NEXTGEN OMICS SPATIAL & DATA US 2026

March 31 - April 01 2026 | Boston, MA

Conference Brochure

Book Now!

Complimentary Guest Passes are Available

Register

Sponsor

Driving the Next Generation of Multi-Omics Research, Data & Technology

9 Content Tracks Across Two Days

10+ Hours of pre-arranged 1:1 Meetings

70+ Partners

600+ Attendees | **50%** pharma/ biotech | **50%** academia / healthcare

Composed of 4 Programs!

- NextGen Omics Data & Analysis
- Spatial Multi-Omics
- Single Cell Analysis
- NGS & Clinical Diagnostics

NextGen Omics Young Scientist Poster Presentations

Honouring outstanding scientific work by a PhD student, PostDoc or early career scientists. Successful applicants will get the opportunity to present on day 2.

More Information

oxfordglobal.com/precision-medicine/events/nextgen-omics-us

Over 70 Expert Speakers Including...

KEYNOTE SPEAKER

STEPHEN BRUCE BAYLIN,
Deputy Director & Associate Director for Research, Sidney Kimmel Comprehensive Cancer Center

Day 2 Keynote Address 08:45; *The Role Of Epigenomics In Cancer Progression*

KEYNOTE SPEAKER

ARUTHA KULASINGHE,
Associate Professor, Lead of Clinical-oMx Lab University of Queensland

Day 1 Keynote Address 09:00; *Decoupling Immunotherapy Responses, One-Cell, One-Niche & One Functional-Unit At A Time*

PANEL DISCUSSION HIGHLIGHTS

REVOLUTIONIZING MULTI-OMICS WITH ARTIFICIAL INTELLIGENCE

Join us for the interactive panel discussion on Day 1 at 6:pm alongside:

SOURAV CHOUDHURY, Group Head, **Sanofi**
SAHIL SETH, Principal Scientist, **Bristol Myers Squibb**
ENRICO MOSSOTTO, Senior Director, Genome Informatics & AI, **MeiraGTx**
SIMONA CRISTEA, Head of Genomics Data Science & AI, **Dana-Farber Cancer Institute**
IULIAN PRUTEANU-MALINICI, Senior Director of Bioinformatics for Pioneering Medicines, **Flagship Pioneering**

WORKSHOP

GESTALT - GLOBAL ALLIANCE FOR SPATIAL TECHNOLOGIES

Join the following GESTALT members as they discuss the latest innovations across their global working groups

- FEI CHEN, Principal Investigator & Assistant Professor, **Broad Institute**
- JIWOON PARK, Founder of the Spatial Atlas of Human Anatomy, **Harvard Medical School & Weill Cornell Medicine**
- GLORIA PRYHUBER, Professor, Department of Pediatrics, Neonatology, **University of Rochester**
- DANIEL JONES, Staff Scientist, Vaccine & Infectious Disease Division, **Fred Hutch Cancer Center**

WELCOME TO

NextGen Omics, Spatial, & Data US 2026

Welcome to NextGen Omics, Spatial, & Data US 2026, Oxford Global's premier US technology event bringing together the leading innovators across omics research at the Sheraton Hotel, Boston from 30 March – April 1.

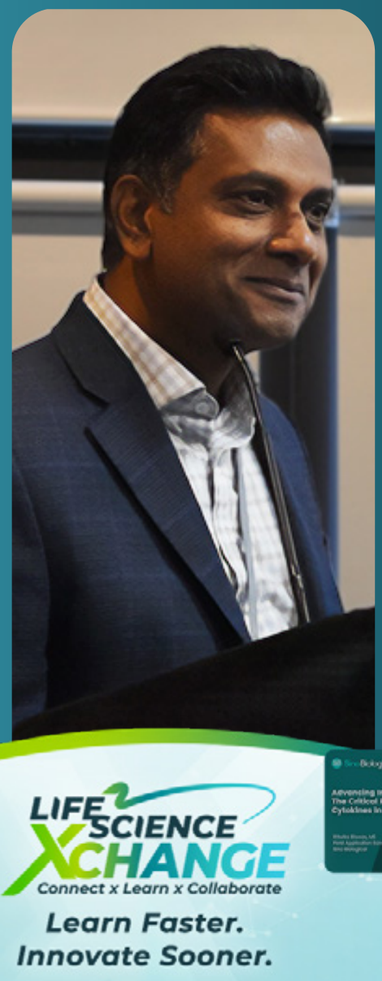
Join us for two immersive days of expertly curated content addressing the most pressing challenges, spotlighting breakthrough innovations, and uncovering emerging technologies across four programs: **NextGen Omics Data & Analysis, Spatial Multi-Omics, Single Cell Analysis** and **NGS & Clinical Diagnostics.**

This year's event features an enhanced agenda with a strong focus on AI/ ML and the revolution it is having on the multi-omics landscape.

Engage in high level discussions and expertly tailored sessions that showcase the latest advancements in AI, data integration & interpretation through to single cell & spatial analysis and genomic sequencing & screening. Hear insights from leading experts as they explore how AI- and ML-driven tools are accelerating the integration of spatial and single-cell insights, enhancing the application of single-cell technologies in clinical development, and informing evolving strategies for utilizing spatial biology. Deep science sessions will examine how AI powered omics techniques and technologies are shaping clinical decision-making, disease understanding, and precision-guided therapies.

In addition to scientific presentations and interactive discussions, this event offers invaluable opportunities to network with industry leaders and stay at the forefront of the next generation of advancements that are set to transform the industry.

Mike Burden
Director of Production & Content – Precision Medicine Brand,
Oxford Global



WHAT'S NEW

Benefits Of Attending

Take a deep dive into the latest strategies for enabling successful multi-omics data integration. Improving efficiency, downstream processing, data streamlining, and the use of artificial intelligence all have a role in harnessing the power of integrated data.

Gain invaluable insights into innovations in emerging spatial technologies and their applications. Key opinion leaders will be addressing the role of spatial omics in precision medicine from diagnostics to therapeutic development.

Explore advancements in single cell analysis. Hear about how insights from single cell data are providing novel targets for investigation and infiltrating clinical decision-making.

Discuss important considerations when choosing your sequencing and screening technologies. Sessions will address questions about which techniques suit particular experiments best and how to make the most of your results.

Benefit from cross-program discussions on artificial intelligence, research under fiscal constraint, and women in genomics. Join these diverse panels to hear opinions and key takeaways that impact anyone conducting research with omics technology.

DON'T MISS THESE

Interactive Panels

NEXTGEN OMICS DATA & ANALYSIS

Overcoming Multi-Omics Data Harmonization & Analysis Challenges

Revolutionizing Multi-Omics Research With Artificial Intelligence

Overcoming Barriers To Integrate Omics Technology With Big Data

SPATIAL MULTI-OMICS

Advancing Spatial Multi-Omics For Discovery

Omics Research & Investment Under Fiscal Constraint

Exploring Novel Uses For Spatial Transcriptomics

Diversifying the Applications of Spatial Biology

Spatial Biology To Advance The Map Of Human Pathology

SINGLE CELL ANALYSIS

Turning Single Cell Insights Into Novel Targets

Translating High Resolution Single Cell & Spatial Data Into Biomarker Discovery & Clinical Impact

How To Optimize Single Cell Sequencing Approaches

NGS & CLINICAL DIAGNOSTICS

How To Choose Your Sequencing & Screening Technologies

Genomics For Diagnosing Patients With Rare Diseases

The Role of Multi-Omics In Precision Medicine

SPECIAL EVENT FEATURES

Big Attendance Meets Intimate Connections

Day One Keynote

ARUTHA KULASINGHE, Associate Professor, Lead of Clinical-oMx Lab, University of Queensland

Day Two Keynote

STEPHEN BRUCE BAYLIN, Deputy Director & Associate Director for Research, Sidney Kimmel Comprehensive Cancer Center

Day One & Day Two: Young Scientist Awards

The NextGen Omics Young Scientist Poster Award recognizes outstanding work by PhD students, postdocs, and early career scientists. Three winners receive a $1,000 travel grant, a LifeScienceXchange Pass, and a chance to present on day two. For details and entry **visit here**

Cross Program Panel Discussions

Revolutionizing Multi-Omics Research With Artificial Intelligence

Discover how industry and academia are approaching the AI revolution alongside:

- MANISHA BRAHMACHARY, Associate Director, Sanofi
- ENRICO MOSSOTTO, Senior Director, Genome Informatics & AI, MeiraGTx
- SIMONA CRISTEA, Head of Genomics Data Science & AI, Dana-Farber Cancer Institute
- IULIAN PRUTEANU-MALINICI, Senior Director of Bioinformatics for Pioneering Medicines, Flagship Pioneering

Omics Research & Investment Under Fiscal Constraint

Hear strategies for sustaining and reshaping research in resource-limited settings from:

- GÁBOR BALÁZSI, Professor, Stony Brook University
- AARNO PALOTIE, Research Director, Institute for Molecular Medicine Finland
- JOCHEN LENNERZ, Chair, EFLM Task Group on Integrated Diagnostics

Population Genomics

Join sessions providing perspectives on population scale genomics, diversity & large-cohort data to advance global health and discovery

Presentation: FinnGen: Leveraging Population-Scale Genomics & Health Registers For Clinical Discovery

Hear from AARNO PALOTIE, Research Director at the Institute of Molecular Medicine Finland as he delves into FinnGen's 500,000 participant project

Closed Door Panel Discussion: Unlocking Population Genomics With Large Scale Cohort Studies

Discover how a variety of projects are leveraging population scale genomic data and fostering cross continent collaboration

Panel Discussion: Spatial Biology To Advance The Map Of Human Pathology

Gain insights on the development of large scale, multi-national cell atlas projects from our panellists:

- EMRE ARSLAN, Associate Director, Takeda
- JIA-REN LIN, Technical Director, Tissue Imaging Platform, Harvard Medical School
- DAVID GALLEGOS, Senior Scientist, Takeda
- AHMET COSKUN, Professor of Biomedical Engineering, Georgia Institute of Technology

Industry Workshop

Day 2: GESTALT - Global Alliance for Spatial Technologies

Uncover a holistic approach to spatial biology, emphasizing integrated data, systems-level thinking, and AI-driven insight from our speakers

- FEI CHEN, Associate Professor of Stem Cell and Regenerative Biology, Harvard University
- JIWOON PARK, Founder of the Spatial Atlas of Human Anatomy, Harvard Medical School & Weill Cornell Medicine
- GLORIA PRYHUBER, Professor, Department of Pediatrics, Neonatology (SMD), University of Rochester Medical Center
- DANIEL JONES, Staff Scientist, Vaccine & Infectious Disease Division, Fred Hutch Cancer Center

WHY PARTNER WITH

OXFORD GLOBAL?

At Oxford Global, our mission is to curate personalised experiences that foster community and inspire innovation.

We believe in the power of networking, connection, and knowledge to deliver quality products and services that exceed expectations. Partnering with Oxford Global means having a dedicated team committed to helping you achieve your goals and navigating the industry's ever-changing landscape.

Arrange 1-1 Meetings

Benefit from guaranteed one-to-one face time with your key prospects, with detailed pre-meeting information provided to enable effective and productive conversations.

Speaking Opportunities

Showcase your company's recent work to a relevant and highly engaged audience.

Host Panel & Roundtable Discussions

Feature alongside key opinion leaders to discuss current hot topics and highlight your company's expertise.

Organise Workshops

Demonstrate best practice within the industry in front of your peers with case studies from your clients.

Exhibit your Products & Solutions

Promote your offerings and ensure delegates know where to find you with a prominent brand presence in the exhibition hall.

Digital Marketing & Lead Generation

Accessing the Oxford Global database, amplify your thought leadership and branding messaging through our digital content initiatives.

LEARN MORE

DRIVE INNOVATION & ACCELERATE RESEARCH

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AGENDA AT A GLANCE

NextGen Omics Data & Analysis

Discuss novel approaches to multi-omics data. Presentations will include using dual filter AI in single cell analysis, AI enabled multi-omics integration, combining spatial biology with agentic AI, and mathematical models.

Join key opinion leaders to advance data focused approaches in multi-omics to advance target discovery.

VPs, Directors & Senior Managers from leading pharma & biotech companies and research institutions in the following fields and more:

- FAIR Data
- Data Integration
- Bioinformatics
- Data Standardization
- Data Analysis
- Big Data
- Spatial Analysis
- Single Cell Analysis
- AI

Formal and informal meeting opportunities offer delegates the chance to discuss key solutions with leading service providers. Formal 1:1 meeting opportunities will be available to arrange prior to the event which take place during the dedicated networking breaks covering:

- FAIR Data
- Machine Learning
- Generative AI
- Data Visualization
- Data Interpretation
- Data Sharing / Repositories
- Bioinformatics Tools
- Statistical Programming
- Quantum Computing
- Workflow Automation
- Data Processing
- Experimental Design Optimization

Day One

Track 1: Multi-Omics Approaches for Data Integration, Harmonisation & Analytics

- Applications of multi-omics data for personalised medicine
- Large-scale multi omics data analysis
- Case studies from omics: proteomics, genomics, transcriptomics, epigenomics
- Bioinformatics & data analytics and approaches
- ML-driven target identification
- AI-driven analytics approaches
- Integrating multiple datasets
- AI/ML toolkits for multi omics datasets
- Novel methods, approaches, and platforms for data integration

NEXTGEN OMICS SPATIAL & DATA US 2026

AGENDA AT A GLANCE

Spatial Multi-Omics

Gain invaluable insights into novel multi-omics technologies for spatial genomics & transcriptomics. Presentations will include translating spatial imaging techniques & approaches into drug development multi-modality processing and spatial transcriptomic databases.

Discuss spatial biology for oncology, immunology and neuroscience. Hear from expert speakers discussing the tumour environment, distribution of immune cells within the tumour and mapping cellular diversity in the brain.

VPs, Directors & Senior Managers from leading pharma & biotech companies and research institutions in the following fields and more:

- Spatial Genomics
- Spatial Transcriptomics
- Spatial Metabolomics
- Spatial Proteomics
- Systems Biology
- Molecular Medicine
- Translational Medicine
- Spatial Omics
- Translational Science

Formal and informal meeting opportunities offer delegates the chance to discuss key solutions with leading service providers. Formal 1:1 meeting opportunities will be available to arrange prior to the event which take place during the dedicated networking breaks covering:

- Spatial Imaging Platforms
- Spatial Data Analysis Tools
- Tissue Imaging & Prep
- Single Molecule Imaging
- Cellular Analysis
- Proteome Analysis
- Spatial Bioinformatics
- Spatial Profiling
- Spatial Mapping
- Spatial Proteogenomics
- Biomarker Profiling

Day One

Track 2: Emerging Multi-Omics Platforms and Applications: Genomics & Transcriptomics

- Spatial transcriptomics innovations
- Techniques & approaches into drug development
- Single cell transcriptome imaging
- Multi-modality processing
- Liquid Biopsies beyond oncology

Track 3: Spatial Biology for Therapeutics Discovery & Development (Oncology & Immunology)

- Spatial biology in the tumour microenvironment
- Understanding cellular & genetic heterogeneity
- Studying immune cell distribution
- Relationship between the immune system and tumour biology to identify novel therapeutic targets
- Genomics and spatial transcriptomics: discovery of novel cell states and cellular interactions in liver physiology and disease biology

Day Two

Track 1: Emerging Multi-Omics Platforms & Applications: Proteomics, Epigenomics, & Metabolomics

- Next gen proteomics – including developing novel technologies for protein analysis & advancements in quantifying protein expression
- Metabolomics & lipidomics, including high resolution profiling
- Spatial distribution of proteins within the cell
- Distribution of metabolites at spatial resolution

Track 2: Spatial Biology for Therapeutic Discovery & Development

- Case studies from varying therapeutic areas including:
- Neurobiology
- Gastroenterology
- Infectious Disease
- Urology
- Includes the GESTALT workshop

NEXTGEN OMICS SPATIAL & DATA US 2026

AGENDA AT A GLANCE

Single Cell Analysis

Hear from and meet with the key innovators in single cell & spatial biology. 2025 attendees include, Vice President, Head of Clinical BioAnalytics & Translational Sciences; Senior Director of NGS; Director of Computational Biology; and of Genomics Data Science & AI.

Advance your understanding emerging of single cell technologies from novel technologies for single cell imaging, through to benchmarking, applying omics in the clinic, and bioinformatics for single cell analysis.

VPs, Directors & Senior Managers from leading pharma & biotech companies and research institutions in the following fields and more:

- Single Cell Analysis
- Cell Biology
- Cell Engineering
- Image Analysis
- Bioinformatics
- Molecular Bioengineering

Formal and informal meeting opportunities offer delegates the chance to discuss key solutions with leading service providers. Formal 1:1 meeting opportunities will be available to arrange prior to the event which take place during the dedicated networking breaks covering:

- Single Cell Profiling
- Single Cell Assays
- Single Cell RNA Seq
- Single Cell Imaging
- Single Cell Bioinformatics
- Single Cell Data Analysis

Day One

Track 4: Single Cell in Translational Drug Development & Clinics

- Novel applications of single cell technologies
- Understanding disease mechanisms at single cell resolution
- Identifying off-target effects
- Uncovering cellular heterogeneity
- Single cell analysis in clinical trials
- Case studies

Day Two

Track 3: Single Cell Analysis: Advanced Tools & Technologies

- Novel technologies for single cell imaging
- Computational tools for single cell analysis
- Updates from single cell multi-omics
- Single cell proteomics & metabolomics
- Implementation of AI

> “Great content, good exhibitor space, nice pre-arranged meetings, and good follow up from Oxford Global”
>
> - EXECUTIVE DIRECTOR, NEOGENOMICS LABORATORIES

NEO GENOMICS

NEXTGEN OMICS SPATIAL & DATA US 2026

AGENDA AT A GLANCE

NGS & Clinical Diagnostics

Hear from and meet with the key innovators in multi-omics. 2025 attendees included: Senior Research Analyst for Medical Policy; Vice President, Head of Clinical BioAnalytics; Senior Vice President, Innovation; and Senior Director of NGS

Discuss the advancements in clinical genomics. Presentations will include applying genome sequencing to disease prevention, reproducibility & validation of variants, real world clinical applications and metagenomics analysis developments

VPs, Directors & Senior Managers from leading pharma & biotech companies and research institutions in the following fields and more:

- NGS
- Multiplex Technologies
- Computational Biology
- Clinical Diagnostics
- Clinical Development
- Big Data
- Newborn Screening
- Precision Medicine
- Multiplex Tools
- Data Analysis

Formal and informal meeting opportunities offer delegates the chance to discuss key solutions with leading service providers. Formal 1:1 meeting opportunities will be available to arrange prior to the event which take place during the dedicated networking breaks covering:

- Library Preparation
- Bioinformatic Tools
- Next Gen Sequencing
- Computational Analysis
- Data Interpretation
- Clinical Development
- Multiplex Tools
- Data Analysis

Day One

Track 5: Advanced Sequencing & Clinical Genomics

Part 1 - Advanced Sequencing & Screening Technologies
- Clinical implementation of genomic medicine
- Delivering personalised cancer care
- Holistic approaches to diagnoses
- Whole genome sequencing
- Computational methods for human genetic diversity

Part 2 - Clinical Genomics
- Clinical trials and real-world applications
- Novel sequencing methods to empower precision medicine
- Long-read RNA sequencing methods
- Improving accessibility and lowering costs of genome sequencing
- New sequencing instruments
- Sequencing beyond DNA, including protein sequencing
- Overcoming bottlenecks between library prep & multiplexed sequencing
- Improving sensitivity of sequencing technologies
- High content microscopy screening

Day Two

Track 4: Precision Multi-Omics & NGS Diagnostic Innovations

Part 1 - NGS Innovations for Diagnostics Development
- Novel NGS analysis techniques in the clinic
- Using transcriptomics for diagnosis of patients in the clinic (RNAseq)
- Diagnostics of rare diseases
- Whole genome sequencing using long & short read sequencing
- Long and short read sequencing in the clinic

Part 2 - Multi-Omics in Precision Medicine
- The role of multi-omics in precision therapeutics
- Advancing precision medicined beyond oncology
- AI & omics analysis
- NGS applications in precision medicine

ALL PROGRAMS

Confirmed Speakers

HIGHLIGHT SPEAKERS

GIORGIO GAGLIA, Head of Systems Biology, Sanofi

ZORA MODRUSAN, Senior Director NGS, Genentech

ENRICO MOSSOTTO, Senior Director, Genome Informatics & AI, MeiraGTx

JING HE, Associate Director, Head of Cohort Disease Understanding, NovoNordisk

ELAINE JOSEPH, Director, Precision Medicine, AstraZeneca

ALEX TAMBURINO, Director, Spatial & Single Cell Multiomics, Merck

SOPHIA GEORGE, Professor, University of Miami

AARNO PALOTIE,
Research Director, Institiute for Molecular Medicine Finland

ADITI SINGH,
Director of Bioinformatics, Wayne State University

AHMET COSKUN,
Professor of Biomedical Engineering, Georgia Institute of Technology

ALEX TAMBURINO,
Director, Spatial & Single Cell Multiomics, Merck

ALI EBRAHIMI,
Associate Director, Takeda

ALINA AINBINDER,
Scientific Associate Director, Takeda

AMANDA DY,
PhD Candidate, Toronto Metropolitan University, PIcc

AMIT MITRA,
Associate Professor, Auburn University

ANITA BANSAL,
Associate Director, Lead Translational Bioinformatics, UCB

ARIDAMAN PANDIT,
Head of Immune Profiling, AbbVie

ARUTHA KULASINGHE,
Associate Professor, Lead of Clinical-oMx Lab University of Queensland

ASHOT HARUTYUNYA,
Academic Associate, McGill University

BANISHREE SAHA,
Associate Director, Global Biomarker and Assay Analytical Lead Takeda

BHARAT THYAGARAJAN,
Associate Professor, University of Minnesota

BRYAN DOWNIE,
Co-Founder, Node Biosciences

CHANDRA SARAVANAN,
Director, Pathology, Novartis

COLLES PRICE,
Co-Founder & Chief Executive Officer, TALOX

DANIEL JONES,
Staff Scientist, Vaccine & Infectious Disease Division, Fred Hutch Cancer Centre

DAVID GALLEGOS,
Senior Scientist, Takeda

DI HE,
Senior Scientist, Merck

ELAINE JOSEPH,
Director, Precision Medicine, AstraZeneca

EMRE ARSLAN,
Associate Director, Takeda

ENRICO MOSSOTTO,
Senior Director, Genome Informatics & AI, MeiraGTx

EUGENIA LYASHENKO,
Senior Principal Scientist, Lab Head, Sanofi

FEI CHEN,
Principal Investigator & Assistant Professor, Broad Institute

FEI ZOU,
Professor, University of North Carolina

GÁBOR BALÁZSI,
Henry Laufer Professor, Stony Brook University

GIORIGIO GAGLIA,
Head of Systems Biology, Sanofi

GLORIA PRYHUBER,
Professor, Department of Pediatrics, Neonatology (SMD), University of Rochester Medical Center

GREGORY MENDEZ,
Principal Scientist, Sanofi

HAGAI MARMOR-KOLLET,
Investment Associate, aMoon Growth

HUA LI,
Director of Computational Biology, Stowers Institute for Medical Research

IOANNIS RAGOUSSIS,
Professor, McGill University

ALL PROGRAMS

Confirmed Speakers

IRENE GHOBRIAL,
Professor of Medicine, Senior Vice President of Experimental Therapy, Lavine Family Chair for Preventative Cancer Therapy, Dana-Farber Cancer Institute

IULIAN PRUTEANU-MALINICI,
Senior Director of Bioinformatics for Pioneering Medicines, Flagship Pioneering

IVAN LEBEDEV,
President, Verdent Center for Spatial Biology

JACKSON BROUGHER,
Assistant Professor, Space Health Research Scientist, Translational Research Institute for Space Health, Baylor College of Medicine

JAN SCHEJBAL,
Senior Scientist I, AbbVie

JEFF JUNE,
Chief Executive Officer, Ischemia Care

JIA-REN LIN,
Technical Director of Tissue Imaging, Harvard Medical School

JING HE,
Associate Director, NovoNordisk

JIWOON PARK,
Founder of the Spatial Atlas of Human Anatomy, Weill Cornell Medicine

JOANN ARCE,
Assistant Professor, Boston Children's Hospital, Harvard Medical School

JOCHEN LENNERZ,
Chair, EFLM Task Group on Integrated Diagnostics

KISHA SIVANATHAN,
Senior Scientist, AstraZeneca

LEONARD LIPOVICH,
Professor, Biology and Biotechnology, Wenzhou-Kean University

MADHUMALA SADANANDAPPA,
Staff Fellow, Dartmouth Health

MAHMUD HOSSAIN,
Senior Scientist II, Sanofi

MANISHA BRAHMACHARY,
Associate Director, Sanofi

MANOJ KANDPAL,
Director of Research Bioinformatics, Rockefeller University

MARIA FORERO,
Senior Advisor, Accelmed

MENGWEI (CAROL) HU,
Senior Scientist, Functional Genomics, Merck

NICOLAS FERNANDEZ,
Senior Computational Scientist, Broad Insitute

NIR BEN CHETRIT,
Assistant Professor, Weill Cornell Medicine

PEI-HSUAN CHEN,
Principal Scientist, Bristol Myers Squibb

QINGQING WANG,
Associate Director, Regeneron

SAHIL SETH,
Principal Scientist, Bristol Myers Squibb

SARA HAMON,
Senior Director, Head of Precision Medicine -Quantitative Translational Sciences, Regeneron

SAUM GHODOUSSIPOUR,
Associate Professor, Rutgers University

SHANYE YIN,
Assistant Professor, Albert Einstein College of Medicine

SHOH ASANO,
Senior Principal Scientist, Pfizer

SHOU-JIANG GAO,
Professor, University of Pittsburgh School of Medicine

SIMONA CRISTEA,
Head of Genomics & AI, Dana-Farber Cancer Institute

SOPHIA GEORGE,
Professor, University of Miami

SOUMYA NEGI,
Senior Advisor, Eli Lilly

SOURAV CHOUDHURY,
Group Head, Distinguished Scientist, Sanofi

STEPHEN BAYLIN,
Head of the Cancer Genetics & Epigenetics Program, Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University School of Medicine

SUHAS VASAIKAR,
Associate Director, Pfizer

SUNHWA KIM,
Associate Scientific Director, Precision Medicine Immunology, AbbVie

TESFAYE MERSHA,
Professor, Indiana University School of Medicine

TIM HARRIS
Venture Parnter, SV Health Investors

UTTIYA BASU,
Professor, University of Columbia, New York

VITALAY FOMIN,
Chief Executive Officer, Numenos

VIRGINIA SAVOVA,
Senior Director, AstraZeneca

YEA JIN KAESER-WOO,
Senior Director, Next Generation Therapeutics, Eli Lilly

YUFEI HUANG,
Professor, University of Pittsburgh

ZONGMEI GAO,
Senior Scientist II, AbbVie

ZORA MODRUSAN,
Senior Director of Genomics, Genentech

PLACES LIMITED - REGISTER YOUR INTEREST

Registration Required Sessions

A space for senior decision-makers to move beyond public narratives: discuss what is actually working, what isn't, and why.

Select these sessions during your event registration to register your interest.

COLLABORATION HUB SESSIONS - GRAND BALLROOM PREFUNCTION

Interdisciplinary learning and knowledge sharing is key to driving Multi-Omics. Our Collaboration Hub sessions will provide a platform to enable experts and innovators from diverse complementary fields to foster collaboration, hear fresh perspectives, encourage innovation, break down silos, and address specific challenges in the field.

Each focused session will last 50 minutes and with only 15 spaces available per hub, registration is essential!

DAY ONE

1:55 - 2:45

Collaboration Hub 1:
Streamlining Multi-Omics Research

Discussion Points:
Managing sample prep requirements from cell separation to tissue, Challenges of integrating single cell and spatial technologies, Data analysis integration and interpretation, Potential rewards of integrated workflows

Invited Specialists:
Academic researchers, translational scientists, spatial biology experts, single-cell researchers, data scientists

Moderator: ETHAN ROHRBACH, Spatial Biology Specialist, **Miltyeni Biotec**

4:55 - 5:45

Collaboration Hub 2:
Harmonizing Protein & Nucleic Acid Biomarkers: Multi-Omics Workflows For Translational & Clinical Research & Diagnostic Settings

Discussion Points:
How harmonized protein and nucleic acid measurement from the same sample can accelerate biomarker discovery & validation, improve data integrity, and reduce operational friction in research and clinical settings

Invited Specialists:
Translational and Clinical Researchers, Biomarker Scientists, Genomics & Proteomics Technology Specialists, Bioinformaticians and Data Scientists, Clinical Diagnostics Lab Leaders

Moderator: JAY GERLACH, Vice President of Marketing, **Codetta Bio**

DAY TWO

11:25 - 12:15

Collaboration Hub 3:
Single Cell Multi-Omics In Clinical Studies

Discussion Points:
How single-cell multi-omics technologies can be effectively integrated into clinical workflows and the key challenges with turning data into actionable clinical understandings

Invited Specialists:
Academic researchers, clinicians, healthcare administrators, technology or knowledge transfer, translational medicine experts

Moderator: ALEX TAMBURINO, Director, Spatial & Single Cell Multiomics, **Merck**

12:15 - 1:05

Collaboration Hub 4:
AI Safety In Genomics Healthcare Systems

Discussion Points:
Making AI driven tools interpretable in healthcare settings & safely using patient data with AI

Invited Specialists:
AI specialists, data scientists, clinicians, academic researchers, technology developers

Moderator: SUHAS VASAIKAR, Associate Director, **Pfizer**

2:25 - 3:15

Collaboration Hub 5:
Building What Works: Pharma, Start-Ups & Academia Partnering in Omics & Precision Medicines

Discussion Points:
How to design and run partnerships between pharma, start-ups and academia that deliver real value in omics and precision medicine, including aligning objectives and timelines, structuring projects and data sharing, managing IP and publications, and moving successful collaborations from pilot stage into long-term strategic relationshipsl

Invited Specialists:
Pharma R&D and translational leaders, external innovation and business development, start-up and biotech founders, academic PIs and clinical investigators, tech transfer, investors, incubator/accelerator leads, health system and hospital research leaders

Moderator: JEFF JUNE, Chief Execuitve Officer, **Ischemia Care**

CLOSED-DOOR PANEL DISCUSSION

DAY TWO - CONFERENCE ROOM 1

12:15 - 1:05

Panel Discussion:
The Omics Investment Landscape - Funding Priorities & Partnership Models

- Building investable omics companies
- Investor appetite - what is fundableand why?
- What investors are looking for? What are the non-negotiables?
- Building partnerships that work
- The role of AI as an enabler
- Success stories & lessons learnt

Moderator: TIM HARRIS, Venture Partner, **SV Health Investors**

Panellists:

IULIAN PRUTEANU-MALINICI, Director of Bioinformatics for Pioneering Medicines, **Flagship Pioneering**

JEFF JUNE, Founder & Board Member, **Ischemia Care**

MARIA FORERO, Senior Advisor, **Accelmed**

HAGAI MARMOR-KOLLET, Investment Associate, **aMoon Growth**

IRENE GHOBRIAL, Professor of Medicine, Senior Vice President of Experimental Therapy, Lavine Family Chair for Preventative Cancer Therapy, **Dana-Farber Cancer Institute**

Other Special Features

ROUNDTABLE DISCUSSIONS

DAY TWO | CONFERENCE ROOM 5

09:15

ROUNDTABLE 1:
Single Cell & Spatial Data As A Validation Tool

Moderator: SAHIL SETH, Principal Scientist, **Bristol Myers Squibb**

ROUNDTABLE 2:
Developing Hybrid Methods In Proteomics

Moderator: MAHMUD HOSSAIN, Senior Scientist II, **Sanofi**

ROUNDTABLE 3:
The Potential Of DRUG-Seq

Moderator: DI HE, Senior Scientist, **Merck**

ROUNDTABLE 4:
Data Analysis Solutions In rAAV Gene Therapy

Moderator: GREGORY MENDEZ, Principal Scientist, **Sanofi**

ROUNDTABLE 5:
AI-Enabled Multi-Omics Integration: From Data Harmonization To Actionable Biological Insight

Moderator: IULIAN PRUTEANU-MALINICI, Director of Bioinformatics for Pioneering Medicines, **Flagship Pioneering**

SPECIAL PRE-EVENT FEATURE

Laboratory Tours

Wednesday, April 1st | Massachusetts General Hospital

Lab Tour of MGH CCIB DNA Core at Massachusetts General Hospital

Join us at 5:30pm on Wednesday, April 1st for an exclusive, behind the scenes tour of the MGH CCIB DNA Core Facility at Massachusetts General Hospital.

Explore the lab space, see the technologies, and hear about the facility's history as well as their impact on translational research

Wednesday, April 1st | Sanofi

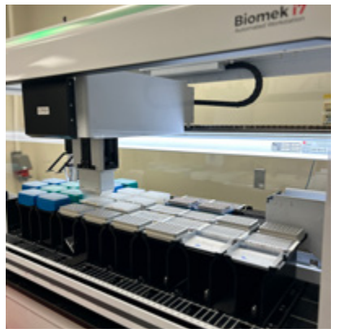
Lab Tour of Exploratory Biomarkers Department Lab at Sanofi

Join us at 5:30pm on Wednesday, April 1st for an exclusive, behind the scenes tour of the Exploratory Biomarkers Department lab at Sanofi.

Explore the lab area, hear about the lab's activities, instrumentations and workflows and participate in a technical & user experience Q&A session.

Spaces are limited to 10 per tour, so secure your place today when you register!

MASSACHUSETTS GENERAL HOSPITAL



Day One | 31 March 2026

8:50 **Conference Room 1 - Oxford Global's Welcome Address**

9:00 ***Conference Room 1- Opening Keynote Address:*** **Decoupling Immunotherapy Responses, One-Cell, One-Niche & One-Functional Unit At A Time**

- Ultra high-plex proteomic profiling of the tumour microenvironment - from 50 to 1200 proteins in tissue
- Single cell and sub-cellular transcriptomic profiling of the tumour microenvironment
- Applications of spatial-omics in clinical cohort studies

ARUTHA KULASINGHE, Associate Professor, **University of Queensland**

NEXT GEN OMICS, DATA, & ANALYSIS	SPATIAL MULTI-OMICS		SINGLE CELL ANALYSIS	NGS & CLINICAL DIAGNOSTICS
CONFERENCE ROOM 1: MULTI-OMICS APPROACHES FOR DATA INTEGRATION, HARMONISATION, & ANALYTICS	CONFERENCE ROOM 2: EMERGING MULTI-OMICS PLATFORMS AND APPLICATIONS: GENOMICS & TRANSCRIPTOMICS	CONFERENCE ROOM 3: SPATIAL BIOLOGY FOR THERAPEUTIC DISCOVERY & DEVELOPMENT (ONCOLOGY & IMMUNOLOGY)	CONFERENCE ROOM 4: SINGLE CELL IN TRANSLATIONAL DRUG DEVELOPMENT & CLINICS	CONFERENCE ROOM 5: ADVANCED SEQUENCING & CLINICAL GENOMICS
Chair: AM- SOPHIA GEORGE, Professor, University of Miami *PM - JING HE, Associate Director, NovoNordisk*	*Chair: IOANNIS RAGOUSSIS, Professor, McGill University*	*Chair: SUNHWA KIM, Associate Scientific Director, Precision Medicine Immunology, AbbVie*	*Chair: NIR BEN CHETRIT, Assistant Professor, Weill Cornell Medicine*	*Chair: DI HE, Senior Scientist, Merck*

Q&A session & transition time between conference rooms

9:30

Using AI To Build Better Gene Therapies

- The problem: Gene therapies hold great promise for treating serious diseases, but they are often very expensive and can cause side effects at high doses, making them difficult for patients to access
- The approach: Using artificial intelligence, we developed a new method to design improved gene therapy delivery vehicles that are both more effective at reaching target tissues and easier to manufacture—something traditional methods have struggled to achieve simultaneously
- The result: The AI-driven approach identified a new delivery vehicle that is 10x better at reaching the target tissue (the back of the eye) and 10x easier to produce, potentially paving the way for more affordable and effective gene therapies for patients

SOURAV CHOUDHURY, Group Head, Distinguished Scientist, **Sanofi**

Spatial Transcriptomics In Diagnosis & Prognosis

- Spatial transcriptomics is evolving from exploratory research into a tool for clinical-trial decisions, stratification, PD/MoA readouts, and response/resistance, when paired with fit-for-purpose design and operational rigor
- Integrating it with digital pathology links morphology to molecular programs, enabling scalable QC, consistent annotations, and interpretable biomarkers across sites and cohorts
- Agentic AI workflows streamline the pipeline by auto-discovering relevant public datasets, generating structured study/donor/sample metadata sheets, and boosting speed, reproducibility, and auditability

EMRE ARSLAN, Associate Director, **Takeda**

From Images to Insight: Spatially Resolved Tissue Biology For Prediction, Mechanism, and Diagnosis

- We will present a unified spatial pathology framework that integrates molecular imaging and histology to link tissue architecture with clinical outcome, disease mechanism, and diagnosis. Applications in colorectal cancer, triple-negative breast cancer, and kidney disease highlight predictive, interpretable, and clinically deployable tissue biomarkers

JIA-REN LIN, Technical Director of Tissue Imaging, **Harvard Medical School**

Unravelling The Complexity Of Single Cell Omics In Translational Drug Development: Insights From A Comprehensive Multi-Omics Analysis Platform

- Presenting PALMO (Platform for Analyzing Longitudinal Multi-Omics), a comprehensive and modular framework designed to address these challenges
- By enabling high-resolution, time-aware insights into molecular dynamics, this platform provides a powerful tool for biomarker discovery, patient stratification, and therapeutic response monitoring in clinical and translational research, paving the way for improved therapeutic strategies and personalized medicine

SUHAS VASAIKAR, Associate Director, **Pfizer**

Direct RNA Sequencing: Advancing Frontiers In Transcriptomics & RNA Modifications

- Direct RNA sequencing (DRS) provides high accuracy of transcript quantification and full-length isoform detection, surpassing cDNA-based long-read sequencing
- DRS uniquely enables identification of RNA modifications, such as m6A, offering new insights into epitranscriptomic regulation
- DRS has been applied to Alzheimer's Disease models to uncover transcriptomic and epitranscriptomic changes, providing novel insights into disease

ZORA MODRUSAN, Senior Director of Genomics **Genentech**

Q&A session & transition time between conference rooms

Day One | 31 March 2026

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9:55	**Eliminating Silos In Multi-Omics: Integrated Protein & Nucleic Acid Analysis In One Harmonized Workflow On Codetta Bio's Concerto System** • Discover how the Concerto system from Codetta Bio is redefining multi-omics by enabling simultaneous, high-sensitivity quantification of proteins and nucleic acids in a single, harmonized workflow • Built on microbead-based target capture and a powerful combination of digital PCR, real-time PCR, and immunoPCR, Concerto leverages proprietary noise-canceling chemistry, advanced optics, and precision thermal control to generate up to six million parallel reactions per run—delivering sub-pg/mL [WH1.1] sensitivity and up to eight logs of dynamic range without serial dilutions • Designed for ease of use, the platform integrates encoded bead sets and automated chip loading to streamline multiplex biomarker detection from liquid biopsies • By consolidating workflows traditionally spread across multiple instruments, Concerto reduces complexity, lowers operational costs, and unlocks deeper, more actionable multi-omic insights for precision medicine research and diagnostics WILLIAM HENLEY, Co-Founder and Vice President of Research & Innovation, **Codetta Bio**	**Conference Room 2: Leveraging High-Plex Spatial Proteomics To Investigate Diseases & Underlying Mechanisms** • High-plex spatial proteomics, in tandem with complementary single-cell and transcriptomic technologies, reveal critical insights in tissue mapping, characterization of the tumor microenvironment, and establishing clinical relevance in CAR T research and development • The MACSima® System enables a flexible and gentle approach to developing spatial panels with antibodies and RNA probes for a wide breadth of applications while incorporating a computational workflow that empowers researchers • Next-level dimensionality employs a 3D light sheet-directed spatial biology workflow to dive deep into the sections that matter SAMUEL HARRISON, Technology and Application Science, **Miltenyi Biotec**		*Attendees are welcome to attend co-located sessions*	*Attendees are welcome to attend co-located sessions*
10:20 - 11:40	MORNING BREAK & REFRESHMENTS				
	1-2-1 Meetings x4			Poster Displays	

Day One | 31 March 2026

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11:40	*Attendees are welcome to attend co-located sessions*	**Leveraging Spatial Transcriptomics Across Analytical Platforms: Assessing The Translatability Of Murine Colitis Models To Human Inflammatory Bowel Disease** TERRY MELIM, Senior Scientist II, Abbvie SHARVARI GUJJA, Data Scientist, Abbvie **10x Genomics**	**From Single-Slide Transcriptomics To IMC: A Multimodal Spatial Workflow For Drug Discovery** • End-to-end Imaging Mass Cytometry™ (IMC™) workflow and highlight how IMC enables high-parameter, spatially resolved profiling of immune architecture in autoimmune disease • Emerging post-transcriptomics IMC workflows to strengthen multimodal biological interpretation, and show how single-cell spatial insights can accelerate advanced translational immunology research and support therapeutic discovery and development ABEER OBAID, Senior Scientist I, AbbVie, **Standard Biotools**	**Perturb-seq At Scale: 100 Million Cells Driving AI-Powered Drug Discovery** • We generated a genome-wide perturb-seq dataset of 100M+ single cells using CRISPRi, CRISPRa, and siRNA perturbations across diverse human cell types (iPSCs and cancer lines), profiled with the Illumina emulsion based single-cell platform (PIP-seq) DULGUUN AMGALAN, Staff Scientist, **Illumina AI Lab**	*Attendees are welcome to attend co-located sessions*
			Q&A session & transition time between conference rooms		
12:05	**Deep Interrogation Of The Tumor Microenvironment For Therapeutic Development Using Single Cell Multi-Modality Profiling** • Profiling the composition and states of immune and tumor cells patients at baseline and upon treatment • Evaluate the effects of therapeutic molecules on immune cell state evolution • Identify new treatment combinations QINGQING WANG, Associate Director, **Regeneron**	**SPACE: Multimodal Spatial CRISPR Screening With Whole-Transcriptome Readout At Subcellular Resolution In 3D Models** • WTX RNA+68-plex protein+CRISPR detection in FFPE 3D spheroids • Unbiased discovery on different aspects of CAF-tumor interplay: • ECM composition, ligand-receptor interaction, spatially variable genes • Cost-effective approach allows profiling hundreds of spheroids (tens of thousands of cells) in one single run MENGWEI (CAROL) HU, Senior Scientist, Functional Genomics, **Merck**	**Spatially Resolved Immunology: Insights From Tissue Atlases** • Spatial transcriptomics to map cellular organization and tissue architecture • Identification of stromal–immune niches that shape tissue homeostasis and disease pathology • Translational implications for immune regulation, target discovery, and biomarker development KISHA SIVANATHAN, Senior Scientist, **AstraZeneca**	**Omics-Guided Prediction Meets Experimental Therapeutics In Preclinical Cancer Drug Development** • Leveraging multi-omics to deconvolute tumor heterogeneity • Rethinking drug discovery with AI-driven single-cell analytics • Prioritizing actionable gene targets/molecular pathways to guide precision medicine AMIT MITRA, Associate Professor, **Auburn University**	**Leveraging NGS To Optimize Gene Therapy Vectors** • Designing large synthetic barcoded libraries to screen cis-regulatory elements (MPRA) • Use of NGS screens to assess CRE activity and infer regulatory grammar in the Gene Therapy context • CLARA - a Deep Learning model - can predict and generalize regulatory elements activity ENRICO MOSSOTTO, Senior Director, Genome Informatics & AI, **MeiraGTx**
			Q&A session & transition time between conference rooms		

Day One | 31 March 2026

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12:30	**Accelerating Bioinformatics & Cheminformatics With AI Powered Serverless HPC** • Computational teams running Nextflow RNA seq pipelines, molecular dynamics simulations with GROMACS and OpenMM, and AI models such as AlphaFold and Boltz face growing challenges around scale, cost control, and operational complexity on the cloud • This session shows how an AI powered, serverless HPC approach on AWS enables organizations to achieve over 100× faster time to insight and 80–85% lower cloud costs while eliminating cluster management and manual execution strategy selection • We will cover how large scale genomics, multi omics, structural biology, and protein modeling workloads can be optimized for sustained performance, predictable costs, and faster experimentation DANIEL CARNEY, Sales Director, **Fovus**	*Attendees are welcome to attend co-located sessions*	**3D Spatially Resolved Multi-Omics In Thick Tissue: Mapping Molecular Organization Across Sub-Cellular & Multicellular Scales** • We present a 3D spatial multi-omics platform combining STARmap and RIBOmap assays with the Pyxa instrument to map gene expression and protein localization across sub-cellular and multicellular scales in intact thick tissue CHANYOUNG PARK, Research Scientist, **Stellaromics**	*Attendees are welcome to attend co-located sessions*	**Accelerating Methods Development With The icon96 System & AutoNorm** • Efficient methods development requires rapid exploration of reaction conditions. Uniform amplification protocols have proved to be a long standing bottleneck, constraining our ability to evaluate individually optimal amplification conditions across samples • This presentation will share examples of how the icon96 system, with its per-well thermal control and AutoNorm adaptive normalization, enables rapid, high-throughput methods development without the constraints of fixed-cycle PCR AZIZ AL'KHAFAJI, Director, Molecular R&D PI, Methods Development Lab, Genomics Platform, Broad Clinical Labs, Broad Institute of MIT and Harvard, **N6**

Day One | 31 March 2026

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12:55 - 1:55

LUNCH BREAK & REFRESHMENTS

1-2-1 Meetings x3

Poster Displays

1:55

INTERACTIVE

***PANEL DISCUSSION:* Overcoming Multi-Omics Data Harmonisation & Analysis Challenges**

- Defining and quantifying "harmonisation" in multi-omics data
- Value of integrated multi-omics datasets
- Moving and streamlining complicated omics data whilst ensuring real-world utility

Moderator:

DAVID GALLEGOS, Senior Scientist, **Takeda**

Panellists:

MANISHA BRAHMACHARY, Associate Director, **Sanofi**

ADITI SINGH, Director of Bioinformatics, **Wayne State University**

VITALAY FOMIN, Chief Executive Officer, **Numenos**

IULIAN PRUTEANU-MALINICI, Senior Director of Bioinformatics for Pioneering Medicines, **Flagship Pioneering**

HANSUELI MEYER, Senior Director, Site Leader & Head of Systems Integration Spatial Technologies, **Miltenyi Biotec**

Analysis Of Immune Responses With Integrated Public Transcriptomics Data

- Data normalization and data quality check
- Analysis results
- Lessons learned from data acquisition and suggestions on depositing high quality/ usable data into public databases

FEI ZOU, Professor, **University of North Carolina**

Q&A session & transition time between conference rooms

AI-Guided Single-Cell Spatial Analysis For Tumor Stratification

- G4X Spatial Platform enables high-resolution mapping of cellular architecture and immune niches within intact tumor tissues
- AI-driven modeling integrates spatial features to predict tumor classification, immunotherapy response, and clinical outcomes
- Scalable, interpretable frameworks bridge spatial biology with translational precision oncology

SHANYE YIN, Assistant Professor, **Albert Einstein College of Medicine**

INTERACTIVE

***CROSS PROGRAM PANEL DISCUSSION:* Omics Research & Investment Under Fiscal Constraint**

- Strategies for prioritising, sustaining, or reconfiguring research in resource limited settings
- Initiatives to fund young researchers
- Cultivating start-ups

Moderator:

GÁBOR BALÁZSI, Henry Laufer Professor, **Stony Brook University**

Panellists:

JOCHEN LENNERZ, Chair, **EFLM Task Group on Integrated Diagnostics**

MADHUMALA SADANANDAPPA, Staff Fellow, **Dartmouth Health**

INTERACTIVE

***PANEL DISCUSSION*: Turning Single Cell Insights Into Novel Targets**

- How to best use multi-omics data to gain new insights
- Rethinking drug discovery for cellular complexity
- How to prioritize which cell populations, pathways, or transitions matter biologically and clinically

Moderator:

SOPHIA GEORGE, Professor, **University of Miami**

Panellists:

QINGQING WANG, Associate Director, **Regeneron**

AMIT MITRA, Associate Professor, **Auburn University**

GIORIGIO GAGLIA, Head of Systems Biology, **Sanofi**

DEEPAK VEEREGOWDA, Chief Executive Officer, **QT Sense**

INTERACTIVE

***PANEL DISCUSSION:* How To Choose Your Sequencing & Screening Technologies**

- How to evaluate trade-offs between coverage, read length, throughput, cost, and sensitivity, dependent on goals
- When is it worth investing in deeper, more precise approaches versus high-throughput, population-level methods?
- How to combine multiple platforms

Moderator:

SIMONA CRISTEA, Head of Genomics & AI, **Dana-Farber Cancer Institute**

Panellists:

ZORA MODRUSAN, Senior Director of Genomics, **Genentech**

IOANNIS RAGOUSSIS, Professor, **McGill Genome Centre**

Q&A session & transition time between conference rooms

FinnGen: Leveraging Population-Scale Genomics & Health Registers For Clinical Discovery

- FinnGen is a large-scale public–private partnership combining genomic data with longitudinal health registry data from over 500,000 participants in Finland
- The Nordic health register system enables lifelong follow-up of healthcare events since the 1960s, providing unique opportunities to study disease onset, progression, and outcomes
- The genetic characteristics of the Finnish population, together with close collaboration between academia, biobanks, hospitals, and 15 international pharmaceutical companies, enable novel insights into disease mechanisms and translational research

AARNO PALOTIE, Research Director, **Institute for Molecular Medicine Finland**

2:20

Q&A session & transition time between conference rooms

Day One | 31 March 2026

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From Spatial Transcriptomics To Multimodal Discovery: Scaling AI-Driven Genomics On Manifold • The explosion of spatial transcriptomics, single-cell, and multi-omic datasets is outpacing researchers' ability to access, integrate, and reason across them • In this session, the Broad Institute and Manifold demonstrate what becomes possible when those bottlenecks are removed — from interactive spatial data exploration to AI-powered cross-modal analysis at scale • Sami Farhi (Broad Institute Spatial Technology Platform) will walk through the STP's spatial transcriptomics pipeline and Celldega, a cloud-native, open-source visualization tool purpose-built for large spatial datasets • He'll show how Celldega running on Manifold enables external collaborators to explore and interact with spatial data directly — no infrastructure setup, no data transfers • The session then shifts to the broader challenge of working across modalities • Gervaise Henry (Manifold) will demonstrate how the platform brings together diverse single-cell, bulk, and reference datasets — including TCGA and CCLE — into a unified environment for cross-modal discovery • He'll show how Manifold's AI Agents let scientists move from raw data to governed, reproducible analysis through natural language, making multimodal exploration accessible to computational and bench researchers alike VINAY MOHTA, Chief Executive Officer & Co-Founder, **Manifold AI** GERVAISE HENRY, Vice President Solutions Engineering, **Manifold AI** SAMI FARHI, Director, Spatial Technology Platform, **Broad Institute**	**Spatial Pathology At Scale** • The field of spatial transcriptomics has been held back by 3 limiting factors: Cost per sample, Experiment throughput, and Multiomics Integration • Enter G4x. Over 10 times more samples per run. Dramatically lower prices per samples. RNA and Protein in the same run. AARON BERLIN, Chief Technology Officer **Singular Genomics**	**Spatial Imaging Of Protein Glycosylation In The Tumor Microenvironment** • Protein glycosylation controls diverse biological functions of multiple cell types within the tumor microenvironment • However, glycans have been notoriously challenging to study using conventional approaches • The first-in-kind Glysite™ Explorer™ in situ Proximity Ligation Assay (isPLA) Glycan Detection Kit overcomes this hurdle by providing an innovative platform for spatial visualization of protein glycosylation of several tissues and cell types. It uses an immunostaining workflow and image analysis pipeline compatible with standard microscopy to deliver same-day results • This next-generation technology is poised to broadly impact the life sciences by accelerating glycobiological knowledge and therapeutic discovery as well as biomarker-based disease detection and prognosis STEVEN BARTHEL, Assistant Professor of Dermatology, Harvard Medical School, Research Associate and Co-Director of the Program of Glyco-Immunology and Oncology at Mass General Brigham **Navinci**	**High-scale Multiomic Drug Profiling** • To systematically dissect the molecular determinants of drug sensitivity and resistance, we employed a high-throughput single-cell multi-omic profiling framework using a PRISM pool, a barcoded co-culture platform of ~400 human cancer cell lines spanning diverse lineages and genetic backgrounds • We treated the PRISM pool with two RAS inhibitors to capture early drug response dynamics. Leveraging SBX as our sequencing engine, we employed a modified 10x Genomics Flex protocol enabling simultaneous capture of the whole transcriptome, target proteome (~320-plex MultiPro Human Discovery Panel), and PRISM identity via expressed DNA barcodes • In this presentation, I will share run performance and how we are leveraging this multiomic information to distill putative mechanisms of drug tolerance AZIZ AL'KHAFAJI, Director, Molecular R&D PI, Methods Development Lab, Genomics Platform, Broad Clinical Labs, Broad Institute of MIT and Harvard **Protein Tech**	*Attendees are welcome to attend co-located sessions*

2:45

Q&A session & transition time between conference room

The Challenge Of The Modern Pathology Laboratory In The Industry Setting: Building Workflows That Balance Efficiency & Scalability Of Digital High-Plex Technologies • Over the past decade, breakthroughs in spatial molecular biology technologies as well as deep digitization and automation of laboratory processes have transformed traditional pathology laboratories • Robust multimodal platforms like COMET or Xenium enable the implementation of higher throughput assays with the generation of extensive molecular data sets from tissue sections in the biopharmaceutical research setting • Such implementation requires proficient infrastructures with quality control checkpoints along the various workflows, from bench to multimodal digital analytical platforms • Herein we will review our multimodal spatial-omic pipelines and provide a few examples of what worked and what did not work SILVIA SISO, Scientist- Pathologist & HEATHER KNIGHT, Senior Scientist, AbbVie **Lunaphore Technologies**	**One Tissue, Eight Omics: A Unified Platform For Spatial Drug, Lipid, Protein, & Transcript Mapping** • Map up to eight molecular and drug classes on a single platform • 3D quad-omic and tri-omic datasets from Alzheimer's tissue experiments • Highlight correlative multi-omic analysis that uncovers deeper biological insights JOHN GILLESPIE, President & Chief Executive Officer, AmberGen COLIN MCDOWELL, Senior Manager, Business Development, **Biodesix**	**Quantum Biomicroscopy Of Mitochondrial Redox Kinetics For Mechanism-Driven Cancer Drug Discovery** • This talk we introduce Quanutm biomicroscopy platform (Quantum Nuova), which uses fluorescent nanodiamond NV-center sensors and T1 relaxometry to quantify free-radical dynamics in live cells with organelle-level targeting • Instead of inferring mechanism from endpoints, the platform is built to capture (i) the first measurable subcellular trigger, (ii) the kinetic profile of the response, and (iii) causal dependency between initiating events and downstream phenotypes • Using mitochondria-proximal quantum sensing, we show how early redox shifts can be detected within the first hour of treatment—well before transcriptomic and multi-omics consequences dominate—creating an upstream "fail-fast" decision gate in lead optimization DEEPAK VEEREGOWDA, Chief Executive Officer, **QT Sense**	*Attendees are welcome to attend co-located sessions*

3:10

Day One | 31 March 2026

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3:35 - 4:55 **AFTERNOON BREAK & REFRESHMENTS**

1-2-1 Meetings x4 | Poster Displays

4:55

Targeting Primate-Specific Long Non-Coding RNA (lncRNA) Genes With RNA Drugs In Diabetes, Obesity, And Beyond: Insights From A Nonhuman-Primate Model

- 65% of the ~ 75,000 Gencode human genes do not encode proteins and have been largely ignored in drug development
- We computed the intersection of single-nucleotide polymorphims (SNPs) from Genome-Wide Association Studies (GWAS) with exons of long non-coding RNA genes
- We identified a lncRNA that controls fasting glucose levels and body weight, and targeted it in-vivo with an RNA drug that can replace insulin for diabetes and GLP1R agonists for obesity

LEONARD LIPOVICH, Professor, Biology and Biotechnology, **Wenzhou-Kean University**

Attendees are welcome to attend co-located sessions

INTERACTIVE

***PANEL DISCUSSION:* Advancing Spatial Multi-Omics For Discovery**

- Evaluating technologies across therapeutic areas
- Choosing the right spatial strategy for your biological question
- How spatially located targets influence R&D decisions; moving from maps of cellular neighbourhoods to actionable insights

Moderator:

NIR BEN CHETRIT, Assistant Professor, **Cornell University**

Panellists:

ALEX TAMBURINO, Director, Spatial & Single Cell Multiomics, **Merck**

BANISHREE SAHA, Associate Director, **Takeda**

AHMET COSKUN, Professor of Biomedical Engineering, **Georgia Institute of Technology**

COLLES PRICE, Co-Founder & Chief Executive Officer, **TALOX**

KISHA SIVANATHAN, Senior Scientist, **AstraZeneca**

Using Single Cell Genomics To Gynecologic Cancers Across Different Populations

SOPHIA GEORGE, Professor, **University of Miami**

INTERACTIVE

***PANEL DISCUSSION:* Genomics For Diagnosing Patients With Rare Diseases**

- Omics techniques to guide rare disease diagnosis
- Moving from diagnostics to clinical trials
- Where are the bottlenecks?

Moderator:

ANITA BANSAL, Associate Director, **UCB**

Panellists:

BHARAT THYAGARAJAN, Professor & Director of Division of Molecular Pathology & Genomics, **University of Minnesota**

JACKSON BROUGHER, Assistant Professor, Space Health Research Scientist, **Translational Research Institute For Space Health, Baylor College of Medicine**

Q&A session & transition time between conference rooms

5:20

INTERACTIVE

***PANEL DISCUSSION:* Overcoming Barriers To Integrate Omics Technology With Big Data**

- How to handle data at the terabyte & petabyte scale
- Making large-scale integration feasible and reliable
- Storage, processing power, cloud adoption, and reproducibility of analyses, as well as the role of AI and machine learning

Moderator:

LEONARD LIPOVICH, Professor,Biology and Biotechnology, **Wenzhou-Kean University**

Panellists:

ALI EBRAHIMI, Associate Director, **Takeda**

MANOJ KANDPAL, Director of Research Bioinformatics, **Rockefeller University**

BRYAN DOWNIE, Co-Founder, **Node Biosciences**

INTERACTIVE

***PANEL DISCUSSION:* Exploring Novel Uses For Spatial Transcriptomics**

- Decoding genotype-to-phenotype relationships
- Charting developmental pathways
- Combining spatial transcriptomics with other technologies (e.g., CRISPR)

Moderator:

CHANDRA SARAVANAN, Director, Pathology, **Novartis**

Panellists:

SHOU-JIANG GAO, Professor, **University of Pittsburgh**

MENGWEI (CAROL) HU, Senior Scientist, Functional Genomics, **Merck**

SOUMYA NEGI, Senior Advisor, **Eli Lilly**

JEFFERY BYLUND, Senior Science & Technology Advisor, **10x Genomics**

Accelerating Discovery In Spatial Biology With Agentic AI

- We introduce spatiAlytica, a graphic user interface powered by multi-agents designed for discovery from spatial datasets. It functions an interactive AI co-scientist for biologists and clinicians to identify, explain, and correlate gene- or cellular-level spatial features with ease by asking questions in natural language
- Multi-agent orchestration and memory advance beyond static explorers to enable extensible, literature-informed spatial discovery, compressing hypothesis validation cycles from weeks to hours

YUFEI HUANG, Professor, **University of Pittsburgh**

Contextualizing & Integrating Pre-Clinical Single Cell Data For Translation

- Cross-species cell type annotation for translational alignment: Using probabilistic latent variable models to integrate scRNA-seq data across species and experimental systems, enabling robust cell atlas alignment and targeted cell type resolution while preserving biologically meaningful translation features
- Linking in vitro perturbations to in vivo biology: Modeling shared perturbation response spaces across species and contexts to predict in vivo-like transcriptional states from in vitro systems, strengthening translational confidence for drug and genetic perturbations
- Batch-aware inference for intercellular and cross-species analysis: Applying covariate-based, batch-aware differential expression approaches to sparse scRNA-seq data and illustrating their impact on downstream analyses such as cell–cell communication and signaling conservation

DAVID GALLEGOS, Senior Scientist, **Takeda**

From Dark Matter To Diagnosis: Resolving Genomic Complexity With Long Read Sequencing

- The evolution of sequencing technologies and describe opportunities and challenges for implementing long read sequencing into clinical diagnostics
- Describe a comprehensive clinical workflow for variant identification using long read sequencing for inherited disorders
- Strategies to incorporate epigenetics to improve clinical diagnostics for inherited disorders

BHARAT THYAGARAJAN, Professor & Director of Division of Molecular Pathology & Genomics, **University of Minnesota**

Q&A session & transition time between conference rooms

Day One | 31 March 2026

NEXT GEN OMICS, DATA, & ANALYSIS	SPATIAL MULTI-OMICS		SINGLE CELL ANALYSIS	NGS & CLINICAL DIAGNOSTICS
CONFERENCE ROOM 1: MULTI-OMICS APPROACHES FOR DATA INTEGRATION, HARMONISATION, & ANALYTICS	CONFERENCE ROOM 2: EMERGING MULTI-OMICS PLATFORMS AND APPLICATIONS: GENOMICS & TRANSCRIPTOMICS	CONFERENCE ROOM 3: SPATIAL BIOLOGY FOR THERAPEUTIC DISCOVERY & DEVELOPMENT (ONCOLOGY & IMMUNOLOGY)	CONFERENCE ROOM 4: SINGLE CELL IN TRANSLATIONAL DRUG DEVELOPMENT & CLINICS	CONFERENCE ROOM 5: ADVANCED SEQUENCING & CLINICAL GENOMICS
Multi-Omics Datasets In Infectious Disease & Vaccine Research JOANN ARCE, Assistant Professor, **Boston Children's Hospital, Harvard Medical School**	**Spatial Single-Cell Atlas Reveals KSHV-Driven Broad Cellular Reprogramming, Progenitor Expansion, Immune & Vascular Remodeling In Kaposi's Sarcoma** • CD34+ progenitor lymphatic endothelial cells are the primary KSHV target cells, with their clonal expansion driving Kaposi's sarcoma growth • KSHV infection reprograms broad cell types into hybrid identities, and drives tumor-specific niche and vascular remodeling, endothelial plasticity, and immune modulation. • KSHV-reprogrammed macrophages drive inflammation, angiogenesis, and immune modulation. • Spatially resolved molecular and cellular signatures predict Kaposi's sarcoma progression, offering novel therapeutic strategies targeting the tumor microenvironment. SHOU-JIANG GAO, Professor, **University of Pittsburgh**	*Attendees are welcome to attend co-located sessions*	*Attendees are welcome to attend co-located sessions*	*Attendees are welcome to attend co-located sessions*

5:45

INTERACTIVE

Conference Room 1 - Cross Program Panel Discussion: **Revolutionizing Multi-Omics Research With Artificial Intelligence**

- How does AI bridge the gap between data and biological insight?
- Ensuring maintenance of interpretability & reproducibility when using AI models
- Challenges with data standardization and privacy
- What are the future possibilities of AI technology in R&D research?

Moderator:
MANISHA BRAHMACHARY, Associate Director, **Sanofi**

6:10

Panellists:
SOURAV CHOUDHURY, Group Head, Distinguished Scientist, **Sanofi**
SAHIL SETH, Principal Scientist, **Bristol Myers Squibb**
ENRICO MOSSOTTO, Senior Director, Genome Informatics & AI, **MeiraGTx**
SIMONA CRISTEA, Head of Genomics & AI, **Dana-Farber Cancer Institute**
IULIAN PRUTEANU-MALINICI, Senior Director of Bioinformatics for Pioneering Medicines, **Flagship Pioneering**

INTERACTIVE

Conference Room 2- Fireside Chat: **Genomics As A Tool For Risk Reduction In Human Spaceflight**

- The profound and rapid changes of spaceflight present a unique opportunity to understand human adaptation at the molecular level
- TRISH established the EXPAND program to collect and store physiological, functional, and environmental data and bio-samples from spaceflight missions
- The database's multifaceted nature will enable analyses between multi-omic, physiological, and functional measurements in humans and allow cross-disciplinary questions to be asked

JACKSON BROUGHER, Assistant Professor, Space Health Research Scientist
Translational Research Institute For Space Health, Baylor College of Medicine

6:45 **NETWORKING DRINKS & END OF DAY ONE**

Day Two | 01 April 2026

Conference Room 5: Complimentary Breakfast - Inclusive Leadership: From Intent To Impact

Come together over breakfast to discuss innovative and inclusive leadership strategies with your peers, following a short presentation of a KOL's personal leadership journey, including their approach, process and how they provide impact for their team and culture!

8:00 ***Opening Address:*** ARIDAMAN PANDIT, Head of Immune Profiling, **AbbVie**

- Leadership journey and pivotal experiences
- Approach to inclusion
- Decision-making processes and habits
- Internal / external collaborations, leadership & interdisciplinary approaches
- Practical habits, decisions, and strategies used to turn intent into measurable impact for teams and culture

8:45

Conference Room 1 - Keynote Address: **The Role Of Epigenomics In Cancer Progression**

- Genetic but also epigenetic abnormalities drive caner evolution and reflect identities of normal cells of cancer origins and their "states of cell programming" that influence tumor development
- Understanding these regulatory layers could prove critical for developing more precise and durable strategies for marking cancer risk and developing strategies for prevention, early interception and durable therapies
- I will stress that how the above science may be exploited for these goals

STEPHEN BRUCE BAYLIN, Head of the Cancer Genetics and Epigenetics Program,
Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University School of Medicine

Conference Room 2 - Keynote Address: **The Power Of The Pre-Competitive Space – Examples From The USA & Europe**

- Pre-competitive collaboration is where trust is built before competition begins — enabling shared standards, aligned evidence, and faster translation of innovation into clinical practice. This session shows how cross-sector communities in the U.S. and Europe are using this space to accelerate safe, scalable AI and integrated diagnostics
- The Pathology Innovation Collaborative Community (PIcc) is a multi-stakeholder forum uniting clinicians, regulators, industry, and policy leaders to advance shared foundations for innovation in pathology and diagnostics. PIcc will present its current project on validation terminology, addressing how consistent language for analytical, clinical, and real-world validation can enable clearer regulatory pathways and more trustworthy deployment of AI in medicine
- The European Federation of Clinical Chemistry and Laboratory Medicine (EFLM) represents laboratory medicine across Europe and leads strategic efforts to shape the future of the profession. EFLM will introduce the Integrative Diagnostics Workforce Task Force, outlining its scope and vision for a new generation of professionals equipped to work across disciplines, data streams, and technologies — ensuring that integrated diagnostics is not only technically possible, but institutionally sustainable
- Together, these perspectives illustrate how the pre-competitive space becomes a catalyst for alignment: turning fragmented innovation into shared progress across the Atlantic

JOCHEN LENNERZ, Chair, **EFLM Task Group on Integrated Diagnostics**
AMANDA DY, PhD Candidate, **Toronto Metropolitan University, PIcc**

Day Two | 01 April 2026

	SPATIAL MULTI-OMICS		SINGLE CELL ANALYSIS	NGS & CLINICAL DIAGNOSTICS
	CONFERENCE ROOM 1: EMERGING MULTI-OMICS PLATFORMS AND APPLICATIONS: PROTEOMICS, EPIGENOMICS & METABOLOMICS	CONFERENCE ROOM 2: SPATIAL BIOLOGY FOR THERAPEUTIC DISCOVERY & DEVELOPMENT	CONFERENCE ROOM 3:SINGLE CELL ANALYSIS: ADVANCED TOOLS & TECHNOLOGIES	CONFERENCE ROOM 4: MULTI-OMICS FOR PRECISION MEDICINE & NGS DIAGNOSTICS
	Chair: AM - ROBERTO DE LUCA, Instructor, Neurology, Harvard Medical School *PM - SOPHIA GEORGE, Professor, University of Miami*	*Chair: AM - ALINA AINBINDER, Scientific Associate Director, Takeda* *PM - VITALAY FOMIN, Chief Executive Officer, Numenos*	*Chair: AM - ZORA MODRUSAN, Senior Director NGS, Genentech* *PM - GÁBOR BALÁZSI, Professor, Stony Brook University*	*Chair: AM - SUHAS VASAIKAR, Associate Director, Translational Sciences, Bioinformatics, Pfizer* *PM -TESFAYE MERSHA, Professor, Indiana University School of Medicine*
	Q&A session & transition time between conference rooms			
9:15	**Integrating Data-Driven & Hypothesis-Driven Mass Spectrometry-Based Approaches For The Quantification Of Complement Compounds In Biofluids** • Utilizes hybrid-DIA mass spectrometry, an intelligent acquisition strategy that integrates: • Data-driven DIA (Data-Independent Acquisition) • Hypothesis-driven PRM (Parallel Reaction Monitoring) • Enables comprehensive proteome profiling and accurate quantification of complement compounds in biofluids • Significantly enhances assay throughput, improving efficiency. • Conserves valuable sample material, making the method resource efficient MAHMUD HOSSAIN, Senior Scientist II, **Sanofi**	**Integrative Analysis Of Single Cell & Spatial Transcriptomics Data In Esophageal Adenocarcinoma Identifies Highly Proliferative Cell Subpopulation & Interactions With Other Tumor & Stroma Cells** • We have utilized modern single cell and spatial transcriptomics technologies from 10X Genomics to characterize transcriptomic profiles of tumor and stromal cell populations in EA and their spatial relationships • We applied Xenium 5,000 human gene spatial transcriptomics on tumor and stroma samples derived from 30 patients, (matched single cell and spatial transcriptomics) • We identified multiple tumor cell subpopulations which displayed spatially distinct distribution. Notably, a minor tumor cell cluster was present in all samples with high expression of proliferation markers • This tumor subpopulation was tightly interacting with other tumor clusters and possibly contributing to tumor propagation • In-depth characterization of all tumor subpopulations will help pinpoint their respective contributions to tumor development and tumor-stroma interactions IOANNIS RAGOUSSIS, Professor, **McGill University** ASHOT HARUTYUNYAN, Academic Associate, **McGill University**	**Application Of Single Cell Analytics To Drug Discovery & Development** • Single cell analytics is enabling unprecedent dissection of disease • Meaningfully impacting drug discovery requires different approaches that academic researchers • Use cases of how single cell analytics can advance novel target identification, understand mechanism of action and delivery, and patient heterogeneity GIORGIO GAGLIA, Head of Systems Biology, **Sanofi**	**CDx Development For TCR-Ts** • Companion diagnostic (CDx) development for T cell receptor therapies (TCR-Ts) • Challenges and solutions to enable precise patient selection for TCR-Ts in advanced solid tumor indications ELAINE JOSEPH, Director, Precision Medicine, **AstraZeneca**
	Q&A session & transition time between conference rooms			
9:40	**Multidimensional Spatialomics Empowers Our Understanding Of Rheumatoid Arthritis Pathobiology** • This study examined the spatial organization of fibroblasts in rheumatoid arthritis (RA) using histology and spatial transcriptomics. We integrated data from Xenium and Visium, or from Xenium and LC/MS proteomics to examine fibroblast pathobiology in RA • In RA synovium, we found distinct laminar histological configuration of up to nine fibroblast subtypes compared to the random organization observed in healthy synovium. This suggests that fibroblast subtypes expand, transition, and support organized cellular niches with distinct pathophysiological roles in RA SILVIA SISO, Senior Principal Scientist - Pathologist, AbbVie **Aspect Analytics**	**Mapping Immunotherapy Resistance: Unlocking Spatial Biology Insights Across the Tumor Microenvironment** • Immunotherapy failure driven by antigen loss, suppressive signaling, and hostile tumor microenvironments can be elucidated through spatial biology, enabling high-resolution mapping of resistance mechanisms to support optimized response assessment Senior Representative, **Neo Genomics**	*Attendees are welcome to attend co-located sessions*	*Attendees are welcome to attend co-located sessions*
10:05 - 11:25	MORNING BREAK & REFRESHMENTS			
	1-2-1 Meetings x4		Poster Displays	

Day Two | 01 April 2026

	SPATIAL MULTI-OMICS		SINGLE CELL ANALYSIS	NGS & CLINICAL DIAGNOSTICS
	CONFERENCE ROOM 1: EMERGING MULTI-OMICS PLATFORMS AND APPLICATIONS: PROTEOMICS, EPIGENOMICS & METABOLOMICS	CONFERENCE ROOM 2: SPATIAL BIOLOGY FOR THERAPEUTIC DISCOVERY & DEVELOPMENT	CONFERENCE ROOM 3:SINGLE CELL ANALYSIS: ADVANCED TOOLS & TECHNOLOGIES	CONFERENCE ROOM 4: MULTI-OMICS FOR PRECISION MEDICINE & NGS DIAGNOSTICS
11:25	**From Discovery to Innovation: New Insights and Technologies Shaping Spatial Biology** • Spatial single-cell insights into early specification of cortical layers and regional boundaries in the developing human brain • Emerging workflow enhancements and spatial multi-omic applications enabling deeper analysis of tissue architecture, organoid models, and cellular interactions XUYU QIAN, Assistant Professor, Department of Pediatrics, Division of Neurology, **Children's Hospital of Philadelphia, Perelman School of Medicine, University of Pennsylvania** JIANG HE, Vice President, Reagents & Sci. Affairs, **Vizgen** vizgen	**Decoding Tissue Biology At Scale: Single-Cell Spatial Insights For Translational Discovery** • Stereo-seq enables scalable, single-cell spatial profiling to map tissue architecture and cell interactions, unlocking insights in disease biology to drive translational research and therapeutic discovery TIBBY DUAN, Senior STOmics Product Manager, **Complete Genomics** Complete GENOMICS	**True Single-Cell Multiomics: RNA & DNA Co-Sequencing At Scale With Semi-Permeable Capsules** • Beyond scRNA-seq: co-sequence RNA and targeted DNA in the same single-cell with Atrandi's Semi-Permeable Capsules (SPCs) • Confirm CRISPR edits, link genotype to transcriptional state, and characterize mutations at scale • Shown on >100k primary PBMCs RAPOLAS ŽILIONIS, Chief Scientific Officer, **Atrandi Biosciences** Atrandi BIOSCIENCES	*Attendees are welcome to attend co-located sessions*
			Q&A session & transition time between conference rooms	
11:50		**Orion™ Spatial Proteomics: Translating Spatial Biomarkers Into Clinical Value** • The Orion spatial proteomics platform reproducibly delivers the biomarker depth at a capacity demanded by clinical trials for precision therapies • Discover how this groundbreaking technology redefines how spatial biology is used for clinical trials TAD GEORGE, Senior Vice President R&D, **Rarecyte** RARECYTE	**Sample Prep Matters: How Cell & Nuclei Preparation Shape Your Single-Cell Data** • Your sample prep method can alter gene expression, distort cell type composition, and even generate artifacts mistaken for biology • We examine case studies illustrating how preparation choices shape downstream single-cell sequencing outcomes. CARINA EMERY, Product Manager **Miltenyi Biotec** Miltenyi Biotec	*Attendees are welcome to attend co-located sessions*

Day Two | 01 April 2026

	SPATIAL MULTI-OMICS		SINGLE CELL ANALYSIS	NGS & CLINICAL DIAGNOSTICS
	CONFERENCE ROOM 1: EMERGING MULTI-OMICS PLATFORMS AND APPLICATIONS: PROTEOMICS, EPIGENOMICS & METABOLOMICS	CONFERENCE ROOM 2: SPATIAL BIOLOGY FOR THERAPEUTIC DISCOVERY & DEVELOPMENT	CONFERENCE ROOM 3:SINGLE CELL ANALYSIS: ADVANCED TOOLS & TECHNOLOGIES	CONFERENCE ROOM 4: MULTI-OMICS FOR PRECISION MEDICINE & NGS DIAGNOSTICS

Q&A session & transition time between conference rooms

12:15

INTERACTIVE

***CLOSED DOOR PANEL DISCUSSION:* The Omics Investment Landscape - Funding Priorities & Partnership Models**

- What are the non-negotiables for building an investable company?
- Platform vs product: does clinical proximity outweigh broad platforms?
- Building partnership models that preserve value
- Where is AI providing acceleration?

Moderator:
TIM HARRIS, Venture Partner, **SV Health Investors**

Panellists:
IULIAN PRUTEANU-MALINICI, Senior Director of Bioinformatics for Pioneering Medicines**, Flagship Pioneering**

IRENE GHOBRIAL, Professor of Medicine, Senior Vice President of Experimental Therapy, Lavine Family Chair for Preventative Cancer Therapy**, Dana-Farber Cancer Institute**

JEFF JUNE, Chief Executive Officer, **Ischemia Care**

HAGAI MARMOR-KOLLET, Investment Associate, **aMoon Growth**

MARIA FORERO, Senior Advisor, **Accelmed**

***WORKSHOP:* GESTALT**

***PRESENTATION 1:* Emerging Spatial Multi-Omics Technologies & Analytical Frameworks**

- How these tools enable high-resolution mapping of tissues and cellular states
- Technological advances, current capabilities, and limitations that shape how spatial data can be generated and interpreted

FEI CHEN, Principal Investigator & Assistant Professor, **Broad Institute**

***PRESENTATION 2:* Spatial Atlas Generation & Large-Scale Spatial Data Analysis**

- How spatial omics datasets are built, integrated, and translated into biologically and clinically meaningful insights
- Applications across disease research and human biology

JIWOON PARK, Founder of the Spatial Atlas of Human Anatomy, **Weill Cornell Medicine**

INTERACTIVE

***PANEL DISCUSSION:* Translating High Resolution Single Cell & Spatial Data Into Biomarker Discovery & Clinical Impact**

- Translating high-resolution tissue data into clinical decision-making and biomarker discovery
- Future directions in therapeutic targeting

Moderator:
IVAN LEBEDEV, President, **Verdent Center for Spatial Biology**

Panellists:

SAUM GHODOUSSIPOUR, Associate Professor, **Rutgers University**

JENNIFER FRAHM, Director, Global Field Applications CTI, **Standard Biotools**

VIRGINIA SAVOVA, Senior Director, **AstraZeneca**

YOUNG SCIENTIST POSTER PRESENTATIONS X3

***PRESENTATION 1:* Spatial Analysis Of Tumor & Adjacent Uninvolved Lung Tissues In Non-Small Cell Lung Cancer**

ISABELLA POLIC, Graduate Student, **The University of Texas MD Anderson Cancer Center**

***PRESENTATION 2:* Radiation-Induced Glial Responses In Mice: Whole-Brain Mapping Via Multiplex Immunofluorescence & Dose Co-Registration**

- We developed a preclinical mouse model to investigate long-term radiation effects in the brain by combining proton irradiation, MRI, and spatially resolved multiplex histology to analyze chronic inflammation and blood–brain barrier disruption at the cellular level
- Microglia showed region-specific activation, with the highest radiosensitivity in periventricular areas and the lowest in the cortex, alongside sustained proliferation in high-dose regions. In contrast, astrocyte responses were more localized to the irradiated hemisphere and white matter tracts.
- Overall, this work establishes a framework for spatially mapping dose-dependent brain responses and will be extended with spatial transcriptomics to uncover molecular pathways and identify potential therapeutic targets for late radiation-induced brain damage

SINDI NEXHIPI, Post Doctoral Researcher, **German Cancer Research Center**

Leveraging Short- & Long-Read NGS To Unravel rAAV Genome Complexity

- Introducing NGS-based analytical approaches for rAAV product characterization, including short-read methods for variant calling and process contaminant quantification, and long-read sequencing for evaluating transgene integrity and complex genome rearrangements
- Challenges in data interpretation and emerging industry efforts to standardize descriptions of unintended genome species are discussed.

GREGORY MENDEZ, Principal Scientist, **Sanofi**

Q&A session & transition time between conference rooms

Endotype Discovery: Integrating Tissue & Genetic Cohorts To Uncover Disease Mechanisms

- Endotypes are biologically defined disease subtypes—based on molecular, cellular, or pathway mechanisms—that predict distinct biomarkers and treatment responses
- In cardiometabolic disease, similar clinical phenotypes can arise from different mechanisms; endotyping identifies the patients represents enriched biological mechanisms
- Here, we show an endotyping framework by integrating tissue omics and human genetics cohorts, with 2 examples illustrating data-driven mechanisms discovery in T2D and hypothesis-driven Obesity endotype identification
- Both approaches demonstrate how cross-modality integration can help prioritize candidate mechanisms, refine patient stratification, and generate testable hypotheses for follow-up studies

JING HE, Associate Director, **NovoNordisk**

12:40

1:05 - 2:25

LUNCH BREAK & REFRESHMENTS

1-2-1 Meetings x4

Poster Displays

Day Two | 01 April 2026

SPATIAL MULTI-OMICS

CONFERENCE ROOM 1: EMERGING MULTI-OMICS PLATFORMS AND APPLICATIONS: PROTEOMICS, EPIGENOMICS & METABOLOMICS

Subcellular Multi-Omic Imaging Of FFPE Tissue At The Whole Transcriptome Level (19000-Plex RNA) & Up To 1200-Plex Protein (Same Slide): Transformational Technology For Translational Research & Drug Development

JOSEPH BEECHEM, Chief Scientific Officer & Senior Vice President of Research and Development, **Bruker Spatial Biology**

CONFERENCE ROOM 2: SPATIAL BIOLOGY FOR THERAPEUTIC DISCOVERY & DEVELOPMENT

Translating ADC Treatment Resistance To Therapeutic Strategy In Bladder Cancer

- Same-slide spatial multiomics of paired bladder biopsies identified layered drivers of Nectin-4 ADC resistance
- FGFR3/SMAD/TGF-β activation promoted M2 polarization and IL-12 insufficiency, establishing immunosuppressive niches that spatially excluded activated T cells implying multi-node blockade may be required

GULPREET KAUR, Cofounder & Chief Business Officer **Elucidate Biotechnologies**

SINGLE CELL ANALYSIS

CONFERENCE ROOM 3:SINGLE CELL ANALYSIS: ADVANCED TOOLS & TECHNOLOGIES

Not All Antibodies Are Created Equal: Why Application-Specific Validation Defines Single-Cell Insights

- Validation isn't just about binding; it's about performance in context
- We explore why application-specific validation is the backbone of single-cell multi-omics, using our Hallmarks of Validation to prevent false protein signals.

GREG WARNER, Senior Field Applications Scientist, **Cell Signaling Technology**

NGS & CLINICAL DIAGNOSTICS

CONFERENCE ROOM 4: MULTI-OMICS FOR PRECISION MEDICINE & NGS DIAGNOSTICS

Single-Cell Multiomics Enables Superior MRD Detection & Therapeutic Insight In Myeloid Malignancies

- Sensitive detection of measurable residual disease (MRD) and therapy-resistant clones is critical in myeloid malignancies, yet standard bulk assays often miss rare subpopulations or misclassify benign clonal hematopoiesis
- Single-cell multiomic profiling overcomes these limitations by simultaneously capturing genotype and phenotype
- This approach offers superior sensitivity over conventional methods, accurately distinguishing leukemic from preleukemic cells while mapping co-mutant subclones and clonal hierarchies
- These high-resolution insights improve relapse prediction, define biomarkers, and characterize resistance mechanisms. Consequently, single-cell multiomics establishes a unified framework that strengthens both clinical monitoring and precision therapeutic development

ANDREW OWENS, Field Application Scientist, **Mission Bio**

Q&A session & transition time between conference rooms

2:25

Leveraging Multi-Omics To Unravel Systemic Sclerosis Pathobiology & Advance Precision Medicine Strategies

- Comprehensive multi-omics profiling across systemic sclerosis subtypes reveals distinct molecular signatures and disease phenotypes, providing deeper insight into disease heterogeneity
- Precision medicine strategies: ongoing efforts and challenges in integrating multi-omics insights to enable data-driven patient stratification and therapeutic development

SUNHWA KIM, Associate Scientific Director, Precision Medicine Immunology, **AbbVie**

INTERACTIVE

WORKSHOP: GESTALT

PRESENTATION 3: **Multi-Modal & Multi-Omics Studies In Human Lung Disease**

- Integrating spatial transcriptomics with complementary modalities such as mass spectrometry imaging
- Translational and disease-focused applications, including bronchopulmonary dysplasia and other inflammatory lung conditions, demonstrating how spatial biology informs therapeutic development

GLORIA PRYHUBER, Professor, Department of Pediatrics, Neonatology (SMD), **University of Rochester Medical Center**

INTERACTIVE

PANEL DISCUSSION: **How To Optimize Single Cell Sequencing Approaches**

- Single cell technology comparison – what to use and when
- Innovative techniques to enhance resolution and accuracy
- Uncovering & identifying novel and rare cell types

Panellists:

EUGENIA LYASHENKO, Senior Principal Scientist, Lab Head, **Sanofi**

IOANNIS RAGOUSSIS, Professor, **McGill University**

DAVID GALLEGOS, Senior Scientist, **Takeda**

REA DABELIC, Senior Staff Product Manager, **Illumina**

Mapping Adaptive Tumor Ecosystems In Bladder Cancer: Translating Spatial Multi-Omics Into Precision Therapy

- Spatial and multi-omic profiling reveals dynamic tumor-stroma adaptive niches that drive therapeutic resistance and disease recurrence
- Integrative computational frameworks and liquid-biopsy approaches enable real-time, non-invasive monitoring of tumor state evolution
- These insights support a new generation of biomarker-guided clinical trials and personalized treatment strategies in urothelial carcinoma

SAUM GHODOUSSIPOUR, Associate Professor, **Rutgers Cancer Institute**

2:50

Q&A session & transition time between conference rooms

Day Two | 01 April 2026

SPATIAL MULTI-OMICS

CONFERENCE ROOM 1: EMERGING MULTI-OMICS PLATFORMS AND APPLICATIONS: PROTEOMICS, EPIGENOMICS & METABOLOMICS

Connecting Studies & Sites: Impactful Advances In LC-MS Based Spatial Proteomics

- Integrating temporally separated spatial proteomics studies using LC-MS. Can we gain insights from comparing data acquired years apart?
- Strategies and insights for optimizing sample shipping and handling across multiple sites, enabling broader adoption of spatial proteomics techniques by cross-functional teams

JAN SCHEJBAL, Senior Scientist I, **AbbVie**

3:15

Q&A session & transition time between conference rooms

INTERACTIVE

PANEL DISCUSSION: **Spatial Biology To Advance The Map Of Human Pathology**

- The role of proteomics and metabolomics in human atlases & disease models
- Using proteomic & metabolomic data to find disease mechanisms
- Developing and maintaining large scale cell and organ atlas projects

Moderator:

YEA JIN KAESER-WOO, Senior Director, Next Generation Therapeutics, **Eli Lilly**

Panellists:

EMRE ARSLAN, Associate Director, **Takeda**

JIA-REN LIN, Technical Director, Tissue Imaging Platform, **Harvard Medical School**

DAVID GALLEGOS, Senior Scientist, **Takeda**

AHMET COSKUN, Professor of Biomedical Engineering, **Georgia Institute of Technology**

3:40

4:05

CONFERENCE ROOM 2: SPATIAL BIOLOGY FOR THERAPEUTIC DISCOVERY & DEVELOPMENT

INTERACTIVE

WORKSHOP: GESTALT

PRESENTATION 4: **Computational & Statistical Challenges Of Analyzing Spatial Transcriptomics & Spatial Multi-Omics Data**

- Addressing data integration, scalability, and interpretability, highlighting what must be solved to translate complex spatial datasets into actionable insights for infectious disease, immunology, and clinical research

DANIEL JONES, Staff Scientist, Vaccine & Infectious Disease Division, **Fred Hutch Cancer Centre**

INTERACTIVE

PANEL DISCUSSION: **Diversifying The Applications Of Spatial Biology**

- The newest areas of application for spatial technologies
- Oncology translation
- Infectious disease
- Rare disease
- Where can spatial go next?

Moderator:

FEI CHEN, Associate Professor of Stem Cell and Regenerative Biology, **Harvard University**

Panellists:

PEI-HSUAN CHEN, Principal Scientist, **Bristol Myers Squibb**

CHANDRA SARAVANAN, Director, Pathology, **Novartis**

JIWOON PARK, Founder of the Spatial Atlas of Human Anatomy, **Harvard Medical School and Weill Cornell Medicine**

SINGLE CELL ANALYSIS

CONFERENCE ROOM 3:SINGLE CELL ANALYSIS: ADVANCED TOOLS & TECHNOLOGIES

Learning Cross-Species Cellular Representations With Single-Cell Foundation Models

- Cell type annotation in emerging model organisms is limited by sparse references, inconsistent gene panels, and cross-species variability in single-cell data
- We evaluated existing single-cell foundation models that learn unified cellular representations across species, enabling more accurate annotation in under-studied organisms
- The models were tested across diverse contexts, including whole-atlas and tissue-specific references, and transfers between both closely and distantly related species

HUA LI, Director of Computational Biology, **Stowers Institute for Medical Research**

CELLestial: An End-To-End Spatial Proteomics Analysis Framework For Rapid Cell Type Annotation And Interactive Visualization At Scale

SIMONA CRISTEA, Head of Genomics Data & AI, **Dana-Farber Cancer Institute**

Q&A session & transition time between conference rooms

Single Cell Analysis For Capsid Discovery & Engineering

EUGENIA LYASHENKO, Senior Principal Scientist, Lab Head, **Sanofi**

NGS & CLINICAL DIAGNOSTICS

CONFERENCE ROOM 4: MULTI-OMICS FOR PRECISION MEDICINE & NGS DIAGNOSTICS

Multi-Omics and Precision Medicine: Bridging Biology and the Bedside

- Integrative Insight: Harnessing genomics, transcriptomics, proteomics, and beyond to unravel complex disease mechanisms.
- Personalized Care: Translating multi-omics data into tailored diagnostics, prognostics, and therapeutic strategies.
- Clinical Impact: Bridging research and real-world application to improve patient outcomes through precision medicine

TESFAYE MERSHA, Professor, **Indiana University School of Medicine**

INTERACTIVE

PANEL DISCUSSION: **The Role Of Multi-Omics In Precision Medicine**

- Predicting treatment response
- Challenges to integrating multi-omics into precision medicine

Moderator: SUNWHA KIM, Associate Scientific Director, Precision Medicine Immunology **AbbVie**

Panellists:

BANISHREE SAHA, Associate Director, Global Biomarker and Assay Analytical Lead, **Takeda**

TESFAYE MERSHA, Professor, **Indiana University School of Medicine**

UTTIYA BASU, Professor, **University of Columbia, New York**

ZONGMEI GAO, Senior Scientist II, **AbbVie**

SARA HAMON, Senior Director, Head of Precision-Quantitative Translational Sciences, **Regeneron**

Decoding Therapy Resistance With Multimodal Real-World & Spatial Data

- Beyond clinical trials: How real-world evidence reveals treatment patterns, patient heterogeneity, and gaps not captured in controlled studies
- Spatial context matters: Using spatial transcriptomics to link tumor heterogeneity to resistance phenotypes in tissue

SAHIL SETH, Principal Scientist, **Bristol Myers Squibb**

Day Two | 01 April 2026

	SPATIAL MULTI-OMICS		SINGLE CELL ANALYSIS	NGS & CLINICAL DIAGNOSTICS
	CONFERENCE ROOM 1: EMERGING MULTI-OMICS PLATFORMS AND APPLICATIONS: PROTEOMICS, EPIGENOMICS & METABOLOMICS	CONFERENCE ROOM 2: SPATIAL BIOLOGY FOR THERAPEUTIC DISCOVERY & DEVELOPMENT	CONFERENCE ROOM 3:SINGLE CELL ANALYSIS: ADVANCED TOOLS & TECHNOLOGIES	CONFERENCE ROOM 4: MULTI-OMICS FOR PRECISION MEDICINE & NGS DIAGNOSTICS
4:30	**Single Cell Spatial Interactomics & Multimodal Barcoding In Cancer, Immunity, & Aging** • Spatially resolved protein-protein interactomics go beyond protein location with its functional single cell post-translational-omics analysis • Spatial metabolomics are barcoded with cell types using super-resolution imaging and generative deep learning • Spatial biomarkers are discovered using a foundational model and visual query answering system in large-scale multimodal spatial omics datasets AHMET COSKUN, Professor of Biomedical Engineering, **Georgia Institute of Technology**	**Challenges & Considerations For Multimodal Clinical Spatial Omics: A Practical Guide** • While spatial technologies are rapidly advancing, their use in clinical applications remains in its early stages and differs from workflows and expectations established in preclinical model systems characterizations • We will present a pilot workflow using a FFPE human colon tissue dataset analyzed with spatial transcriptomics via the 10x Genomics Xenium platform, followed by post Xenium multiplexed imaging with Akoya • We will share key lessons learned, along with practical laboratory considerations and sample selection criteria, to help ensure robust data quality in multimodal spatial assays SHOH ASANO, Senior Principal Scientist, **Pfizer**	**Celldega: Toolkit For Analysis & Visualization Of Spatial & Single-Cell Data** • Visualization and analysis of single-cell and spatial transcriptomics data • Scalable and linked visualizations for large spatial datasets • Novel neighborhood-level analysis NICOLAS FERNANDEZ, Senior Computational Scientist, **Broad Institute**	**Somatic Hypermutation Mechanisms During B Cell Lymphoma Progression** • B cells undergoing physiologically programmed or aberrant genomic alterations provide an opportunity to study the causes and consequences of genome mutagenesis • Using three DNA alteration processes--(i) VDJ recombination, (ii) class switch recombination (CSR), and (iii) somatic hypermutation (SHM)—driven by DNA mutator proteins RAG1/2 recombinase (i) or Activation Induced Deaminase (AID) (ii, iii), B cells somatically mutate their antibody-encoding genes to incorporate mutations in the Ig gene loci IgH and IgL • Here, we discuss identification and characterization of lymphoma causing mutations identified from a patientss UTTIYA BASU, Professor, **University of Columbia, New York**
4:55	**END OF CONFERENCE**			

VENUE INFORMATION

Experience Boston's Back Bay

NextGen Omics Spatial & Data US 2026 will be held at the Sheraton Boston Hotel.

Nestled in the historic Back Bay neighborhood and directly connected to the Prudential Center and the Hynes Convention Center, experience outstanding service and an incredible location in downtown Boston.

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Sheraton Boston Hotel

39 Dalton Street, Boston,
Massachusetts, USA, 02199

Explore the Hotel

DIRECTIONS BY AIR

Boston Logan International Airport:
Sheraton Boston Hotel is 4 miles from the International Airport. A single taxi ride to the hotel will cost approx. $26-$35 and will take around 11 minutes. Additionally, you could get subway from Prudential- Government Center then to Airport.

DIRECTIONS BY TRAM/BUS

The closest bus stop to the venue is Boylston Street, which is a 5min walk away. If you're wanting to get to South Station Train Terminal you will need to walk to Stuart St and dismount at Lincoln St, a short 2 minute walk you will find the station.

DIRECTIONS BY SUBWAY / TRAM

The closest subway/tram stop to the venue is Prudential, which is a 3-min walk away. If you're wanting to get to South Station Train Terminal you will need to walk to Prudential get the E tram change over at Park Street on the Red line to South Station.

PARKING

There is self-parking available (garage parking) at the hotel for $30 (this may be subject to state local taxes). There is no valet parking at this venue. For further information please contact the hotel directly.