2025
Genetic Resources Core Facility (GRCF) Symposium Guide

Keynote Address: **"Molecular genetic studies of CNS vascular development and disease"**

Jeremy Nathans, M.D., Ph.D.

Samuel Theobald Professor of Ophthalmology
Professor of Molecular Biology and Genetics
Professor of Neuroscience
nvestigator, Howard Hughes Medical Institute
Johns Hopkins Medical School

Come to Learn, Engage, and Network

April 9, 2025, 9:30 am - 2:00 pm, Turner Concourse

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

Welcome to the 2025 Annual GRCF Symposium!

We are delighted to welcome you to this year's GRCF Annual Symposium, a premier event that brings together our core facility community, innovative vendors, leading researchers, and cutting-edge technologies. More than just a meeting, this symposium serves as adynamic platform for collaboration, discovery, and networking—driving progress in genetics, genomics, and beyond.

As we continue this valued tradition, we are excited to showcase the vital research support provided by the GRCF, highlight the latest advancements in genet ic and genomic research, and foster connections that fuel scientific innovation. Whether you're here to explore emerging technologies, exchange ideas, or engage with industry leaders, we hope this symposium provides inspiration, knowledge, and new opportunities for your work.

Thank you for being part of this year's event—we look forward to an engaging and productive gathering!

See you there!

The GRCF Team

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AGENDA

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2025 GRCF SYMPOSIUM AGENDA

Start Time	End Time	Event	Room	Featuring	Title
9:30:00 AM	2:00:00 PM	**Exhibit Floor**	Turner Concourse	GRCF & GRCF Suppliers	
10:00:00 AM	10:50:00 AM	**Breakout Session I**	G-01	Illumina, Inc.	Leveraging Illumina Sequencing with the NovaSeq X Plus
			G-03	Zymo Research	Unlocking the Full Potential of Liquid Biopsy and FFPE Samples with Advanced Purification and Library Preparation Technologies
			West Room	QIAGEN	Quantification using the QIAcuity dPCR System
11:00:00 AM	11:50 AM	**Breakout Session II**	G-01	10X Genomics	The neXt generation of single cell starts with GEM-X
			G-03	New England BioLabs	Streamlined RNA and DNA Library Construction Methods to Overcome the Challenges of High-throughput Sequencing
			West Room	MilliporeSigma	Next-Gen Tools for Biomedical Research: From 3D Organoids to Biomarker Analysis with MILLIPLEX® and SMC® Technolo
12:00 PM	12:50:00 PM	**Lunch**	Turner Concourse	Rosina Gourmet	
1:00 PM	2:00 PM	**Keynote Address**	Tilghman	Jeremy Nathans	Molecular genetic studies of central nervous system vascular development and disease
2:00 PM		**Event's Conclusion**			**Thank you for attending!**

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Keynote Address

TITLE: "Molecular genetic studies of central nervous system vascular development and disease"

PRESENTER: Jeremy Nathans, M.D., Ph.D., Samuel Theobald Professor of Ophthalmology, Professor of Molecular Biology and Genetics, Professor of Neuroscience, Investigator, Howard Hughes Medical InstitutionJohns Hopkins Medical School

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TIME: 1:00 pm - 2:00 pm

ROOM: Tilghman Auditorium

ABSTRACT: During development, the central nervous system (CNS) vasculature grows to precisely meet the metabolic demands of neurons and glia. In addition, most of the CNS vasculature acquires a unique set of molecular and cellular properties – collectively referred to as the blood-brain barrier (BBB) – that minimize passive diffusion of molecules between the blood and the CNS parenchyma. An analogous system in the retina is referred to as the blood-retina barrier. Both processes are controlled by signals that originate in neurons and glia. A unifying feature of angiogenesis and BBB formation and maintenance throughout the central nervous system (CNS) is their dependence on beta-catenin signaling (also called canonical Wnt signaling), with Wnt7a and Wnt7b serving as the dominant ligands in the brain and spinal cord, and Norrin serving as the dominant ligand in the retina. In contrast to CNS angiogenesis, development of the peripheral vasculature is largely independent of beta-catenin signaling. This lecture will describe some of the experiments that serve as the foundation for our current understanding of CNS vascular development and maintenance, and the connections between this work and human disease

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Breakout Session I

Illumina Innovations - What's new and what's on the horizon, Bao Ho, Ph.D., Sequencing Specialist,Illumina, 10 am - 10:50 am, MRB G-01.

Abstract: Illumina sequencing has led researchers to impactful insights into biological phenomena. As we continue to deliver transformative tools, we endeavor to drive these insights to higher resolutions across multiple modalities. Hear from us about our latest innovations in single cell: how we address barriers in cell preparation, scale, and cost with a microfluidic-free workflow. Check out our new proteomics assay that leverages aptamers to characterize over 9,000 unique proteins and how it differentiates from antibody-based methods. Learn about our new product updates in library prep-free comprehensive genome, our approach to methylation with 5-base sequencing, and how Illumina continues to enable breakthrough science in multiomics.

Unlocking the Full Potential of Liquid Biopsy and FFPE Samples with Advanced Purification and Library Preparation Technologies, Ian Ward, Senior Research Associate, Zymo, 10 am - 10:50 am, MRB G-03.

Abstract: Liquid biopsy and FFPE samples are critically challenging materials for oncology research, requiring precise handling to unlock their full potential in genomics, epigenomics, and transcriptomics. Zymo Research leads innovation with high-performance solutions for these applications. The Novel MAGicBead™ Technology enables quick and automatable isolation of cell-free DNA (cfDNA) with highest yield from plasma, serum, and a wide variety of other biofluids, preserving both short and long fragments essential for DNA methylation and fragmentomic studies, directly compatible with the Zymo-Seq SPLAT DNA Library Kit for efficient NGS library construction. Additionally, the Zymo-Seq RiboFree Total RNA Library Kit provides an FFPE-compatible solution for whole transcriptome profiling of degraded samples from any species, broadening RNA analysis beyond common models for further insights.
Join us to learn more about how Zymo Research empowers scientists with streamlined approaches to analyze liquid biopsy and FFPE samples efficiently for new discoveries in cancer biology and therapeutics

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Quantification using the QIAcuity dPCR System, Will Johnson: Digital PCR Specialist, Ph.D.,QIAGEN, 10:00 am -10:50 am, West Room.

Abstract:

Not provided

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Breakout Session II

The neXt generation of single cell starts with GEM-X, Bradley Toms, M.S. Senior Science and Technology Advisor, 10X Genomics, 11:00 am -11:50 apm, MRB G-01.

Abstract: See how 10x Genomics is helping researchers uncover molecular insights from fresh or fixed samples, including FFPE tissues. Explore cellular heterogeneity with Chromium Single Cell solutions that let you dissect cell-type differences, investigate the innate and adaptive immune system, identify rare cell types, detect novel biomarkers, and map the epigenetic landscape cell by cell.

Streamlined RNA and DNA Library Construction Methods to Overcome the Challenges of High-throughput Sequencing, Jeanne Geskes Field Applications Scientist, NGS, New England BioLabs, 11:00 am -11:50 pm, MRB G-03.

Abstract: New England Biolabs has developed three new NEBNext UltraExpress® kits aimed at simplifying the processing of samples of various input amounts, accommodating a range of sample types, and streamlining workflows, thus allowing for automation compatibility. Optimizations enable the processing of samples across various inputs with a single adaptor concentration and a single condition for PCR cycling. NEBNext UltraExpress® RNA, UltraExpress® DNA (mechanically sheared), and UltraExpress® FS DNA (enzymatically sheared) workflows represent, single-tube solutions, incorporating master mixed reagents, reduced incubation times, and fewer clean-up steps, resulting in faster, more streamlined workflows generating less plastic consumable waste while maintaining high-quality sequencing metrics.

Next-Gen Tools for Biomedical Research: From 3D Organoids to Biomarker Analysis with MILLIPLEX® and SMC®, Dr. M. Zulfiquer Hossain, 11:00 am -11:50 am, West Room.

Abstract: In this presentation, we highlight the transition from traditional 2D cell cultures to 3D organoid models, focusing on the use of induced pluripotent stem cell (iPSC) derived and patient-derived organoids in recapitulating complex tissue structures and functions. Furthermore, we introduce MILLIPLEX® multiplex assays and Single Molecule Counting (SMC®) technology, which enhance the accuracy and precision of protein quantification in precious and/or low-abundance samples, including those derived from organoid models. These advances improve disease modeling, drug efficacy testing, and biomarker discovery, ultimately reducing clinical trial failures. Integrating these tools into research workflows promises to bridge the gaps between in vitro and in vivo models and lead to more accurate, reliable, and physiologically relevant biomedical research outcomes.

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Arima Genomics

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biomodal

Bio-Rad

Integrated DNA Technologies (IDT)

Illumina, Inc.

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New England BioLabs (NEB)

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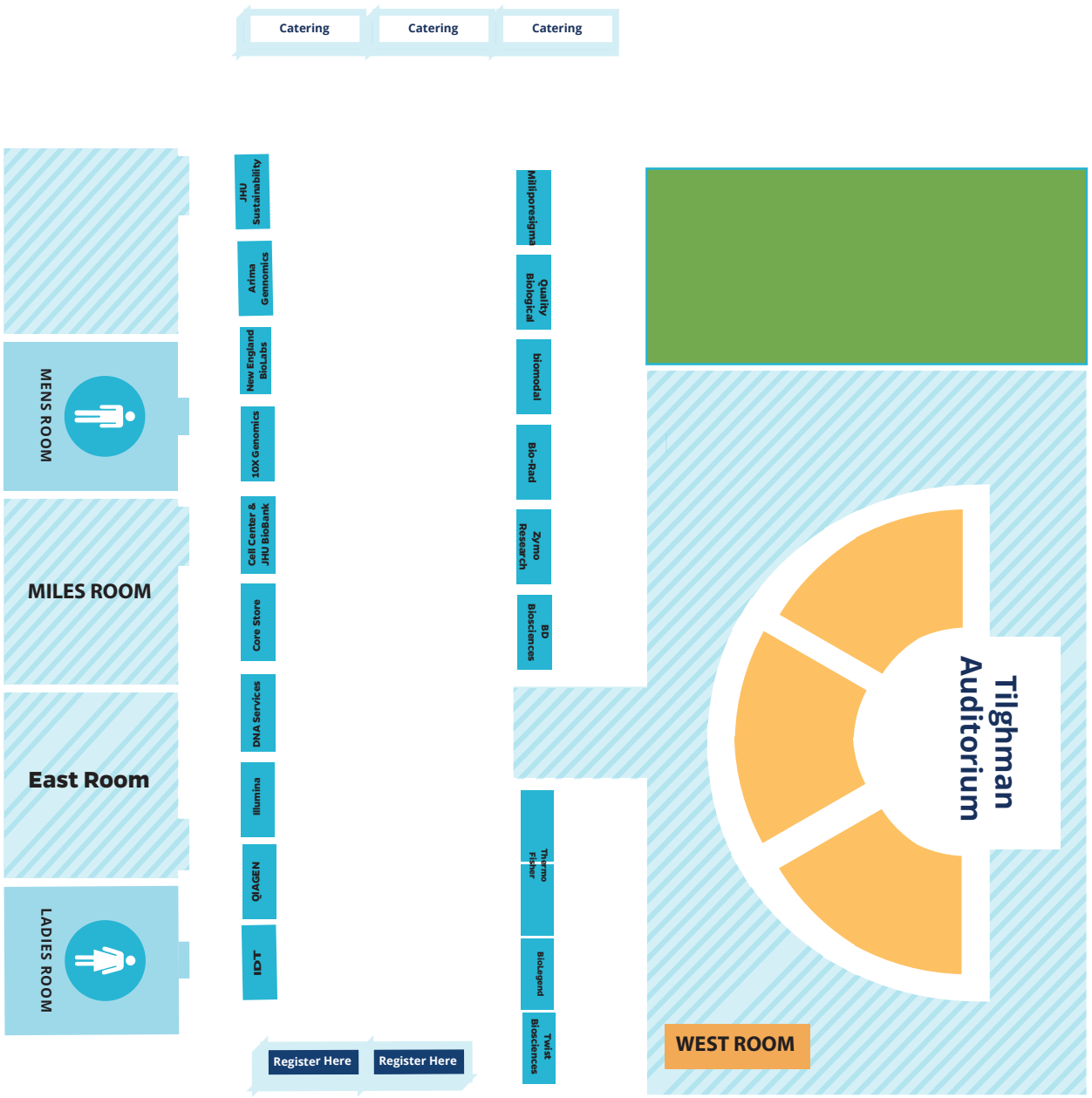
2025 GRCF Symposium



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