2026 Spring Conference

Accelerating Discovery:

Automation, Integration, Innovation

Wednesday April 22, 2026
DoubleTree Hotel St. Louis - Chesterfield

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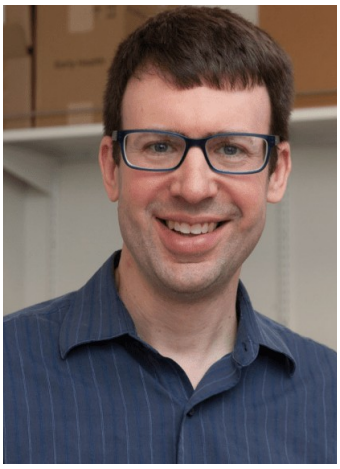
Accelerating Discovery
2026 Midwest LRIG
Spring Conference Program

11:00am: Doors Open, Registration, Exhibits Open
12:00pm: Lunch (Ballroom B)
12:45pm: Introduction, Platinum Sponsor Rapid Fire Talk: ***Nova Biomedical***
1:00pm: **Keynote: "Engineering Consistency in Human iPSC Neuronal Cultures for Image-Based Phenotyping and Functional Genomics"**
William Buchser, Washington University- St. Louis
1:30pm: Rapid Fire Talk: ***Biosero***
1:40pm: "Design and Implementation of Modular Automation for Genomics Assays"
Duane Currier, St. Jude Children's Research Hospital
2:10pm: Break, Visit Exhibits
2:40pm: "Innovating for Impact: How Bayer's Genotyping and Automation Are Powering Sustainable Agriculture"
Amy Caruano-Yzermans & Abbie Stack, Bayer Crop Sciences
3:10pm: Rapid Fire Talk: ***Dynamic Devices***
3:20pm: Break, Visit Exhibits, passed hors d'oeuvres/beverages in Exhibit Hall
Mike Williams Memorial Scholarship Announcement
4:15pm: "Scalable Approaches for Modeling Rare Disease in Patient-derived Organoid Systems" **Scott T. Younger, Children's Mercy Research Institute**
4:45pm: **Roundtable Discussion– Accelerating Discovery in 2026: AI²**
Moderator: Joshua Bauer, Vanderbilt University
Panelists: William Buchser, WashU
Duane Currier, St. Jude
Amy Caruano-Yzermans & Abbie Stack, Bayer
Scott T. Younger, Children's Mercy
5:30pm: Social Networking Reception- Dinner Served, Exhibits Open
7:00pm: Exhibits Close

Exhibitors:

Aurora Microplates | Azenta | BioNex | BlueCatBio | BMG Labtech | Copia Scientific
eMolecules | Formulatrix | Future Drop | Gilson | Grenova | IMCS
Integra Biosciences | LabSource | Omega Bio-tek | Opentrons | Revvity Health Sciences | Scinomix | ThermoFisher | Zinsser Analytic

Speakers

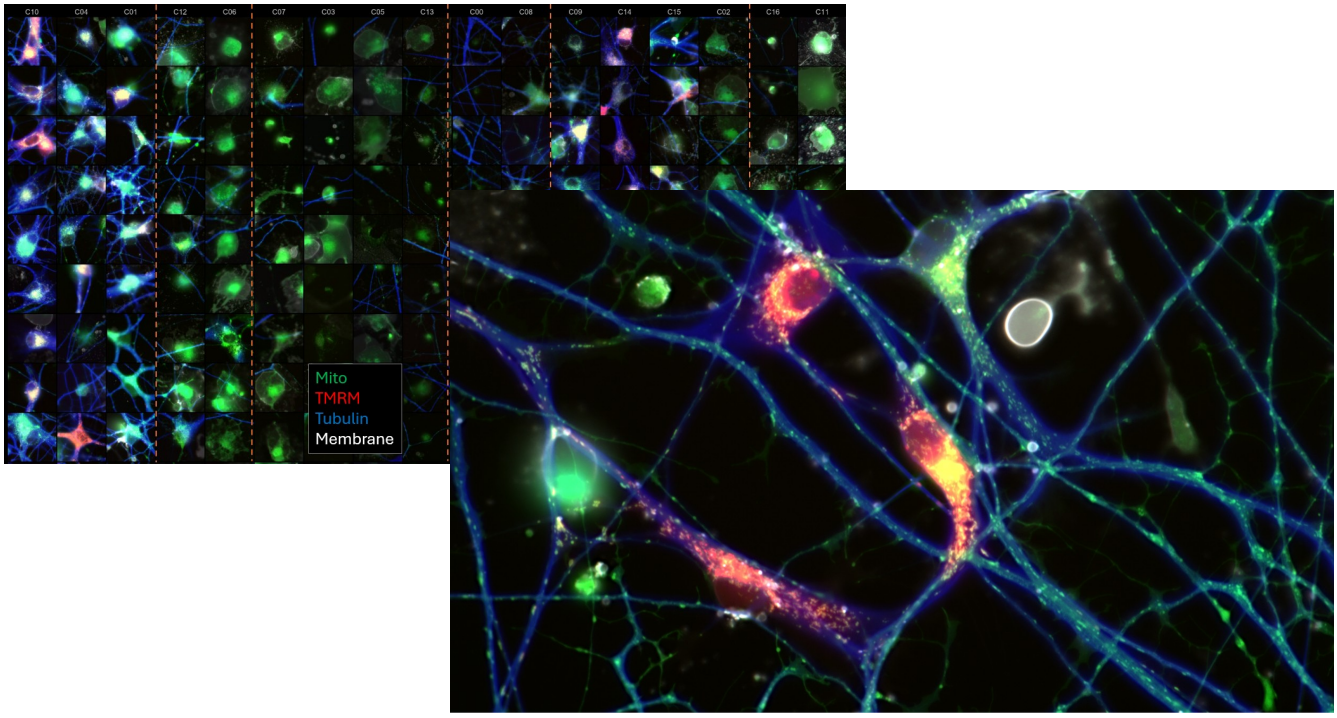


Keynote Speaker:

William Buchser, Ph.D.
Associate Professor
Department of Genetics
Director F.I.V.E.- Functional Imaging for Variant Elucidation
Washington University in St Louis, School of Medicine

Engineering Consistency in Human iPSC Neuronal Cultures for Image-Based Phenotyping and Functional Genomics

A major biological feature of neurodegenerative disease is that neurons carrying the same genetic alleles can show striking differences in sensitization depending on neuronal subtype. Studying this biology requires experimental systems that produce highly consistent human iPSC-derived neuronal cultures while supporting complex perturbational designs at scale. This talk will describe an integrated workflow that combines automated liquid handling, nanoliter dispensing, high-content confocal imaging, fast data infrastructure, and machine learning to enable single-cell, image-based phenotyping and functional genomics in human neuronal models. It will highlight studies in motor and sensory neuropathies spanning multiple chemical stressors, doses, timepoints, and genetic backgrounds. It will also discuss Raft-Seq, a pooled image-based microraft screening approach for linking genetic perturbations to cellular phenotypes. Together, these studies show how automation, integration, and quantitative imaging can help reveal the biological basis of neuronal vulnerability while highlighting the experimental challenges that remain.



Speakers

Duane Currier
Director of Laboratory Operations for
PARADIGM Automation Engineering
St. Jude Children's Research Hospital

Design and Implementation of Modular Automation for Genome Editor Assays

CRISPR genome editors, enzymes that can be simply programmed with a short guide RNA to change the DNA of living cells, are becoming next-generation personalized genomic medicines that can correct patient disease mutations. A key step is identifying editors and guide RNA combinations that are both highly active and specific for their intended target. Engineering these editors and characterizing their activity poses a throughput challenge due to the proliferation of design permutations. Each target may require testing of a few editor variants, target-specific guide RNAs may explore a range of editing windows, and protein engineering campaigns may produce multiple editor constructs.

Accelerating the development of genomic medicines requires increasing the throughput of editor engineering and activity assessment beyond current manual bench protocol capability. While automation can achieve higher throughput, genomic assays pose distinct challenges such as sample expansion and pooling and workflows that branch and merge.

To enable rapid discovery and characterization of highly active and specific genome editor and target combinations for therapeutics, we designed a flexible, high-throughput, robotic system. The system is capable of performing genome-wide on- and off-target activity assays, such as cellular GUIDE-seq and biochemical CHANGE-seq, with minimal human intervention. Sample expansion and pooling are supported through adaptable sample-mapping strategies. Branching and merging workflows leverage modular protocol units that can be reconfigured into complex workflow patterns.

Our system integrates both acoustic and tip-based liquid handling, multiple thermocyclers, high-capacity automated storage and other devices required for automated plate-based assays. The system's flexibility is enabled by a state-aware approach of coordinating execution between the scheduler and the liquid handlers. The liquid handlers maintain deck state between method runs, allowing the scheduler to issue generalized instructions that function across configurations and pipette method versions. In addition, we developed highly parameterized protocols that accommodate variable sample numbers, plate layouts, and execution parameters.

As a result, we have decoupled minor differences between assay steps from the core execution logic. A workflow orchestration layer, currently under development, will integrate these protocols in assay appropriate sequences. With this core automation infrastructure, we establish a scalable platform capable of supporting rapid development and characterization of genome editors.

Speakers

Amy Caruano-Yzermans, Ph.D.
Genome Marker Design Lead

Abbie Stack
Genotyping Innovation and Technologies Lead

Bayer Crop Sciences

Innovating for Impact: How Bayer's Genotyping and Automation are Powering Sustainable Agriculture

Precision Genomics in Bayer Crop Science R&D is transforming how plants are developed by uniting world-class automation and cutting-edge genotyping/genomics at unprecedented scale. This presentation will highlight how Bayer leverages decades of expertise in laboratory robotics and genomics to process millions of samples annually and generate billions of data points that accelerate seed and trait pipelines. Through real-world examples attendees will see how Precision Genomics converts complexity into actionable insights Bayer is innovating for impact—delivering faster, more reliable solutions that empower breeders, support growers worldwide, and advance the future of sustainable agriculture.

Speakers

Scott T. Younger, Ph.D.
Director, Disease Gene Engineering
Associate Professor of Pediatrics,
University of Missouri-Kansas City School of Medicine
Research Assistant Professor of Pediatrics,
University of Kansas School of Medicine

Children's Mercy Research Institute

Scalable Approaches for Modeling Rare Disease in Patient-derived Organoid Systems

Personalized antisense oligonucleotides (ASOs) have achieved positive results in the treatment of rare genetic disease. As clinical sequencing technologies continue to advance, the ability to identify rare disease patients harboring pathogenic genetic variants that may be amenable to this therapeutic strategy is likely to improve. To support this expanded patient population, we have established a platform to facilitate the rapid characterization of preclinical ASO leads. We developed a highly efficient and scalable pipeline for the derivation of iPSCs. Our noninvasive iPSC reprogramming method requires as few as 50K PBMCs (commonly available from prior genetic testing) and is typically complete within 2-3 weeks. A parallelized format enables the simultaneous reprogramming of dozens of patient samples, allowing the straightforward generation of nearly 300 patient-derived iPSC lines in under 6 months with >93% reprogramming success rates. Pairing our iPSC reprogramming pipeline with optimized organoid differentiation protocols further enables the functional profiling of patient-specific disease phenotypes at scale. As proof of principle, we designed personalized ASOs targeting a splice-disrupting intronic variant in the dystrophin gene of a Duchenne muscular dystrophy (DMD) patient and confirmed the reversal of contractile dysfunction in patient-derived cardiac organoids. We then selected a cohort of undiagnosed rare disease patients with complex neurological phenotypes, prioritized predicted splice-disrupting intronic variants based on genome sequencing data, designed patient-specific ASOs targeting candidate variants for each patient, and identified several ASOs that resulted in abatement of seizure-associated neuronal hyperactivity in patient-derived brain organoids. Our platform provides the foundation for an expedited path towards the design and preclinical evaluation of personalized ASO therapeutics for a broad range of rare diseases. Importantly, this platform is not limited to the characterization of ASOs and can be used to evaluate patient-specific responses to alternative therapeutic modalities including small molecules and biologics.

About Midwest LRIG

*The Midwest LRIG is a registered 501(c)(3) non-profit with a **mission** to provide and foster an open collaborative environment where professionals can exchange ideas and advance discovery and application of innovative life science technologies. The **goal** is to provide scientific educational opportunities to the community by stimulating multi-disciplinary scientific collaboration and encouraging networking among representatives of academic, professional, scientific, and business communities through regular meetings and conferences.*

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