting advancements across our portfolio—spanning transcriptomics and proteomics—we will illustrate how these tools reveal rare cell niches and drive discovery in oncology, immunology, and beyond. Join us to see how bridging the gap between resolution and context provides a transformative lens for modern biological research.

Breaking Through Bias to Redefine Precision in Small RNA Library Prep, Jeanne Geskes, Senior NGS Application Scientist, 11:00 am -11:50 am, MRB G-03.

Abstract: Bias in Small RNA library prep is an important factor that can impact the accuracy of sequencing data, skewing the representation of small RNA species present in a sample. Efforts at New England Biolabs to understand and overcome this bias has resulted in a novel method that utilizes a randomized splint adaptor to avoid any ligase preference towards the terminal ends of small RNA species. This approach provides a method for accurate sequencing-based analysis of small RNAs present in a cell, offering insight into the wide variety of cellular functions they regulate.

From Slide to Insights: Spatial Transcriptomics Without Bioinformatics Barriers, Jason Whitham, 11:00 am -11:50 am, West Room.

Abstract: Takara Bio's Trekker is a novel spatial technology that delivers true single-cell resolution while simplifying downstream bioinformatics. By tagging nuclei rather than relying on image segmentation and signal deconvolution, Trekker avoids many of the challenges common to imaging- and sequencing-based spatial platforms. This approach produces single-cell data enriched with spatial context that can be analyzed using standard tools. In this talk, we highlight key analyses that showcase the power of true single-cell spatial transcriptomics and outline both service and DIY analysis options.

Exhibitors

Hopkins Exhibitors

Johns Hopkins Integrated Genomics Center: *Membership of the new Integrated Genomics Center to combine, the Genetic Resources Core Facility (GRCF), Experimental and Computational Genomics Core (ECGC), and the Single Cell and Transcriptomics Core (SCTC).*

- **Core Store**
- **Computational Analysis**
- **JHU Biobank & Cell Center**
- **Nucleic Acid Services & Technologies & HTS**
- **Single Cell & Functional Genomics**

Other Hopkins Affiliates

- Office of Climate & Sustainability
- JHU Office of Sesquicentennial

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