# 2018 SEASR Annual Meeting – June 27 – 29
# Emory Conference Center and Hotel - Atlanta, GA

# Welcome 2018 SEASR Annual Meeting!

As President of the Southeastern Association of Shared Resources (SEASR) I want to thank you for registering for the 2018 SEASR Annual Meeting. The meeting will be held at the Emory Conference Center Hotel and begins on Wednesday (6/27). The Emory Conference Center Hotel is located at 1615 Clifton Rd, Atlanta, GA 30329. The organizing committee is excited to bring to you a number of professional development,
scientific, and networking sessions that we hope meet your needs as a core director, administrator, manager, or staff member. Our strong vendor turnout will allow us to showcase the latest technologies and has also permitted us to offer free meeting registration. If you registered prior to this free meeting registration offer, you will be receiving a refund shortly. Please visit our website for the latest schedule of events: http://seasr.abrf.org/program-schedule

Below is some logistical information that may help you when you arrive.

**Parking**
Parking at the hotel is $15 per day.

**Badge Pickup**
You may pick up your badge at the SEASR meeting registration desk located in the Hearth Room from 11 am - 3 pm on Wednesday (6/27) or from 7:30 am-2 pm on Thursday (6/28). If you are attending the opening reception, we encourage you to pick up your badge on Wednesday as you will receive your drink tickets at that time.

**Pre-meeting Workshop**
If you arrive early on Wednesday, please join Cell Signaling Technologies for a free workshop entitled "Separating the truth from fiction in antibody validation" from 11am-3 pm at the Hotel in the Hickory Room. Lunch will be provided and you will be able to take part in an interactive roundtable discussion regarding best practices for working with antibodies.

**Opening Reception**
The Opening Reception will take place at the Wisteria Lanes on Wednesday evening from 6 - 9 pm. We will be serving complimentary drink tickets and light food. Don't forget to sign up for a bowling team when you register!

Please contact the SEASR Organizing Committee (oc@seasr.abrf.org) if you have any questions. I look forward to seeing you in Atlanta!

Sincerely

David Blum

David L. Blum, Ph.D
President, SEASR

# SEASR 2018 Annual Meeting - Emory Conference Center Hotel Schedule at a Glance

Wednesday, June 27 2018

| Start | End | Event | Location |
|---|---|---|---|
| 11:00am | 3:00pm | Registration Desk Open | Hearth Room (Upstairs) |
| 11:00am | 3:00pm | Pre-meeting Workshop<br>Cell Signaling Technologies | Hickory Room |
| 3:00pm | 12:00am | Exhibitor Setup | Vendor Hall (Salons III, IV, & V) & Lullwater Ballroom Foyer |
| 6:00pm | 9:00pm | Opening Reception | Wisteria Lanes (on site) |

Thursday June 28, 2018

| Start | End | Event | Location |
|---|---|---|---|
| 7:00am | 8:30am | Breakfast | Lullwater Ballroom Foyer |
| 7:30am | 2:00pm | Registration Desk Open | Lullwater Ballroom Foyer |
| 7:30am | 8:30am | Breakfast Workshop #1 - Ultra-sensitive Immunoassay Technology Platforms for Biomarker Detection, Quanterix | Hickory Room |
| 7:30am | 8:30am | Breakfast Workshop #2 – NGS quality control, Agilent Technologies | Mountain Laurel Room |
| 8:30am | 9:00am | Opening Remarks David Blum, Director, Bioexpression & Fermentation Facility, University of Georgia, President, Southeast Chapter, ABRF<br>Andy Chitty, Director, University Shared Resources at OHSU \| Oregon Health & Science University, President, ABRF | Salons I & II |
| 9:00am | 10:00am | Plenary Talk Kevin Knudtson, Director, Iowa Institute for Human Genetics, University of Iowa | Salons I & II |
| 10:00am | 10:30am | Coffee Break | Vendor Hall |
| 10:00am | 7:00pm | Exhibit Hall Open (Vendors Show) | Vendor Hall |
| 10:30am | 11:30am | Keynote Lecture - "Open Science"<br>Tim Errington, Lead of metascience activities, Center for Open Science | Salons I & II |
| 11:30am | 12:30pm | Lunch | Dining Hall |
| 12:30 | 1:00pm | Sponsored Lunch Workshop Best Practices to get reproducible data for extracellular vesicles research Beckman | Salons I & II |
| 1:00pm | 3:00pm | Professional Development Strategies to Launch your career to the next level - Staff | Hickory Room |

| | | | |
|---|---|---|---|
| | | Kim Dahlman, PhD, Assistant Professor of Medicine and Director, Innovative Translational Research Shared Resource, Vanderbilt University Medical Center | |
| 1:00pm | 3:00pm | Professional Development Strategies to Launch your career to the next level - Directors<br>Claudius Mundoma, Director, Physical Biochemistry Facility, Florida State University | Mountain Laurel Room |
| 3:00pm | 3:30pm | Coffee Break | Vendor Hall |
| 3:30pm | 4:30pm | Promoting reproducible omics research to increase likelihood of successful clinical translation.<br>Lisa McShane, Acting Associate Director, Division of Cancer Treatment and Diagnosis, Biometric Research Program, National Cancer Institute, NIH | Salons I & II |
| 4:30pm | 5:30pm | Quality Systems Primer and How to write SOPs<br>Michael Hellerstein, President, Hellerstein Consulting, LLC | Salons I & II |
| 5:30pm | 7:00pm | Poster Session (Wine and Hors D'oeuvres) | Garden Overlook |

Friday June 29, 2018

| Start | End | Event | Location |
|---|---|---|---|
| 7:00am | 8:30am | Breakfast | Lullwater Ballroom Foyer |
| 7:30am | 8:30pm | Breakfast Workshop #3 - Swift and Easy Library Preparation Swift | Hickory Room |
| 7:30am | 8:30pm | Breakfast Workshop #4 Cyagen | Mountain Laurel Room |
| 8:00am | 12:00pm | Exhibit Hall Open (Vendors Show) | Vendor Hall |
| 8:30am | 9:30am | Keynote Lecture - Biomedical research reproducibility: many dimensions and shared responsibilities<br>Lisa McShane, Acting Associate Director, Division of Cancer Treatment and Diagnosis, Biometric Research Program, National Cancer Institute, NIH | Salons I & II |
| 9:30am | 10:30am | Understanding the Science Behind Branding When Branding for Science<br>Chris Dillon, Director of Communications, ICBR/University of Florida | Salons I & II |
| 10:30am | 11:00am | Coffee Break | Vendor Hall |
| 11:00am | 12:00pm | Get the data where you want it, when you want it there: High Throughput WGS Mapping and Calling Using AWS Rich Johnston, Ph.D., Core Director, Emory Integrated Computational Core | Hickory Room |
| 11:00am | 12:00pm | Dealing with external customers David Blum, Director, Bioexpression & Fermentation Facility, University of Georgia | Mountain Laurel Room |

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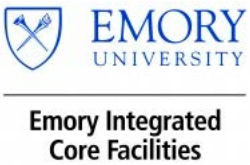
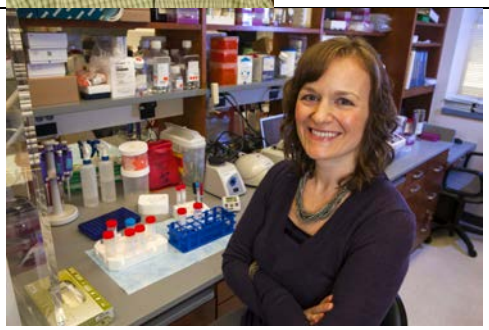
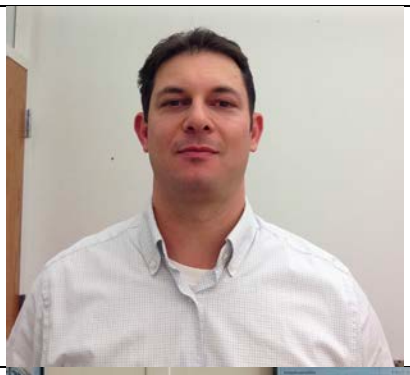



## Institutional Silver Sponsors


## Institutional Bronze Sponsor

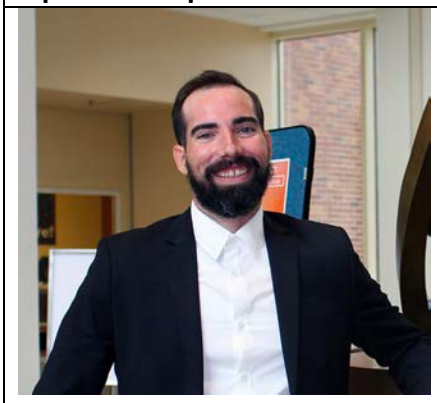
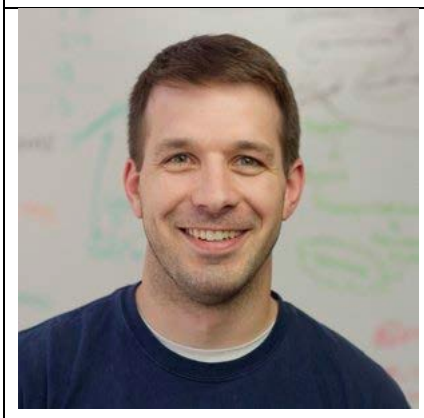
# SEASR Organizing Committee

| | |
|---|---|
| David Blum, President<br>University of Georgia<br>Director, Bioexpression and Fermentation Facility |  |
| Kim Dahlman, President- Elect<br>Vanderbilt University<br>Assistant Professor, Department of Cancer Biology<br>Director, Innovative Translational Research Shared Resource |  |
| Thayumanasamy Somasundaram, Treasurer<br>Florida State University<br>Director, IMB X-Ray Facility |  |
| Susan Constable, Secretary<br>Moffitt Cancer Center<br>Manager, Basic Science Shared Resources |  |

| | |
|---|---|
| Jason Goldstein, Sponsor Coordinator<br>Annular Biotechnology<br>Founder |  |
| Dennis A. Bagarozzi, Jr.<br>Centers for Disease Control and Prevention<br>Branch Chief, Reagent and Diagnostic Services |  |
| Steven Madore<br>University of Florida ICBR<br>Associate Director of Science |  |
| Claudius Mundoma<br>Director, Physical Biochemistry Facility<br>Florida State University |  |

| | |
|---|---|
| Michael Zwick<br>Emory University<br>Assistant Vice President for Research |  |

# Speaker Biographies

| Speaker photo | Speaker Biography |
|---|---|
|  <br>Chris Dillon | Chris Dillon is the Communications Director for the University of Florida's Interdisciplinary Center for Biotechnology Research (UF ICBR). Chris first arrived at the University of Florida in 2011, serving as the Communications Coordinator to the Vice Principal of Development & Alumni Affairs for the $1.72B Florida Tomorrow Campaign. The following year, he would go onto serve as Strategic Project Manager at the University of Florida Foundation with a focus on branding, development and UFF Board engagement. In 2016, he took over the communications department at UF ICBR, emphasizing the center's rebranding project, website redesign and marketing efforts. |
|  <br>Tim Errington | Tim is lead of metascience activities at the Center for Open Science (COS; https://cos.io) that aims to increase openness, integrity, and reproducibility of scientific research. In that position he collaborates with researchers and stakeholders across scientific disciplines and organizations to design, implement, and analyze projects aimed to understand the current research process and evaluate initiatives designed to increase reproducibility and openness of scientific research.<br>He is currently spearheading the Reproducibility Project: Cancer Biology (https://osf.io/e81xl/wiki/home/), which is a collaboration between COS and Science Exchange, with eLife as the publisher, to independently replicate selected results from a substantial number of high-profile papers in the field of cancer biology. The project will provide evidence about reproducibility in cancer biology research, and to identify factors that influence reproducibility more generally. Tim received his PhD in Microbiology, Immunology, and Cancer Biology from the University of Virginia, MA in Molecular and Cell Biology at UC Berkeley, and earned a BS in Biology and Chemistry at St. Lawrence University. |

| | |
|---|---|
|  <br>Mike Hellerstein | Mr. Hellerstein serves as Director of Regulatory Affairs and Quality Systems at GeoVax, a clinical-stage biotechnology company developing vaccines against infectious diseases and cancers. He also applies his expertise in quality and regulatory affairs in his part-time consulting business, Hellerstein Consulting, which assists biotech startups and university labs. Initially trained as a molecular biologist, Mr. Hellerstein joined GeoVax in 2005 and has progressively expanded his job responsibilities. He has managed quality control since 2006, quality systems since 2007, outsourced manufacturing since 2008, regulatory affairs since 2014, and project management and government contracting since 2015. He founded Hellerstein Consulting in 2012. Prior to joining GeoVax, Mr. Hellerstein worked at several companies including Pfizer, Cell Signaling Technology, and Blue Sky Biotech, which he co-founded. Mr. Hellerstein obtained his A.B. in biology from Harvard University in 1999. |
|  <br>Rich Johnston | Rich received his PhD from the Johns Hopkins University Institute of Genetic Medicine. His area of expertise is in whole genome sequencing and population genetics. He is currently working on projects to leverage Emory cloud-based computing resources for bioinformatics. |
|  <br>Kevin Knudtson | Kevin Knudtson received his PhD from Iowa State University and was a post-doctoral fellow at the University of Utah prior to accepting a position at the University of Iowa that included directing their DNA Sequencing Facility. His facility has since grown and has expanded to serve both the basic research community in supporting their genomics-based studies and the clinical community in providing NGS-based clinical genetic testing. He is currently the Director of the Genomics Division of the Iowa Institute of Human Genetics. He has also been an active member of the ABRF for over 17 years and has served on numerous ABRF research groups and committees. He is currently the chair of the Committee on Core Rigor and Reproducibility. |

Lisa McShane

Lisa Meier McShane, Ph.D., is an Acting Associate Director for the Division of Cancer Treatment and Diagnosis (DCTD), U.S. National Cancer Institute, National Institutes of Health. Dr. McShane heads the Biometric Research Program (BRP) within DCTD. BRP comprises the Biostatistics and Computational and Systems Biology Branches with members including statisticians, bioinformaticians, and computational biologists. Dr. McShane is internationally recognized for her expertise on development of tumor markers for prognosis, therapy selection, and disease monitoring; omics-based predictors for clinical use; and reporting guidelines for health research studies. She holds a Ph.D. in Statistics from Cornell University and is a Fellow of the American Statistical Association. Her statistical research interests include biomarker-driven clinical trial design, analysis of high-dimensional omics data, multiple comparisons methods, surrogate endpoints, measurement error models, and biomarker assay analytical performance assessment. She co-led efforts to develop "Reporting guidelines for tumor marker prognostic studies (REMARK)" and "Criteria for the use of omics-based predictors in clinical trials." She has coauthored numerous statistical and biomedical papers and the book *Statistical Design and Analysis of DNA Microarray Investigations*.

Dr. McShane serves on the Scientific Advisory Board for *Science Translational Medicine* and the Editorial Board for *BMC Medicine*. She has served on American Society of Clinical Oncology committees that developed guidelines for *HER2* and hormone receptor testing in breast cancer, *EGFR* mutation testing in lung cancer, and biomarkers in early stage breast cancer. She has served as a member of the Institute of Medicine *Committee for Management of the Air Force Health Study Data and Specimens*, the *Consensus Committee on Management of the Air Force Health Study Data and Specimens-Report to Congress*, and the *Committee on the State of the Science in Ovarian Cancer Research*.

# Abstracts

#1
**Affiliation:**
Emory University
**Poster Travel Award:**
No
**Authors and Affiliations:**
Daniel J. Kota, Emory University; Marco A. Garcia, Emory Healthcare; Shahnaz Akbarpour, Emory Healthcare; Muna Qayed, Emory University
**Topic:**
Technical
**Poster Title:**
Emory Personalized Immunotherapy Core
**Poster Abstract Text:**
The Emory Personalized Immunotherapy Core (EPIC), one of the Emory Integrated Core Facilities (EICF), was created to foster development of cellular pharmaceuticals and biotherapies for the treatment of human catastrophic illnesses. From conception to execution, EPIC offers a variety of services to help translate cellular products from research into clinical application.

#2
**Affiliation:**
Illumina, Inc.
**Poster Travel Award:**
No
**Authors and Affiliations:**
Anu Khanna1, Joshua Burgess1, Steve Bruinsma1, Daniel Schlingman1, Agata Czyz1, Natalie Morrell2, Katie Ballenger1, Heather Meinholz1, Lindsay Freeberg1, Rooz Golshani3, Haiying Grunenwald1, Niall Gormley2 , and Gary P Schroth3 Illumina, Madison, WI1; Illumina, Chesterford, UK2; Illumina, San Diego, CA3
**Topic:**
Technical
**Poster Title:**
NexteraTM DNA Flex: A revolutionary library preparation method for Whole Genome Sequencing
**Poster Abstract Text:**
The Nextera DNA Flex Library Preparation Kit features a revolutionary workflow that combines DNA extraction, quantitation, fragmentation, and library normalization to deliver the fastest and most flexible library prep workflow in the Illumina portfolio for WGS. This method uses a novel On-Bead Tagmentation chemistry that supports a wide range of DNA input amounts and sample types and also eliminates the need for separate DNA extraction of whole blood and saliva. On-Bead Tagmentation has produced major improvements in library preparation performance, yielding libraries with highly uniform and consistent insert sizes (300–350 bp) across a wide DNA input range (1-500 ng) without careful transposome:DNA ratio optimization as a means of controlling fragment length. On-Bead Tagmentation also delivers uniform and consistent library yields across a wide DNA input range (100-500 ng); at 100 ng DNA input, beads become saturated, leading to consistent, normalized yields, thereby eliminating the need for time-consuming library quantitation and normalization steps before pooling for sequencing. Beyond the workflow improvements supported by bead-based technology, the most significant

advantage of consistent and uniform insert sizes and library yields is more even and uniform coverage across the genome for both human and nonhuman species. Even genomes with high or low GC content show remarkably even coverage without region-specific bias. The extended applications of the kit include colony-direct library prep from microbial genomes of difficult composition, reduced input, PCR amplicons, and FFPE DNA. Nextera DNA Flex is a user-friendly, automation compatible workflow and has been optimized for performance across all Illumina sequencing platforms.

#3
**Affiliation:**
Agilent Technologies
**Poster Travel Award:**
No
**Authors and Affiliations:**
Eva Graf, Agilent Technologies; Zsuzsanna Mayer, Kimberly Krueger, Abel Bronkhorst, Stefan Holdenrieder, German Heart Center Munich
**Topic:**
Technical
**Poster Title:**
Sample quality control of cell-free DNA
**Poster Abstract Text:**
Sequencing of cell-free DNA (cfDNA) extracted from blood specimens or other body fluids is possible due to the establishment of low input library protocols for next-generation sequencing workflows. Accurate quantification of cfDNA samples is essential to determine suitable input amounts for cfDNA library preparation prior to sequencing. The main component of cfDNA samples is the mononucleosome with a size around 170 bp, sometimes with additional species representing nucleosome multimers. Further, cfDNA samples may contain larger DNA fragments dependent on preanalytical sample treatment or extraction method. High molecular weight material can negatively influence library preparation and subsequently result in lower sequencing depth. Therefore, reliable quantification of cfDNA requires a method that separates DNA fragments by size, such as electrophoresis. This poster shows the use of an automated electrophoresis platform performing cfDNA quantification with region analysis. Moreover, the results include sample purity as a score to qualify cfDNA samples according to their contamination level with high molecular weight material. The analysis features are described with examples of typical sample patterns.

#4
**Affiliation:**
ForteBio
**Poster Travel Award:**
No
**Authors and Affiliations:**
ForteBio
**Topic:**
Technical
**Poster Title:**
Fragment screening process improvement with Pioneer FE and dynamic injection SPR
**Poster Abstract Text:**
Fragment-based drug design (FBDD) has become an increasingly popular platform for the identification and design of lead candidates in drug discovery programs. The detection and characterization of

chemical fragment binding events is facilitated by sensitive biophysical technologies capable of detecting low affinity interactions of low molecular weight compounds

#5
**Affiliation:**
Vanderbilt-Ingram Cancer Center; Vanderbilt University Medical Center
**Poster Travel Award:**
Yes
**Authors and Affiliations:**
Jamye F. O'Neal, Vanderbilt University Medical Center; Heather Barnes, Vanderbilt University Medical Center; Kimberly B. Dahlman, Vanderbilt University Medical Center
**Topic:**
Administrative
**Poster Title:**
Tracking biospecimen collection deviations to improve clinical trial outcomes
**Poster Abstract Text:**
Biospecimen collection deviations are detrimental to clinical trial outcomes and operations; they may result in spurious data, are costly, time-consuming, and may be inconvenient to patients. As a result, it is necessary to systematically track these deviations in order to identify when, and to what extent, they are occurring. Historically, the clinical trials management system used by the Vanderbilt-Ingram Cancer Center (VICC) did not have a convenient method for extracting these data for comprehensive analyses. The objective of our project was to create a better system for tracking and extracting deviated biospecimens data. Furthermore, it was important to learn whether or not deviations were occurring, and if so, how often, what type, and, what action was needed to reduce deviation frequency. Using the REDCap reporting tool, we built and launched a database that included 17 cancer groups and their respective studies across 22 different Vanderbilt University Medical Center clinic locations. Data from 494 REDCap records collected from February 2016 through January 2018 were analyzed. During this timeframe, across a total of 166 studies, 24,763 parent samples were slated for collection. The data revealed that 4.6% (n = 1,130) of all parent samples were deviated. The most common reasons for biospecimen collection deviations were: (1) untimely sample processing (23.8%; n = 132), (2) missed sample collections within clinics (17.3%; n = 96), and (3) inadequate notification of specimen collection scheduling by research teams (11.7%; n = 65). For the first time, we have a comprehensive overview of total biospecimen collections and deviations collected by the Clinical Trials Processing Core at the VICC. We are refining and automating our collection and analysis methods as well as performing cost analyses to determine what resources are lost due to deviations. These initiatives will improve the quality and standards of the clinical trials enterprise at the VICC.

#6
**Affiliation:**
NuGEN Technologies, Inc.
**Poster Travel Award:**
No
**Authors and Affiliations:**
Marissa Cooke, Benjamin Schroeder, Zulfiqar Gulzar, I-Ching Wang, Lin Pham and Douglas Amorese
**Topic:**
Technical
**Poster Title:**
Customized Depletion of Unwanted Transcripts from RNA-Seq Libraries

**Poster Abstract Text:**
RNA-Seq has become a standard NGS tool for many avenues of research. There are, however, many variations to the technique, such as total RNA vs poly-A selected RNA input, methods of ribosomal RNA depletion, and various methods of maintaining strand orientation. Here we describe a flexible, modular workflow for generating RNA-Seq libraries from any organism. Users can select an upfront poly-A isolation module, or use total RNA as input. A high complexity, stranded library is generated from the core module using a mixture of oligo dT and random priming, resulting in complete 5' to 3' coverage of transcripts. Libraries can be sequenced directly, or further processed with a transcript depletion module. Targeted depletion of highly expressed transcripts can decrease sequencing costs and enrich low expressing transcripts which may be more biologically informative. Ribosomal transcripts are commonly targeted for depletion; however our method is capable of depleting any cDNA fragment from the sequencing library without affecting the other remaining cDNA fragments, due to the coupling of a simple oligonucleotide probe with enzymatic targeting specificity. For example, we have successfully applied this workflow to deplete globin transcripts from poly-A selected mRNA derived human whole blood. In another example of the utility of this modular, customizable workflow we show successful depletion of the 4 most abundant External RNA Controls Consortium (ERCC) spike-in transcripts, which comprise 70% of the total ERCC reads. Depletion of these highly abundant ERCC transcripts resulted in a 2 fold enhancement of low expressing ERCC transcript representation, making them detectable with less than 4 million reads. Depletion of highly abundant, non-informative transcripts provides the investigator with a cost-effective method to detect low expressing transcripts which are biologically relevant to the experimental hypothesis.

#7
**Affiliation:**
Georgia Institute Of Technology
**Poster Travel Award:**
No
**Authors and Affiliations:**
Anton Bryksin Naima Djeddar Shweta Biliya
**Topic:**
Technical
**Poster Title:**
Molecular Evolution and High Throughput DNA Sequencing
**Poster Abstract Text:**
Certain techniques of molecular evolution – the generation and selection of functional molecules using biological mechanisms "in the test tube" – are well established, but still only used by a limited number of laboratories. Principal examples include phage display, SELEX, and yeast hybrid selection methods. These techniques provide an access to peptides and polynucleotides with an enormous range of properties. Many labs often desire to gain access to such tools, but make do without them because often it is too difficult and time consuming to get the project off the ground. The underlying principle for Molecular Evolution core facility is to serve as a hub for routine access to these methods in conjunction with next generation sequencing. Our hope is that an easy access to these techniques will serve as the starting point for new ways of inventing catalysts, therapeutic agents, and functional materials in many labs.

#8
**Affiliation:**
Nexcelom Bioscience

**Poster Travel Award:**
No
**Authors and Affiliations:**
Leo Chan and William Rice-- Nexcelom Bioscience, Lawrence MA John Tigges, Eric S. Zigon, Vasilis Toxavidis-- Beth Israel Deaconess Medical Center, Flow Core, Boston MA
**Topic:**
Technical
**Poster Title:**
Validating and optimizing single cell sorting of FACS using Celigo image cytometry
**Poster Abstract Text:**
One of the major applications that is commonly performed on a fluorescence activated cell sorting (FACS) instrument is single cell sorting. Single cell sorting application is mainly used for research such as cell line development to ensure monoclonality for protein production. In addition, regenerative medicine often uses single cell sorting to study stem cell proliferation from single cell to single colony. Currently, single cell sorting is validated via light microscopy several days after initial sorting, where the cells have grown into an observable colony. However, manual observation using microscopy is highly tedious and time-consuming. Therefore, there is a need for a high-throughput, practical, and accurate detection to validate and optimize single cell sorting of FACS. In this work, we demonstrate a novel high-throughput detection method to validate and optimize single cell sorting using the Celigo Image Cytometry (Nexcelom Bioscience, Lawrence, MA). The instrument was used to image the entire well of all 96 wells on a microplate to detect a single object sorted into the well in less than 4 min. Initially, the FACS (MoFlo Astrios EQ) was used to sort single green fluorescent bead into multiple 96-well microplates in two separate experiments. The microplates were used without any buffer, thus the number and location of beads can be accurately detected. Next, the results from the two experiments showing a sort efficiency of 82 and 90% were used to optimize the FACS to increase the efficiency closer to 100%. The ability to rapidly detect single cell in multi-well microplates is highly important to both flow core laboratories to optimize their sorting instruments as well as to the users, who would like to confirm single cell in each well. The proposed method can highly improve the efficiency of work flow for both flow core managers and users.

#9
**Affiliation:**
University of Florida
**Poster Travel Award:**
Yes
**Authors and Affiliations:**
Mengde Cao, University of Florida; Ning Zhu, University of Florida; Jin Koh,University of Florida; Ran Zheng,University of Florida; Fanchao Zhu,University of Florida; Sixue Chen, University of Florida
**Topic:**
Technical
**Poster Title:**
Targeted Mass Spectrometry (MRM or SRM) Applications in Biological and Medical Research
**Poster Abstract Text:**
Multiple reaction monitoring (MRM, also known as Selective Reaction Monitoring – SRM) is a highly specific and sensitive mass spectrometry technique that can selectively quantify compounds such as proteins, peptides, amino acids, hormones, vitamins, metabolites, and lipids from plasma, serum, urine, hair and other biological samples. This technique uses a triple quadrupole MS that firstly targets the ion corresponding to the compound of interest with subsequent fragmentation of that target ion to produce

a range of daughter ions. One (or more) of these fragment daughter ions can be selected for quantitation purposes. Only compounds that meet both these criteria, i.e. specific parent ion and specific daughter ions corresponding to the mass of the molecule of interest are isolated within the mass spectrometer. By ignoring all other ions that flow into the mass spectrometer the experiment gains sensitivity, whilst maintaining exquisite accuracy. We developed highly sensitive and selective quantitative assays with MRM for small molecule detection from marijuana-derived and tobacco-derived samples using Thermo Scientific™ TSQ Altis Triple Quadrupole Mass Spectrometry coupled with Vanquish horizon ultra-high performance liquid chromatography-electrospray (UHPLC-ESI-MS-MS) and ABI 4000 QTrap Triple Quadrupole Mass Spectrometer with Agilent 1200 HPLC system. We successfully detected sample specific metabolites, including THC, OH-THC, COOH-THC, CBD and CBN from marijuana-derived sample and nicotine and cotinine from tobacco-derived, 20 amino acids, peptides, 13 plant hormones and other targeted compounds. Results showed good reproducibility in the MRM analyses, and high consistency in the targeted quantitation results for different targeted compounds with our established assay methods. The MRM as a highly reliable technique can be broadly applied in biological and medical research.

#10

**Affiliation:**

University Of Florida

**Poster Travel Award:**

Yes

**Authors and Affiliations:**

Jin Koh, University of Florida Sung O. Park, University of Florida Mi-Jeong Yoo, University of Florida Sixue Chen, University of Florida Peter P. Sayeski, University of Florida

**Topic:**

Technical

**Poster Title:**

Proteomic profiling in hematopoietic tissues of Jak2 conditional knock-out mice

**Poster Abstract Text:**

Janus Kinase 2 (Jak2) is essential for mammalian life, hence germline deletion of Jak2 in mice results in embryonic lethality at E12.5 due to impaired hematopoiesis. In our early study, deletions of Jak2 at various stages of prenatal and postnatal life were demonstrated by using of conditional knockout of Jak2. Specifically, deletion of Jak2 beginning at E12.5 resulted in 100% embryonic death characterized by a lack of hematopoiesis. Furthermore, deletion of Jak2 in young adults was characterized by blood cytopenias, abnormal erythrocyte morphology, decreased marrow hematopoietic potential, and splenic atrophy. However, adult death rate was observed in only 20% of the mutant mice. Furthermore, our analysis of these mice suggested that the increased survivability was due to an incomplete deletion of Jak2 and subsequent re-population of Jak2 expressing cells. Since Jak2 dependent-protein expressions were regulated at several stages after transcriptions, observing mRNA transcriptional levels does not correlate a full picture of the effects of genetic alterations on the protein output. Thus, we conducted comprehensive, quantitative proteomic analysis in key points of hematopoietic status from Jak2 deficient mice. Briefly, multiple populations of protein samples from adult bone marrow and fatal liver among 2 genotypes, 4 different mouse stages were compared. These tissue proteins were subjected to 8-plex iTRAQ, which gives ratios of the levels of each labelled form of peptides, and subsequently yield quantitative proteomic information. Based on the data set, anticipated large scope of Jak2-dependent bioinformatics data sets will be evaluated to determine how Jak2 deficient alterations affect protein levels in hematopoietic tissues.

#11
**Affiliation:**
University Of Florida
**Poster Travel Award:**
Yes
**Authors and Affiliations:**
Jin Koh, University of Florida Mengde Cao, University of Florida Ran Zheng, University of Florida Ning Zhu, University of Florida Fanchao Zhu, University of Florida Sixue Chen, University of Florida
**Topic:**
Technical
**Poster Title:**
Proteomics and Mass Spectrometry Applications in Biological and Medical Research
**Poster Abstract Text:**
Proteomics and mass spectrometry have provided unprecedented tools for fast, accurate, high throughput biomolecular separation and characterization, which are indispensable towards understanding the biological and medical systems. Studying at the protein level allows researchers to investigate how proteins, their dynamics, modifications, and interactions affect cellular processes and how cellular processes and environment affect proteins. The mission of our facility is to provide excellent service and training in proteomics and mass spectrometry. Here we present our capabilities in proteomics, highlighting differential proteomics, which include two-dimensional difference gel electrophoresis (2D-DIGE), isobaric tags for relative and absolute quantitation (iTRAQ), tandem mass tags (TMT), iodoTMT, Stable isotope labeling with amino acids in cell culture (SILAC), quantification of proteins by label-free LC-MS/MS, and the analysis of protein post translational modifications (PTM). Along with the capacity of separating thousands of proteins and characterizing differential protein expression, we have a suite of state-of-the-art mass spectrometers available for biomedical sciences and advanced technology research.

#12
**Affiliation:**
University Of Florida
**Poster Travel Award:**
Yes
**Authors and Affiliations:**
Haeyoung Shin, Logos Biosystems Inc. Jin Koh, University of Florida Sung Olivia Park, Logos Biosystems Inc.
**Topic:**
Technical
**Poster Title:**
Make tissue Clearing Simple, Rapid, and reproducible with the X-CLARITY
**Poster Abstract Text:**
X-CLARITY™ is a tissue clearing method developed by the Deisseroth lab at Stanford University and based on Clear Lipid-exchanged Acrylamide-hybridized Rigid Imaging / Immunostaining /in situ-hybridization-compatible Tissue hYdrogel. Tissues are inherently three dimensional in nature, which makes imaging intact tissues a necessity for a more complete studies into the relationship between structure and function and the system-level study of cellular mechanisms. Conventional sectioning and microscopic method is extremely time and labor -consuming histological process but this method has been extensively used for decades. Tissue clearing as relevant and enhanced process has become an important step for imaging tissues in 3D at single-cell resolution. In summary of the X-CLARITY™ process,

tissues are embedded in a hydrogel matrix and lipids are actively extracted through electrophoresis to create a stable and optically transparent tissue-hydrogel hybrid that is chemically accessible for multiple rounds of antibody labeling and imaging. Native cytoarchitecture remains intact and even endogenous fluorescence proteins are well preserved for robust fluorescence imaging downstream. The X-CLARITY™ system which is a collection of systems to standardize, simplify, and accelerate of the tissue clearing process.

#13
**Affiliation:**
Emory Integrated Computational Core
**Poster Travel Award:**
No
**Authors and Affiliations:**
Rich Johnston, Emory University; Viren Patel, Emory University; Ashok Dinasarapu, Emory University; Wayne Harris, Emory University; Michael Zwick, Emory University
**Topic:**
Administrative
**Poster Title:**
Emory Integrated Computational Core
**Poster Abstract Text:**
The Emory Integrated Computational Core (EICC) is a member of the Emory Integrated Core Facilities. The EICC is comprised of a cross-disciplinary team of bioinformatics, statistics, and computing experts. We work closely with other data generating cores and researchers to provide complete data analysis workflows. These include data download and delivery, QC and analyses using standard software and pipelines, data storage and backup, and data submission to national repositories.

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