grcf

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A component of Johns Hopkins Genomics

CORE SYMPOSIUM – May 2nd, 2017, 10:00 a.m. – 2:00 p.m.

Turner Concourse

Genetic Resources Core Facility (GRCF) Mission

To provide high quality, cost effective research services and products to investigators throughout the Johns Hopkins Scientific Community.

The Genetic Resources Core Facility (GRCF), a part of JH Genomics, is a JHU service center that includes **the Core Store,** the **Biorepository & Cell Center and DNA Services**. Collectively, these groups produce a number of products and services to aid researchers performing studies in cell biology, molecular biology and genetics. It is our mission to provide high quality, cost-effective research services and products to investigators throughout the Johns Hopkins scientific community and the general scientific community at large.

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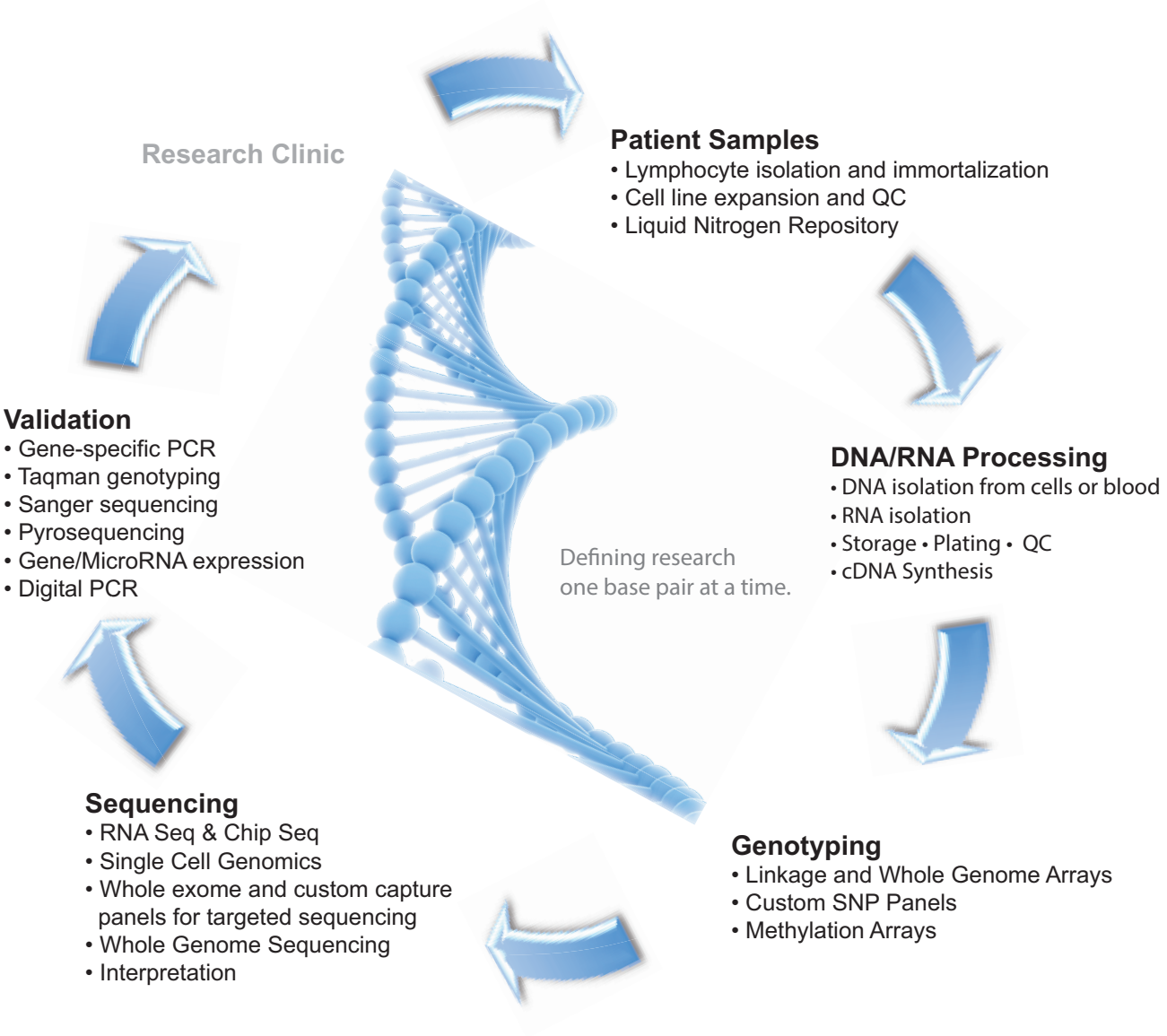
JOHNS HOPKINS
SCHOOL of MEDICINE



The diagram above illustrates the many ways we work to fill the needs of researchers studying genetic disorders. Our goal is to assist in collecting, processing and banking patient samples. From these clinical samples, we have expertise in generating immortalized cell lines that can be used in future biological studies, or for isolating a single cell for genomic analysis. Furthermore, DNA and RNA from various sources can be genotyped on as few as one variant to over 5 million. If more detail is required, we offer a variety of high throughput sequencing protocols from the capture of exomes or genomic regions of special interest to RNA-seq. All of our high quality data is processed through our end-to-end pipeline which provides alignment files, variant calls and customizable reports, enabling our researchers to utilize the most appropriate tools for interpreting results. Once a variant is found, we can provide validation by other technologies such as Taqman, digital PCR, Sanger sequencing, etc. In the epigenetic realm, we are able to assist with methylation studies either through genotyping, pyrosequencing or any of the high throughput sequencing options such as CHiP-seq and Methyl-seq. Our union with Johns Hopkins Genomics has expanded our capabilities to allow seamless integration of clinical testing, making the circle from discovery to application complete.

GRCF Services

The Core Store provides one-stop shopping for more than 300,000 products from 17 of the leading life science companies. In addition to its product offering the store charges no shipping and handling fees and has free delivery to three campuses East Baltimore, Bayview and Homewood. There is also convenient 24/7 access to several hundred products via the Core Store 24/7 at these locations Blalock 1026, CRB 1 B02A and the Asthma and Allergy Building 1st floor. For more information go to http://grcf.jhmi.edu/core-store/

Biorepository & Cell Center facilitates basic and clinical scientific research by providing expertise and service in all mammalian cell culture, single cell genomics, clinical trial support and long-term cryogenic storage of biospecimens. The GRCF Biorepository & Cell Center proudly maintains the international quality and regulatory recognition of CAP (the College of American Pathology) Accreditation. To help further support leading edge research at Johns Hopkins University, the GRCF has worked to develop a single cell genomics facility. Through the joint effort of the GRCF Biorepository & Cell Center and GRCF DNA Services we are able to offer a one-stop single cell isolation (DNA or RNA), sequencing and analysis service. For more information go to http://grcf.jhmi.edu/biorepository-cell-center/.

The DNA Services group works together to provide solutions for all of your DNA and RNA needs. We handle basic needs like DNA isolation, plating and storage, "traditional" core services like Sanger sequencing, PCR support and genotyping, and the more complex needs presented by the constantly changing field of next generation sequencing. For more information on these services please go to https://grcf.jhmi.edu/dna-services/ .

Scientific Exhibitors

10X Genomics

Agilent

Bio-Rad

Corning Cellgro

GE Healthcare Life Sciences

Integrated DNA Technologies

Illumina

Lonza

MilliporeSigma

New England Biolabs

Peprotech

Promega

QIAGEN

Quality Biological

Thermo Fisher Scientific

Zymo Research Corp.

Keynote Address – 11:30 a.m. – 12:30 p.m.

Title: "The functional genomics of retinal development"

Room: Tilghman Auditorium **Time:** 11:30 a.m. – 12:30 p.m. **Sponsor:** GRCF

Presented by: Seth Blackshaw, Ph.D., Professor of Neuroscience, Johns Hopkins University

Abstract: The vertebrate central nervous system (CNS) is an amazingly complex structure composed of distinct subtypes of neurons and glia. Proper development of these cell types is critical in the regulation of physiology and behavior. We use the accessible and well-characterized mouse retina as a system for investigating the molecular mechanisms that control cell fate specification. The retina is perhaps the best-characterized region of the central nervous system, and provides an excellent system to identify the novel molecular mechanisms that regulate neuronal cell fate. The retina is comprised of seven major cell types, each identified by morphology and molecular markers, and changes in their differentiation are easily measured. Over the past 15 years, we have used a variety of high-throughput approaches to identify genes that control retinal cell fate specification. I will discuss recent work from my group that uses single-cell RNA-Seq to comprehensively characterize both heterogeneity among retina progenitors and changes in gene expression associated with the differentiation of individual cell types. I will also discuss our analysis of the epigenomic landscape of retinal progenitor cells, and the use of this data to identify transcriptional regulatory networks that control temporal patterning in retinal progenitors. Finally, I will discuss other studies that investigate the mechanisms by which the transcription factor Lhx2 is able to control multiple different and temporally discrete aspects of retinal development.

Seminar Directory: 10:00 a.m. – 11:00 a.m.

Title: "StemFlex™ Medium: Evolving Your Medium System for Modern Stem Cell Applications"

Room: West Room **Time:** 10:00 a.m. – 11:00 a.m. **Sponsor:** Thermo Fisher

Presented by: Dr. Alexandria Sams

Abstract: The newest stem cell medium from the Gibco brand, StemFlex Medium, is the only medium designed to deliver superior performance in the innovative applications and technologies used in today's stem cell research. StemFlex Medium is uniquely formulated to maximize performance in today's more challenging applications that have traditionally stressed pluripotent stem cell cultures, such as reprogramming, single-cell passaging, and gene editing. In addition to core performance enhancements, it also delivers the modern conveniences of a flexible feeding schedule (including weekend-free options) and the ability to switch between the matrix and passaging reagents best suited for a chosen application.

Title: "Immuno-Oncology Research Enabled Through Advanced Genomic Techniques"

Room: MRB-G01 **Time:** 10:00 a.m. – 11:00 a.m. **Sponsor:** Illumina

Presented by: Gourab Bhattacharjee, Ph. D.

Abstract: Recent advances in our understanding of how the immune system interacts with and fights cancer have revolutionized cancer research and treatment. The power of genomics in Immuno-Oncology is just starting to be comprehended and applied to this dynamic space. Immune cell repertoire sequencing, RNA-Seq and expression analysis of the tumor microenvironment, and the detection and prediction of immune stimulatory neoantigens are all examples of how genomics can help to answer many of the unknown questions that still exist.

Title: " Non-Viral Transfection – A Closed system – Sterile Nucleofection of up to 109 cells Real scalability – Optimization in small scale"

Room: MRB –G03 **Time:** 10:00 a.m. – 11:00 a.m. **Sponsor:** Lonza

Presented by: Curtis Henry, Product Support Specialist, Lonza

Abstract: Lonza's Nucleofector LV System expands the proven 4D system to closed transfection of up to 1x109 cells. Small-scale protocols can be transferred to larger scale without the need for re-optimization – uniting small- and large-scale transfection applications in one system, based on the highly efficient Nucleofector™ Technology.

Transfection is a powerful tool used to study and control gene expression by delivering DNA, RNA, or even proteins into cells. Various applications within translational research require the generation of large numbers of transiently modified cell lines or primary cells. Such applications include modification of cells via genome editing or the generation of CAR-T cells for ex-vivo cell therapies, production of transient proteins or antibodies for construct screening, and generation of disease models via genome editing for cell-based assays.

Nucleofector™ Technology is an efficient, non-viral transfection method for primary cells and hard-to-transfect cell lines. Due to its flexibility with different substrates, such as DNA and mRNA, Nucleofector™ Technology is being used to drive research in numerous cell types and applications, including non-viral iPSC generation via episomal vectors, as well as genome editing using various ZFN-, TALEN- or CRISPR-related cargo combinations.

Title: "The Future of Screening: RNAi and CRISPR"

Room: West Room **Time:** 10:00 a.m. – 11:00 a.m. **Sponsor:** MilliporeSigma

Presented by: Joe Frangipane, Ph.D.

Abstract: RNAi screening has made it possible to identify new genes and networks that are involved in a variety of biological processes. The technology continues to help researchers gain critical insights into the mechanisms of human disease and accelerate the development of treatments for a host of disorders.

The intersection between RNAi and complementary approaches such as CRISPR/Cas9-mediated genome editing has created new opportunities for assay development, screening and validation studies in numerous cell lines and model systems. We will present on validating RNAi screens with CRISPRs as well as our offering for CRISPR libraries, pooled and arrayed. Additionally, RNAi rescue experiments using LentiORFs serve an important role in further validating and boosting the confidence of screened hits. This seminar will cover workflow strategies to improve genome-wide RNAi screening and validation, augmenting its utility as a valuable research tool.

Seminar Directory – 1:00 p.m. – 2:00 p.m.

Title: "The Next Generation of NEBNext® Library Preparation Methods to reduce input amounts, streamline workflows and increase accuracy in NGS analysis"

Room: West Room **Time:** 1:00 p.m. – 2:00 p.m. **Sponsor:** New England Biolabs

Presented by: Daniela Munafo, Ph.D., New England Biolabs NGS Field Application Scientist

Abstract: With its unprecedented throughput, scalability, and speed, next-generation sequencing (NGS) is expanding its applications from research to clinical diagnostics. Unfortunately, many clinical samples go unanalyzed because they do not yield sufficient quantities or quality of DNA or RNA. To enable the increased use of NGS in clinical settings we have developed library prep methods that address these challenges. The NEBNext® Ultra™ II FS DNA library prep kit includes a streamlined fragmentation system library construction method that can accommodates sub-nanogram quantities of DNA. This single-tube method enables the user to go from DNA to sequence-ready libraries in less than 3 hours. Additionally, the workflow incorporates unique molecular identifies (UMI's) to distinguish true mutation from PCR or sequencing-based errors, as well as identify and filter out PCR duplicates. The NEBNext® Ultra™ II Directional RNA library prep kit enables the use of lower input amounts and fewer PCR cycles and all with a streamlined, automatable workflow that delivers high quality data. The NEBNext Direct® technology utilizes a novel approach to selectively enrich nucleic acid targets without sacrificing specificity. It's a unique target enrichment technology that combines a simple workflow with highly specific, uniform enrichment of gene targets.

Title: "Master the Art of CRISPR Editing"

Room: MRB-G01 **Time:** 1:00 p.m. – 2:00 p.m. **Sponsor:** Thermo Fisher

Presented by: Abby Sukman

Abstract: The powerful CRISPR gene editing technology has the potential to transform research at an astonishing rate. While CRISPR-based knock out in mammalian cells is very effective, precise insertion via homology directed repair continues to be challenging. We will cover understanding and choosing the best gRNA and donor DNA formats for your experiment, factors affecting and optimization of CRISPR-Cas9 delivery, optimizing knockout experiments, designing the optimal gRNA and donor DNA for knock-in experiments, quantifying editing efficiency and screening for positive clones, isolating and validating CRISPR-edited clones and screening for off target effects.

Title: "CRIPSR"

Room: MRB-G03 **Time:** 1:00 p.m. – 2:00 p.m. **Sponsor:** Agilent

Presented by: Jonathan Levine, Ph.D.

Abstract: Genome-wide CRISPR libraries are a powerful new tool for high-throughput screening and discovery. Data integrity and interpretation depend on knockout uniformity, also known as representation. Poor representation from subpar gRNA libraries can lead to detrimental artifacts. This seminar will provide an introduction to the scientific principles of CRISPR/Cas genome editing technology and describe how Agilent's pooled CRISPR libraries harness the SurePrint and SureVector technologies to provide better representation than other commercially available solutions. Whether pre-defined or custom, every SureGuide CRISPR library is printed with the same exceptional quality.

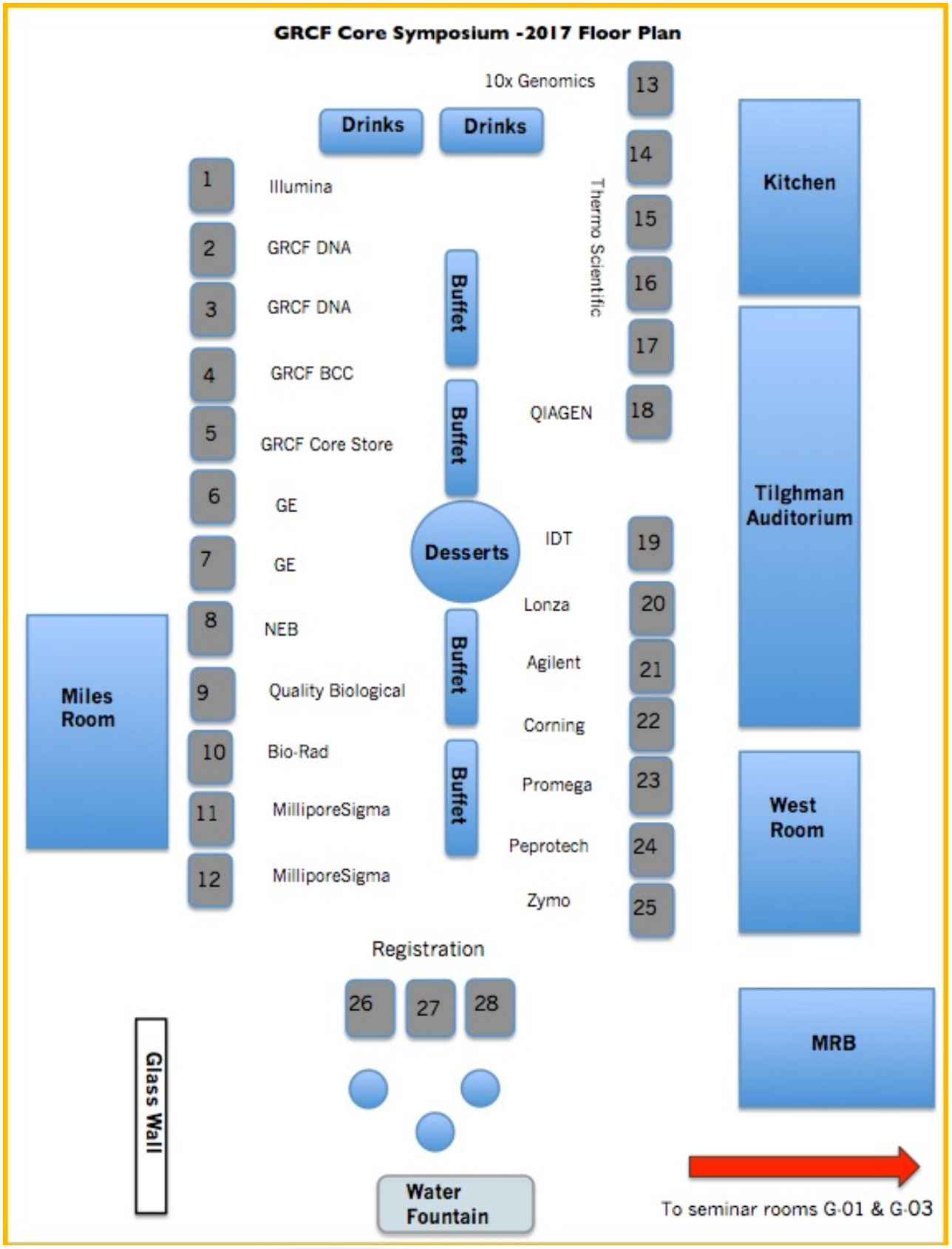
Title: "Imaging Beyond the Diffraction Limit"

Room: Tilgham Auditorium **Time:** 1:00 p.m. – 2:00 p.m. **Sponsor:** GE Healthcare

Presented by: Peter Franklin, Cell Analysis Segment Manager, Asia

Abstract: Optical lenses cannot bend light over a certain angle to achieve resolution beyond the diffraction limit. This is currently defined by Raleigh or Sparrows resolution limits. This limitation exists in all modern microscopes and is a fundamental limitation of optical physics.

There are basically two approaches to optical super-resolution imaging. 1) Localization Microscopy which seeks to determine the spatial localization of a fluorophore in the specimen, and 2) Illumination Manipulation that modifies the illumination system of the microscope to achieve higher resolution. Both of these are typically associated with different applications in cell biology; Localization Microscopy is normally performed in TIRF (Total Internal Reflection Fluorescence Microscopy) based applications whilst Illumination Manipulation (3D-Structure Illumination Microscopy) allows one to image relatively thick samples which are not directly in contact with the cover slip. We will discuss the methodologies and the advances in Super Resolution Imaging to enable one to see biology in higher definition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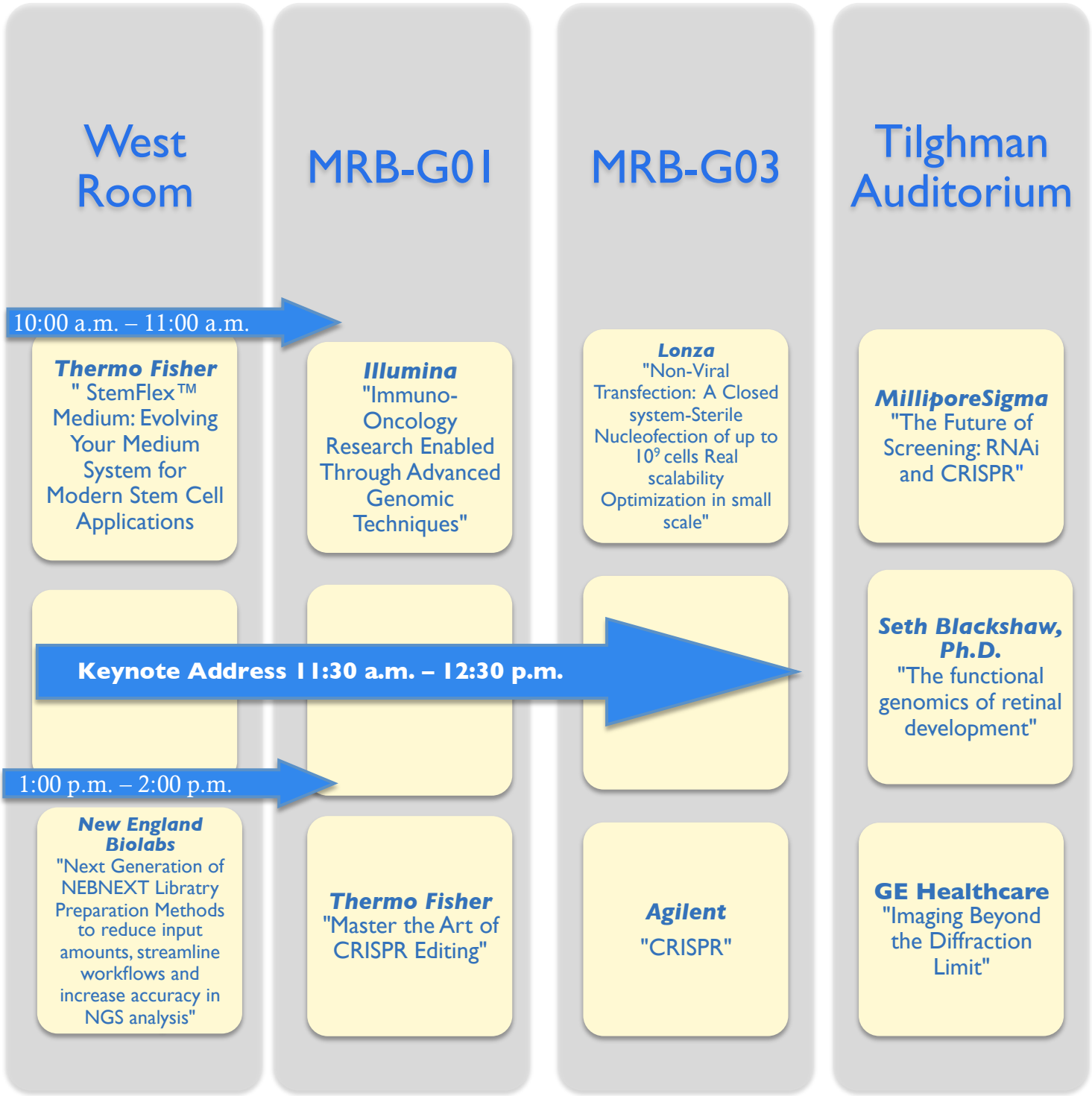
CORE SYMPOSIUM SEMINAR SCHEDULE

Turner Concourse, May 2nd, 2017



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