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 is a JHU service center including the Core Store, Biorepository & Cell Center and the DNA Services. Collectively, these groups produce a number of products and services to aid researchers performing studies in 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.
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 the Johns Hopkins campuses – East Baltimore, Bayview, and Homewood. For more information, go to https://grcf.jhmi.edu/core-store/

Biorepository & Cell Center facilitates basic 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 Pathologist) 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 http://grcf.jhmi.edu

Scientific Exhibitors

10X Genomics
Agilent
BD Bioscience
BioLegend
Bionano Genomics
Bio-Rad
Cell Signaling
IDT
Illumina
Lonza
MilliporeSigma
New England Biolabs
Oxford Nanopore Technologies
Promega
Quality Biological
ThermoFisher Scientific
Twist Bioscience
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: “Identification of Autism risk factors: from genes to environment”

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

Presented by: Christine Ladd-Acosta, PhD, Assistant Professor, Department of Epidemiology, Associate Director of Genomics, Wendy Klag Center for Autism & Developmental Disabilities, Johns Hopkins Bloomberg School of Public Health

Abstract: Autism Spectrum Disorder (ASD) is a common complex neurodevelopmental disorder thought to involve both genetic and environmental risks. Identification of potentially modifiable risk factors and biologic mechanisms for ASD can inform prevention, intervention, and treatment strategies to reduce ASD disabilities. In this talk, I will discuss recent work by our group to identify genetic, epigenetic, and environmental risk factors through their integration in an epidemiologic framework. I will also present proof-of-principle results showing the potential for epigenetics to serve as a biomarker of past exposure which has the potential to shape future epidemiology study designs and open new avenues of research.

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

Title: “Multidimensional Quantitative Cellular Imaging and Analysis – Utility of CellInsight High Content Platforms for Drug Discovery”

Room: West Room  
Time: 10:00 a.m. – 11:00 a.m.  
Sponsor: ThermoFisher Scientific

Presented by: Sesha Tekur

Abstract: Quantitative Cell based assays using fluorescence Microscopy not only produces awesome Images but also generates high content data providing scientists a deeper understanding of phenotypic changes, as well as key insight into intra and extra cellular processes. This can be in response to genetic manipulations as well a drug and compound treatments. Popularly referred to as High Content Assays of HCA, these have become a staple for most laboratories studying quantitative cell Biology and drug discovery. Since HCA uses fluorescence microscopy, it allows the scientists to multiplex a cell based assay by taking advantage of probes/ targets across the fluorescent spectrum (blue thro near infra red). Biotech companies, CROs and large pharma have historically capitalized on the multiplexing capabilities of HCA to get a better insight into the mechanism of action and sequence of events in response to genetic manipulations (CRISPR is a classic example) as well as drug and compound treatments in fixed end point as well as live kinetic situations to tie HCA as a bridge between cell biology and large scale drug discovery. The ThermoFisher high content portfolio consist comes from legacy Cellomics which invented High content and includes the CellInsight platforms for automated imaging and analysis. The Thermo Scientific CellInsight HCA imaging platform comes with up to 7 powerful LEDs or lasers that can excite from blue through near IR region of the light spectrum, allowing scientists to probe and multiplex several targets within cells and tissues on a variety of plate types and slides. Off late HCA is graduated from doing 2D monolayer imaging and analysis to 3D biology. The confocal capabilities built into some of the CellInsight Platforms allow scientists get deeper into Organoid and spheroid biology as well as get a better understanding of cell-cell interaction in a multidimensional space. The seminar will focus on the capabilities of the CellInsight imaging platforms for multidimensional imaging (2D monolayers, 3D spheroid/ Organoids and multi cellular environments) and quantitative analysis with some hard hitting examples of biology ranging from Cell Cycle, signaling, Toxicology and more, in response to drugs, compounds and genetic manipulations.

Title: “Nanopore Sequencing - The Long and the Short of It”

Room: MRB-G01  
Time: 10:00 a.m. – 11:00 a.m.  
Sponsor: Oxford Nanopore

Presented by: Monolina Binny, Field Application Specialist

Abstract: No abstract provided
Title: "Innovation for CRISPR, NGS, qPCR, and Synthetic Biology by Integrated DNA Technologies"

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

Presented by: John R Wilhelm III, MBA

Abstract: This is a presentation that will discuss the many applications of IDT products from PCR to qPCR to NGS and CRISPR. Stop by and listen and see how IDT has used its considerable experience in the synthesis and production of oligos over the past 30 years to parlay this into a full suite of products to help with every facet of your molecular research needs.

Title: "Advances in multi-modal single cell analysis and spatial transcriptomics"

Room: Tilghman Auditorium          Time: 10:00 a.m. – 11:00 a.m.          Sponsor: 10X Genomics

Presented by: Nirav Patel, MS Science & Technology Advisor, 10x Genomics

Abstract: No abstract provided.

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

Title: "Simplicon™"

Room: West Room          Time: 1:00 p.m. – 2:00 p.m.          Sponsor: MilliporeSigma

Presented by: M. Zulfiquer Hossain, Ph.D., Research Technology Specialist, Advanced Cell Models and Analysis

Abstract: A Next Generation In-Vivo Protein Expression System Simplicon™ is a novel protein expression system that enables immediate, sustained, and yet tunable expression of multiple genes in human cells without any risk of genomic integration. This platform employs a single, synthetic, polycistronic, self-replicating RNA strand which is based on the Venezuelan equine encephalitis (VEE) genome and has been engineered to mimic cellular RNA. The Simplicon™ RNA contains four genes (nsP1-4) encoding the VEE RNA replication machinery. However, it does not include the structural proteins that are required to make an infectious particle. Multiple transgene(s) of interest can be cloned into the Simplicon™ Cloning Vector (E3L) plasmid, and the Simplicon™ RNA can easily be generated from this plasmid through in vitro transcription. Up to a total of 8.3kb of transgene(s) has been successfully cloned into the Simplicon™ Cloning Vector for high sustained protein expression in BJ human foreskin fibroblasts. The Simplicon™ RNA can be transfected into a wide variety of cell types including human induced pluripotent stem cells (iPSCs), LX2 human hepatic stellate cells, human mesenchymal stem cells, and human primary T cells. In an exciting application of this technology, we have used the Simplicon™ RNA to successfully generate human iPSCs from BJ human foreskin fibroblasts. An RNA strand encoding the four reprogramming factors, OCT-4, KLF-4, SOX-2 and GLIS1, induced extremely efficient reprogramming after a single transfection step without any viral intermediates or host genome integration. Once iPSCs were generated, the reprogramming RNA was selectively degraded by removing B18R from the culture media. The Simplicon™ platform simplifies gain-of-function analysis in cell types which are not amenable to plasmid transfection or lentiviral transduction. It can also be used for protein expression in rescue experiments after gene knockout or knockdown with CRISPR or RNAi methods. In this presentation we will review this cutting-edge technology and its application in basic research as well as drug screening efforts.
Title: “ddPCR as an orthogonal platform for NGS”

Room: MRB-G01 Time: 1:00 p.m. – 2:00 p.m. Sponsor: Bio-Rad

Presented by: Mario Aragon, PhD, BioRad Genomics Field Applications Specialist

Abstract: Next Generation Sequencing (NGS) excels as a discovery technique and is ideal for performing global analyses. By looking at all possible targets, NGS allows for the discovery of new molecules or pathways that were not known to have a specific biological function. However, once new targets have been identified, confirmation using an alternative testing platform is strongly recommended. Droplet digital polymerase chain reaction (ddPCR™) was developed to provide high-precision, absolute quantification of nucleic acid target sequences with a wide range of applications. Compared to traditional real time PCR, ddPCR has an increased signal-to-noise ratio and allows for the removal of PCR efficiency biases. As a result, ddPCR can be used to analyze events that require a high level of sensitivity. The advantages of ddPCR make it an ideal platform for orthogonal validation of NGS data.

Title: “Enhancing Transcript Detection Sensitivity for a Range of Sample Types”

Room: MRB-G03 Time: 1:00 p.m. – 2:00 p.m. Sponsor: New England Biolabs

Presented by: Siva Chavadi, Ph.D., Senior Field Applications Scientist

Abstract: The expanding range of RNA-seq applications and technologies increasingly face the challenge of extremes of very low input amounts and degraded samples. RNA samples can also include a large dynamic range of transcript expression, and highly expressed transcripts with minimal biological interest can dominate readouts, masking detection of more informative low-abundance transcripts. Our RNaseH-based method for depletion of abundant RNAs is optimized for high performance with FFPE samples as well as high quality inputs, and probe sets developed for this method include rRNA from human, mouse, rat and bacteria, as well as adult, fetal and embryonic globin transcripts from blood. For samples composed of single cells or picogram amounts of total RNA, detection of low-abundance transcripts is challenging but can be achieved by full-length transcript sequencing using a robust method incorporating template switching and enzymatic fragmentation to provide uniform transcript coverage.

Title: “TotalSeq™, Revolutionary Highly Multiplexed Protein Analysis in Single-Cell Multi-Omics”

Room: Tilgham Auditorium Time: 1:00 p.m. – 2:00 p.m. Sponsor: BioLegend

Presented by: Josh Croteau, PhD, Technical Applications Scientist II, BioLegend Inc

Abstract: Antibody-DNA Oligo conjugates are enabling a new era of single cell analysis. Single cell multiomics now allows for simultaneous profiling of RNA and protein from single cells. CITE-Seq (Cellular Indexing of Transcriptomes and Epitopes by Sequencing) and similar methods seamlessly integrate antibody-oligo conjugates with existing single-cell sequencing workflows allowing antibody directed quantification of cellular proteins simultaneously with the RNA transcriptome. BioLegend’s revolutionary TotalSeq™ oligo conjugated antibodies provide a standardized process for antibody directed protein characterization. This allows for measurement of cell surface proteins without the multiplexing limitation of fluorophores or heavy metals; more than 220 proteins currently. TotalSeq™ Cell Hashing antibodies also allow for sample multiplexing by targeting ubiquitously expressed surface proteins. TotalSeq™ Cell Hashing antibodies combined with antibody directed protein analysis enable extensive sample data cells incorporating targets from both the proteome and transcriptome of single cells. Join us to review the use of TotalSeq™ antibodies in exciting applications such as CITE-seq, and, how it interfaces with commercial scRNASeq solutions such as the 10X Genomics system with Feature Barcoding Technology™. We will discuss technical considerations, collaborator data, new products in development, and more.
GRCF Core Symposium Seminar Schedule
March 11, 2020, 10 a.m. – 2 p.m.

West Room

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MilliporeSigma
"Simplicon™"

1:00 p.m. – 2:00 p.m.

MRB-GO1

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MRB-GO3

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Christine Ladd-Acosta, PhD
"Identification of Autism risk factors: from genes to environment"

BioLegend
"TotalSeq™, Revolutionary Highly Multiplexed Protein Analysis in Single-Cell Multi-Omics"

For more information visit us at grcf.jhmi.edu