



A component of Johns Hopkins Genomics

CORE SYMPOSIUM – April 17th, 2018, 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 clinical science, 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.

Contents

GRCF Services

Each of the GRCF's Services will have an exhibit table with representatives to answer questions.

Scientific Exhibitors

Nineteen of the GRCF's Corporate Partners will have exhibit tables. Please visit their exhibits to learn about their products and services.

Keynote Address

Alan F. Scott, Ph.D., Institute of Genetic Medicine, Johns Hopkins University, page 4.

Exhibit Floor Plan

A map of the exhibit floor and seminar rooms is provided on page 7.

Seminar Schedule

A schedule of all seminars is provided on the back cover of this guide.



# GRCF Services

**The Core Store** provides one-stop shopping for more than 400,000 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 I 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, qPCR, diPCR, DNA/RNA QC, Cel line authentication, mycoplasma testing. . For more information on these services please go to, <https://grcf.jhmi.edu/dna-services/>

## Scientific Exhibitors

I0X Genomics

Agilent

BioLegend

Bio-Rad

Cell Signaling

Corning Cellgro

GE Healthcare Life Sciences

Horizon Discovery

Integrated DNA Technologies (IDT)

Illumina

Lonza

MilliporeSigma

New England Biolabs

Oxford Nanopore Technologies

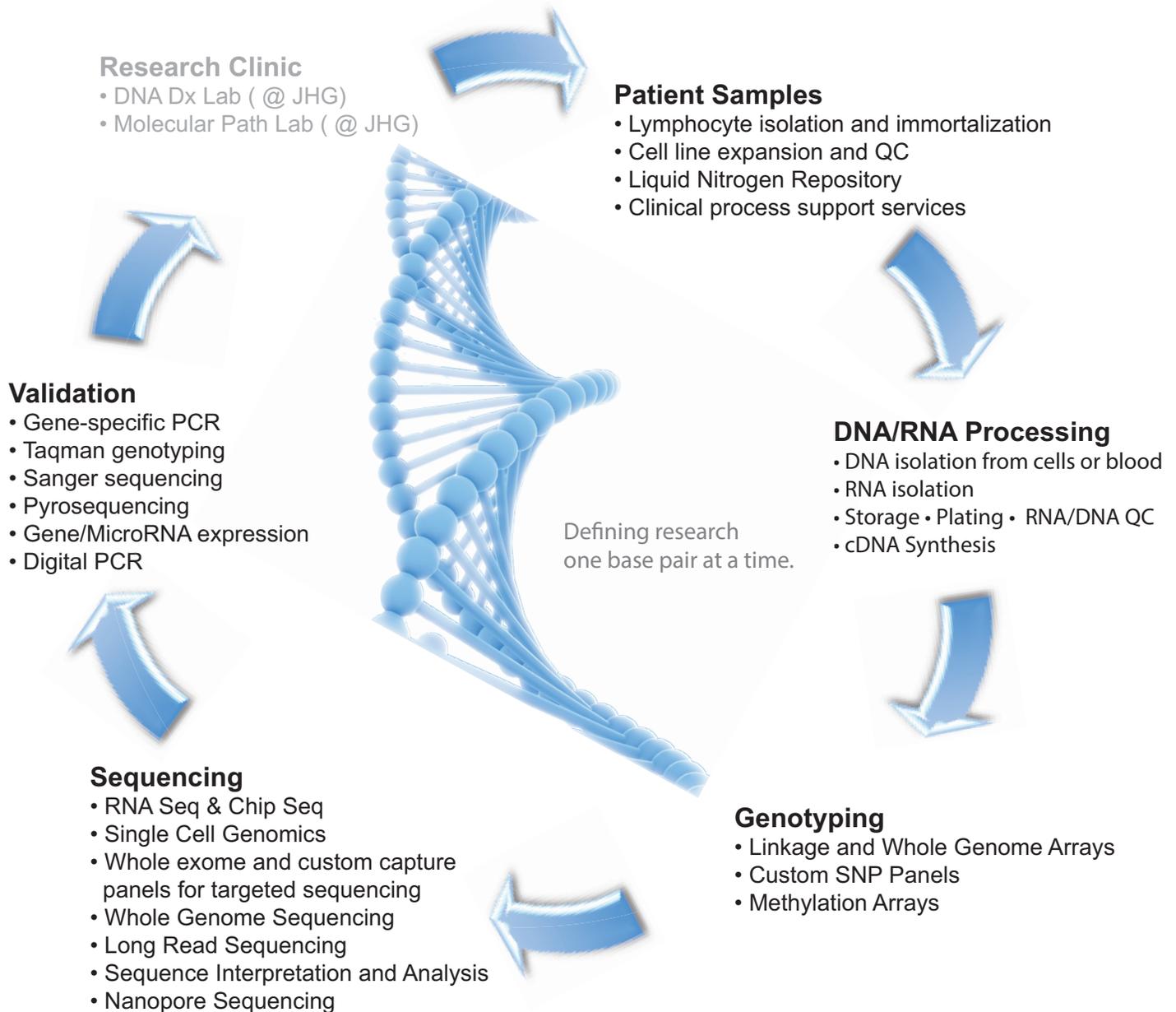
Peptidech

QIAGEN

Quality Biological

Thermo Fisher Scientific

Zymo Research Corp.



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. By joining Johns Hopkins Genomics we have expanded our capabilities to allow seamless integration of clinical testing, making the circle from discovery to application complete.

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

**Title:** “The Genomics of Mass Extinction”

**Room:** Tilghman Auditorium

**Time:** 11:30 a.m. – 12:30 p.m.

**Sponsor:** GRCF

**Presented by:** Alan F. Scott, Ph.D., Assoc. Professor, Director, Genetic Resources Core Facility, Johns Hopkins University SOM

**Abstract:** Earth is undergoing a planet-wide loss of biodiversity and increased rates of extinction unprecedented since the age of the dinosaurs as a consequence of human activities.

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

**Title:** “From CRISPR to Combinations: Empowering Human Disease Research and Personalized Medicine with Horizon Discovery Solutions”

**Room:** West Room

**Time:** 10:00 a.m. – 11:00 a.m.

**Sponsor:** Horizon Discovery

**Presented by:** Vipat Raksakulthai

**Abstract:** Personalized medicine has changed the landscape of drug discovery. Tools such as panels of isogenic cell lines, functional genomic screening platforms and biologically relevant assays all contribute to greater understanding of disease and more accurate prediction of patient responses to drugs and drug combinations.

We'll be discussing:

- \* How to use CRISPR screening for target ID and validation, understanding drug MOA and patient stratification
- \* The screen design, quality control and how to evaluate success of your screening program
- \* Horizon's latest developments to the platform
- \* Horizon's novel approaches to target validation screening

Horizon is a fully integrated life science company offering a full spectrum of products, services and research programs to scientists engaged at every stage of the healthcare continuum from sequence to treatment.

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**Title:** “Discovery depends on detection: Emerging Technologies in Biomarker Identification and Quantitation”

**Room:** MRB-G01

**Time:** 10:00 a.m. – 11:00 a.m.

**Sponsor:** MilliporeSigma

**Presented by:** Amy. R Johnson, Ph.D., Immunoassay Platform Specialist

**Abstract:** Once identified, circulating disease biomarkers provide vital information regarding disease progression or remission and the overall health of an individual. However, the utility of any biomarker depends on the specificity of the biomarker to the disease of interest, as well as robust detection methods capable of repeatedly quantitating the biomarker accurately and resolving minimal – but critical - concentration changes. In this seminar, we will discuss how protein-based analysis using Milliplex® multiplexing and ultra-sensitive Single Molecule Counting (SMC™) technologies can synergize to provide reliable, robust biomarker identification and quantitation over a quantitative 7 log dynamic range. We will highlight the combined use of the Milliplex® and SMC™ protein detection technologies from recently published literature and will be available to discuss specific study-design questions

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**Title:** "Considerations for Magnetic Cell Isolation: Immunophenotyping and Cytokine Profiling"

**Room:** MRB-G03

**Time:** 10:00 a.m. – 11:00 a.m.

**Sponsor:** BioLegend

**Presented by:** Josh Croteau, Ph.D.

**Abstract:** Magnetic cell isolation has become a convenient and versatile tool for isolating specific cell populations from a variety of sample types. There are a number of experimental considerations that may impact the utility of magnetic isolation approaches in day to day research. We will explore some of these considerations using BioLegends Mojosort™ magnetic separation system on multiple cell types (T & B cells, macrophages, dendritic cells, and microglia). Analyses include surface immunophenotyping using flow cytometry and multiplexed cytokine analysis using the LEGENDplex™ assay in response to cell stimulation. Additionally, we will review a few relevant, exciting tools to facilitate immunobiological research and more.

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**Title:** "Real time DNA sequencing using Oxford Nanopore Technologies 'nanopore sensing'"

**Room:** Tilghman Auditorium

**Time:** 10:00 a.m. – 11:00 a.m.

**Sponsor:** GRCF

**Presented by:** James Brayer, Associate Director, Market Development

**Abstract:** Oxford Nanopore Technologies has developed a disruptive platform for the direct, electronic analysis of single molecules. Our instruments the MinION™, the GridION X5™ and the PromethION are adaptable for the detection and analysis of a range of analytes that include DNA, RNA, proteins and small molecules. At the heart of our platform is a biological protein called a 'nanopore'. A single nanopore creates a hole in a membrane made from a proprietary synthetic polymer. An electric potential is applied across the membrane resulting in a current flowing only through the aperture of the nanopore. Single molecules that enter the nanopore cause characteristic disruptions in the current, by measuring these disruptions single molecules from a sample are identified. The MinION is a small device that is designed for portability and simplicity of its workflow. The MinION plugs into a standard PC or laptop. The GridION X5 is a compact benchtop system designed to run and analyse up to five MinION Flow Cells. The PromethION is a standalone high throughput benchtop instrument that provides the flexibility to run up to 192 libraries in an asynchronous manner. Both the GridION and PromethION allow for large projects that requires the flexibility and throughput to interrogate complex eukaryotic genomes. The GridION is commercially available while the PromethION is still in early access. Oxford Nanopore is integrating the data produced by the MinION, the GridION X5 and the PromethION into a cloud-based analytics company, Metrichor. Metrichor is powered by its EPI2ME platform. Metrichor is providing tools to automate data analysis workflows to help people track, trend and predict biological data resulting in real time actionable interpretation of their data. Users of the technology have access to our 'Nanopore Community'. The Nanopore Community helps new users get started with technical documentation as well as user driven forums and encourages discussion and collaborative experimentation using our technology. There is a growing list of publications on the many uses for our nanopore sensing platform that include field based applications, real time pathogen detection and surveillance, metagenomics analysis, anti-microbial resistance detection, education and many more including sequencing on the International Space Station. I look forward to sharing with you the unique opportunities enabled by our nanopore sensing approach.

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

**Title:** "rhAMP up your Genotyping with the new rhAMP SNP"

**Room:** West Room

**Time:** 1:00 p.m. – 2:00 p.m.

**Sponsor:** IDT

**Presented by:** Mitchell Gore, Ph.D. Field Application Manager Genotyping

**Abstract:** The new rhAMP SNP genotyping system utilizes a combination of RNase H2-mediated primer extension, a highly discriminatory Taq polymerase, and a universal reporter to produce fluorescent signals with greater intensity and improved cluster separation compared to traditional systems.

- Virtually eliminates non-specific amplification and primer dimer formation.
  - Works well across the current instrument platforms.
  - Generate the highest level of performance with >99.5% call accuracy for over 90% of assays tested.
  - Generate the highest level of performance with pack commercially available.
  - Interrogate SNPs in difficult sequence regions with amplicon sizes as small as 40 bp
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**Title:** “Unraveling biology and identifying targets with functional genomics approaches supported by LentiArray CRISPR library screens”

**Room:** MRB-G01

**Time:** 1:00 p.m. – 2:00 p.m.

**Sponsor:** Thermo Fisher

**Presented by:** Abby Sukman, Sr. Technical Specialist, Synthetic Biology and Genome Engineering

**Abstract:** At Thermo Fisher Scientific, we are dedicated to driving innovative technologies that result in improved tools and reagents to help accelerate your research. Utilization of CRISPR for functional genomics screening is becoming more prevalent as lentiviral and gRNA libraries are now available and assays utilizing this powerful tool are developed. Please join us to learn more about how our CRISPR screening tools and services are being used in industry and academic settings. Case studies and new data is presented.

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**Title:** “Agilent in the Fight against cancer”

**Room:** MRB-G03

**Time:** 1:00 p.m. – 2:00 p.m.

**Sponsor:** Agilent

**Presented by:** Jane Romm M.S. Business development specialist

**Abstract:** Agilent has a complete portfolio to enable researchers and clinicians with multiple options to fight cancer and enable personalized medicine

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**Title:** “Ultra-Deep Sequencing to Unlock the Secrets of Complex Diseases”

**Room:** Tilgham Auditorium

**Time:** 1:00 p.m. – 2:00 p.m.

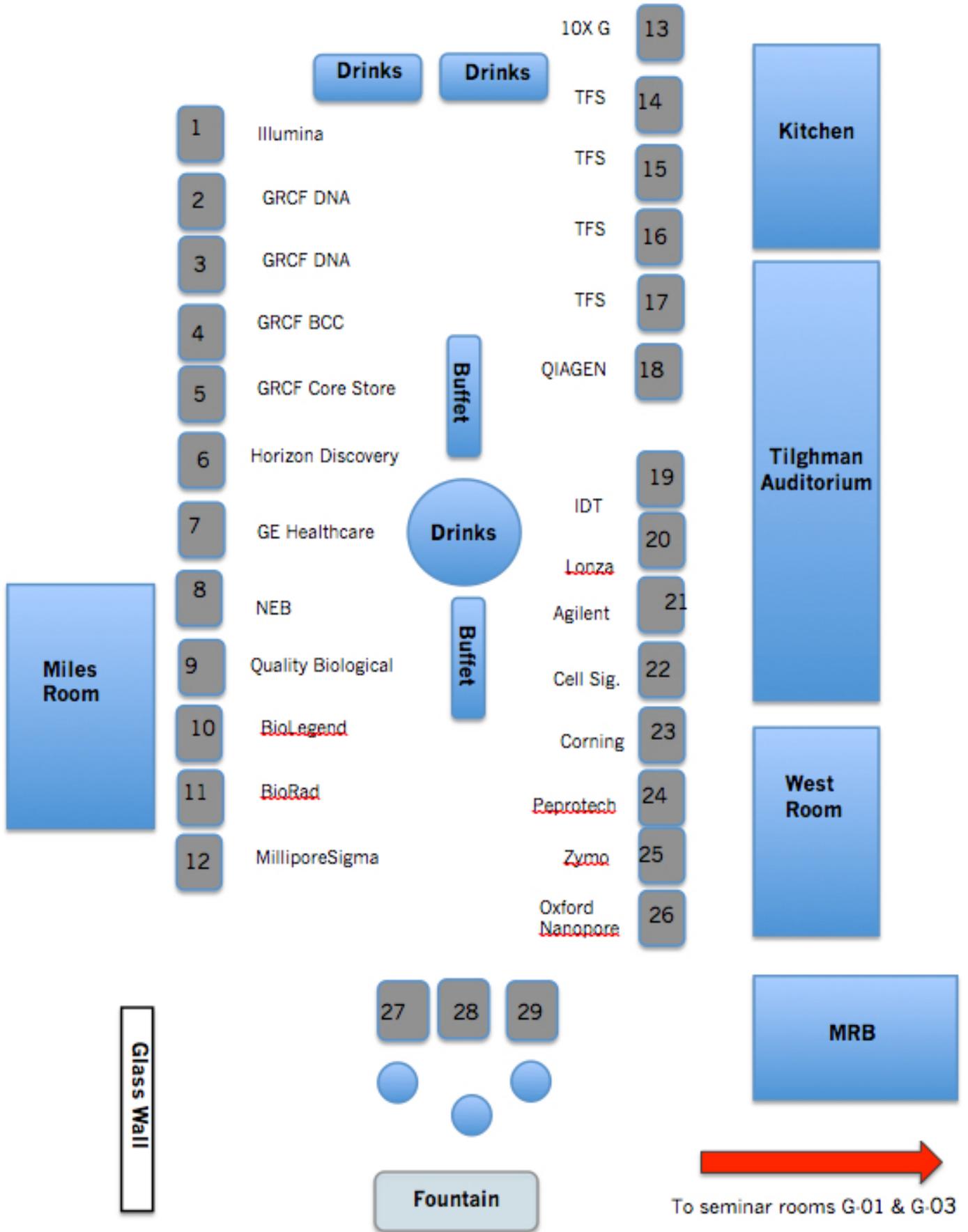
**Sponsor:** Illumina

**Presented by:** Brian J. Henson PhD,Sr. Sequencing Specialist, Mid-Atlantic,Illumina, Inc.

**Abstract:** This presentation will focus on Next Generation Sequencing methods that are being used to unlock the secrets of complex diseases. These technologies are enabling researchers to better understand the molecular mechanisms that underlie development and progression. Methodologies to be discussed include whole genome sequencing, whole genome bisulfite sequencing, whole exome sequencing, transcriptome sequencing, and single cell sequencing.

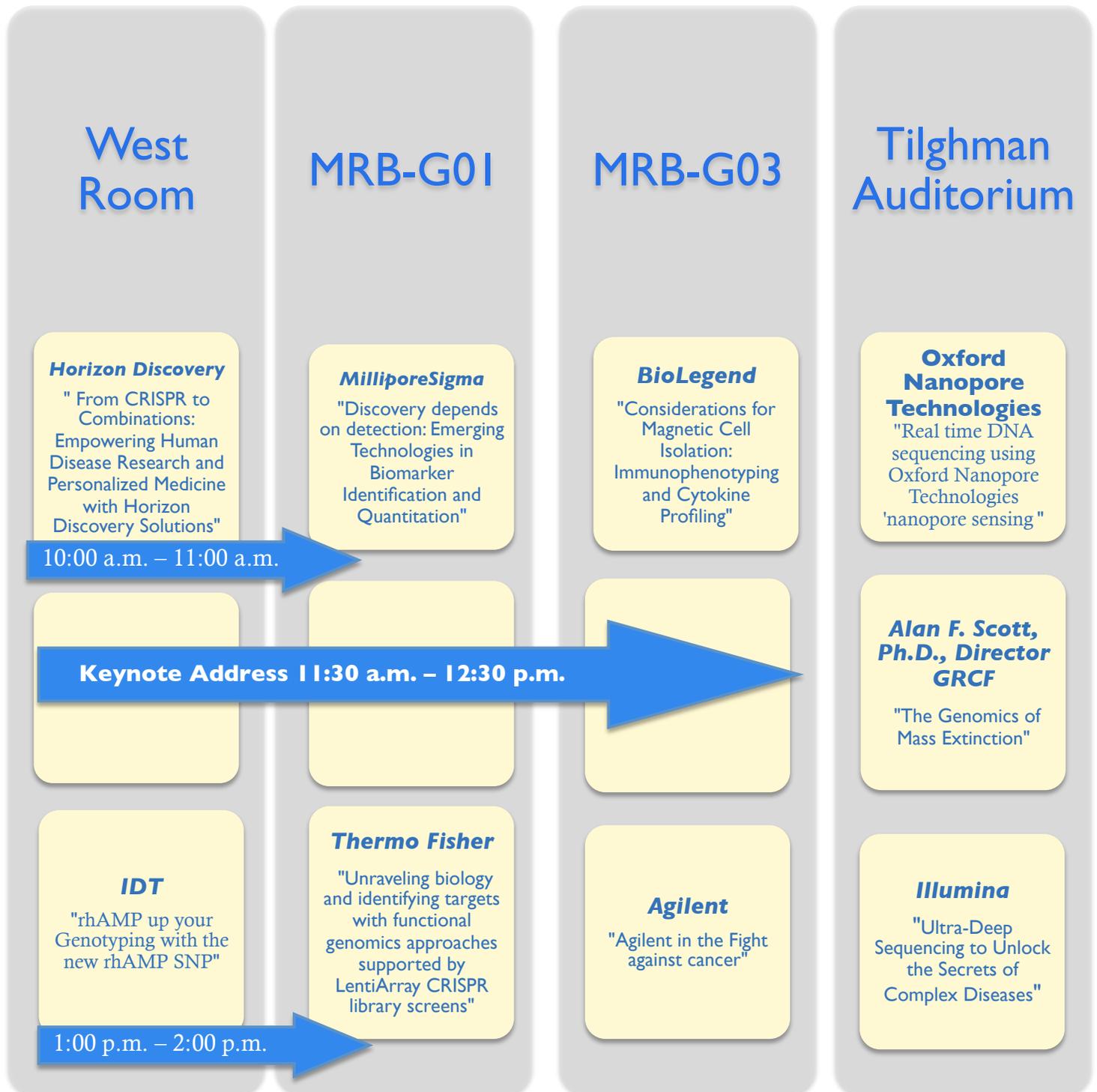
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## 2018 GRCF Core Symposium Floor Plan



# CORE SYMPOSIUM SEMINAR SCHEDULE

Turner Concourse, April 17<sup>th</sup>, 2018



For more information visit us at [grcf.jhmi.edu](http://grcf.jhmi.edu)