



2023 Northeast Regional Laboratory Staff and Core Directors Meeting
October 18th-20th
Hilton Burlington Lake Champlain Hotel
Burlington, VT

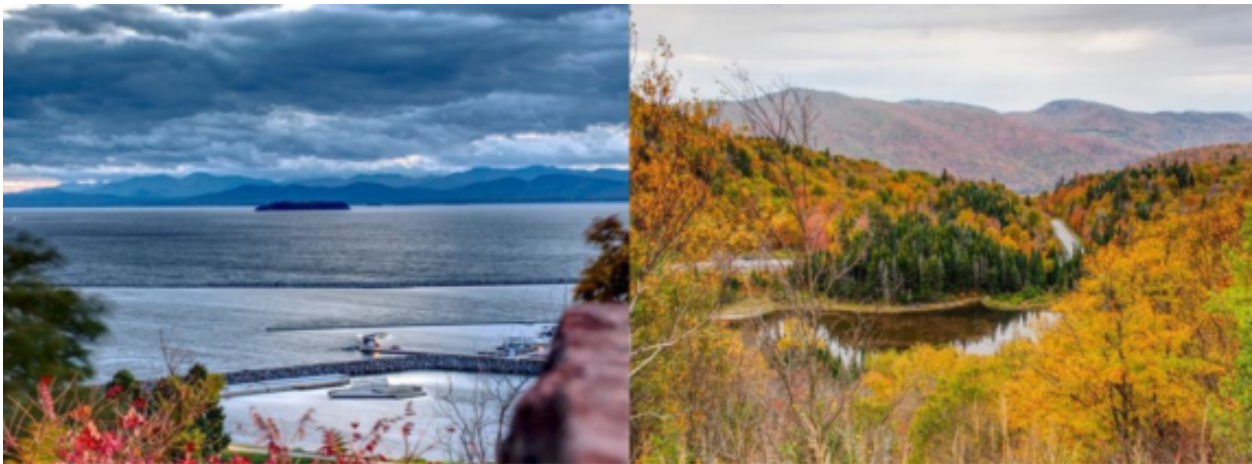


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Welcome to NERLSCD 2023

Thank you for joining us for the 18th annual meeting of the Northeast Regional Laboratory Staff and Core Directors (NERLSCD) meeting.

This year's meeting is hosted by the University of Vermont Burlington, VT, at the Hilton Burlington Lake Champlain, Burlington, VT, USA. This year's meeting continues the grand tradition started at the first meeting, held at Cornell University, Ithaca, NY, USA, of presenting an outstanding regional forum for core facility administrators, directors, managers, and staff. The meeting offers opportunities to network with colleagues, to learn about biotechnology advances and applications, and to discuss the challenges of implementing shared research resources.

This meeting would not be possible without the support of our speakers, who have graciously donated their time to come and share their experiences with us. Active discussion and participation by all meeting attendee's is one of the hallmarks of the NERLSCD meeting, and we encourage you to continue that traditions.

A meeting of this nature cannot be held without the generous support of our partners and sponsors. Their financial support is crucial for the continued success of this meeting. Take time to browse the 40 exhibitors who are here for this meeting.

Sincerely,

The NERLSCD Organizing Committee

NERLSCD 2023 Organizing Committee

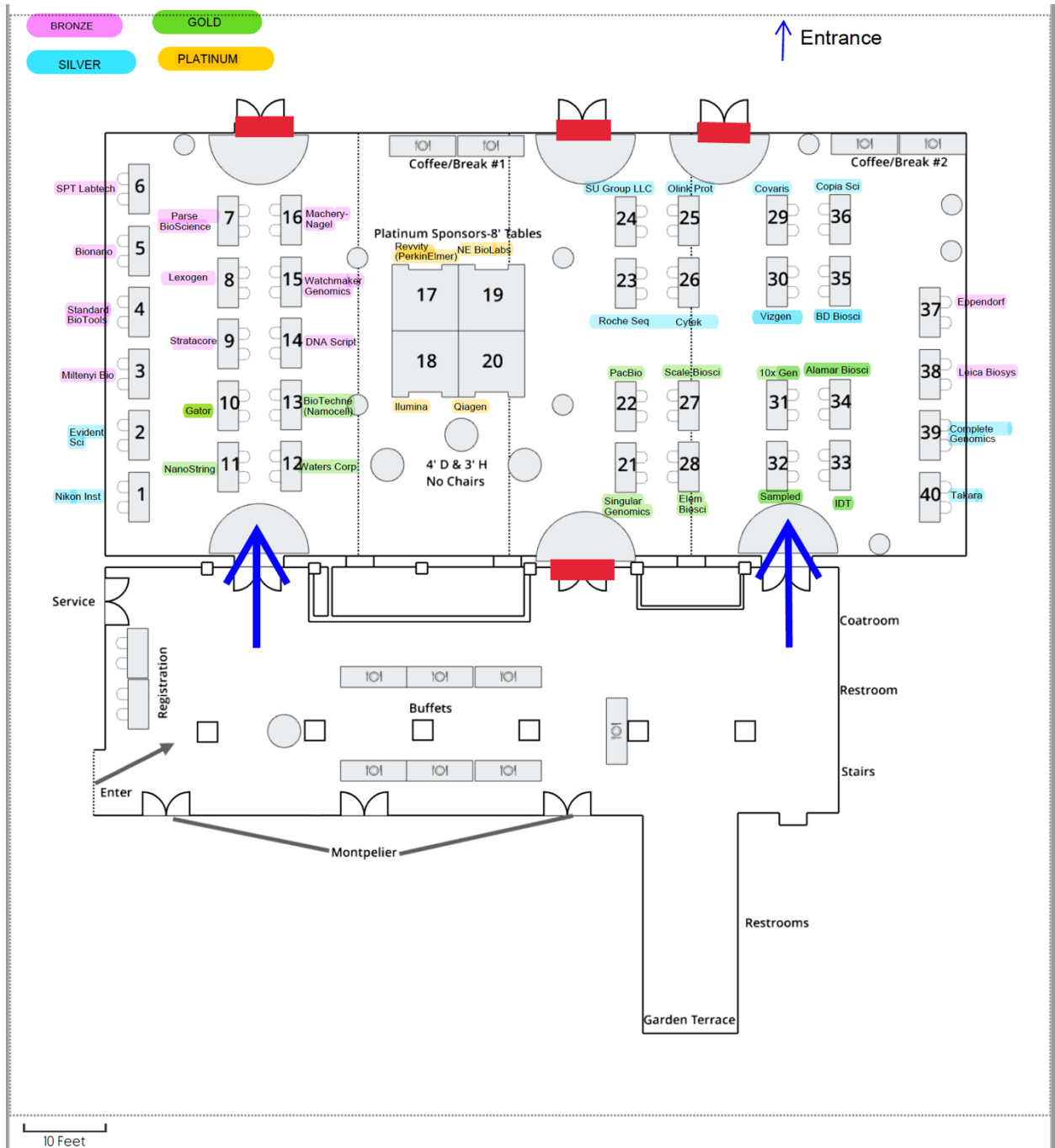
Meeting Hosts

<p>Julie Dragon Director, Vermont Integrative Genomics Resource Director, Vermont Biomedical Research Network Data Science Core University of Vermont Burlington, VT</p>	<p>Roxana del Rio-Guerra Flow Cytometry and Small Particle Detection Facility Director Center for Biomedical Shared Resources University of Vermont/Larner College of Medicine Burlington, VT</p>
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Organizing Committee

<p>President Stuart Levine Director, MIT BioMicro Center Massachusetts Institute of Technology Cambridge, MA</p>	<p>Treasurer/ Webmaster Tim Bushnell Director, Center for Advanced Research Technologies Scientific Director, Flow Cytometry Resource</p>
<p>Corporate Liaison Shahina Maqbool Director, Epigenomics Shared Facility Albert Einstein College of Medicine, Bronx, NY</p>	<p>Corporate Liaison Robert Steen Director, Biopolymers Facility Department of Genetics Harvard Medical School, Boston, MA</p>
<p>Webmaster Andrew Vinard, Core Facilities Director Institute for Applied Life Sciences University of Massachusetts, Amherst, MA</p>	<p>Christian Lytle, Administrative Coordinator for Shared Resources Laboratory Manager, Molecular Biology & Proteomics Core Facility Norris Cotton Cancer Center Geisel School of Medicine at Dartmouth Hanover, NH</p>
<p>Academic Liaison Susanna Perkins Director, Research Cores and Operations Research Core Administration Office of Research University of Massachusetts Chan Medical School, Worcester, MA</p>	<p>John Ashton Genomics Research Center Director Functional Genomics Resource Director Wilmot Cancer Institute Shared Scientific Resources Rochester, NY</p>
<p>Robert Donnelly Director, NJMS Molecular Resource Facility Rutgers Biomedical and Health Sciences The State University of New Jersey Newark, NJ</p>	<p>Dan Mielcarz Director, Immune Monitoring and Flow Cytometry Shared Resource Dartmouth Cancer Center Lebanon, NH</p>
<p>W. Kelley Thomas Director, Hubbard Center for Genome Studies University of New Hampshire Durham, NH</p>	<p>Host 2024 Sridar Chittur Director, Microarray & HT Sequencing Core State University of New York Albany, NY</p>
<p>Host 2024 Marimar Lopez Director Research Cores Rensselaer Polytechnic Institute Albany, New York</p>	<p>Host 2024 Richard Cole Director Light Microscopy & Image Analysis Core Wadsworth Center NYS Department of Health New Paltz, NY</p>

Sponsor Exhibition Room (Adirondack)-Layout



NERLSCD 2023 PROGRAM

Registration from Wednesday, Oct-18th at noon time through Friday, Oct-20th at noon time.

WEDNESDAY, OCT-18TH

Pre-Meeting Workshops

1:00-2:30 pm

- Illumina (Montpelier A): Interactive user group discussion with the local Illumina technical team.
- New England Biolabs (NEB) (Montpelier C): New tools and techniques for your NGS toolbox: the latest additions to the NEBNext family of products for NGS library prep.

2:30-4:00 pm

- QIAGEN (Montpelier A): Advances in sample preparation through NGS & dPCR detection from liquid biopsy samples.
- Revvity (PerkinElmer) (Montpelier C): Single cell RNA sequencing workshop.

UVM-Larner College of Medicine Core Tours

2:00 pm to 4:00 pm

University of Vermont, Larner College of Medicine-Center for Biomedical Shared Resources (CBSR), Firestone Bldg.-First Floor, 149 Beaumont Avenue, Burlington, VT

Opening reception

6:00 pm – 9:00 pm

-At ECHO Leahy Center for Lake Champlain. 1 College St, Burlington, VT. At walking distance from the Hilton Hotel.

THURSDAY, OCT-19TH

9:00 am WELCOME TO NERLSCD 2023

9:30 am: Keynote 1

Rita Colwell. “Oceans, climate, and human health: cholera as a model for global pandemics”. (@ Green Mountain)

10:15 am: Platinum talk: Qiagen. Speed up and simplify your RNA and DNA biomarker workflows using NGS and digital PCR. (@ Green Mountain)

10:30 am: Morning break and Networking (@ Adirondack)

10:45 am: Round-table

Valeria Mezzano-Robinson (NYU Langone) and Nicole Contaxis (NYU Langone). Data management and data sharing: What is the role of Shared Research Resource Facilities/Cores? (@ Green Mountain)

11:45 am: Platinum talk: NEB. Streamlined for speed: new library prep for DNA & RNA. (@ Green Mountain).

12:00 pm: LUNCH and Networking (@Montpelier and Adirondack)

1:30 pm: Concurrent Breakout Sessions, 1 hr./vendor talk 10 minutes

1) Genomics

Scott Tighe (U of Vermont). Implementation of Long Read Sequencing and Data Analysis in Core Facilities. (@ Green Mountain)

Vendor talk: PacBio. Game-changing products for high accuracy sequencing. (@ Green Mountain)

2) Flow-Informatics

Tim Bushnell (U. of Rochester MC). Evaluating flow cytometry software. (@ Montpelier A)

Vendor talk: Bio-Techne (Nanocell). Empowering single cell workflow with fast and gentle single cell sorting. (@ Montpelier A)

3) Imaging

Doug Taatjes (U. of Vermont). Reproducibility in publishing microscopy imaging data. (@ Montpelier B)

Vendor talk: NanoString Technologies. TBD. (@ Montpelier B)

4) Research Facilities

Ying-Wai Lam (U. of Vermont). Regional Analytical Resource Cores. (@ Montpelier C)

Vendor talk: Alamar Biosciences. High-sensitivity proteomics at the push of a button. (@ Montpelier C)

2:45 pm: Afternoon break and Networking (@ Adirondack)

3:00 pm: Keynote 2

Bill Parker. Creating prototype devices for novel research applications in the core lab. (@ Green Mountain)

4:00 pm: Platinum talk: Illumina. Enabling core laboratories to expand access to genomics. (@ Green Mountain)

4:15 pm: Afternoon break and Networking (@ Adirondack)

4:30 pm: Concurrent Breakout Sessions, 1 hr./vendor talk 10 minutes

5) Spatial Transcriptomics

Sridar Chittur (Albany U.). Spatial Transcriptomics, tales from the core. (@ Green Mountain)

Vendor talk: Sampled. TBD. (@ Green Mountain)

6) Facilities

Nate Herzog (U. of Vermont). Facility tools for enabling reproducible research: The Core Marketplace and the Micro Meta App. (@ Montpelier A)

Vendor talk: Scale Biosciences. Combinatorial indexing for single cell sequencing with CRISPR. (@ Montpelier A)

7) Administration

Susanna Perkins (UMass Chan Medical School). Cost saving measures in core facilities: options & experiences. (@ Montpelier B)

8) Informatics

Ramiro Barrantes-Reynolds (U of Vermont). Reproducibility in Bioinformatics. (@ Montpelier C)

Vendor talk: IDT. Not just oligos...IDT is here to help. (@ Montpelier C)

5:45 pm to 7:15 pm: Vendor show and poster session (@ Adirondack)

7:15 pm - : Dinner on your own

9:30 pm - : NERLSCD afterdark. Drinks sponsored by Complete Genomics at the Beacon Bar & Lounge/Hilton Hotel.

FRIDAY, OCT-20TH

7:30 am- 12:00 pm REGISTRATION

9:00 am Concurrent Breakout Sessions, 1 hr./vendor talk 10 minutes

9) Caroline Shamu (Harvard U). Labor disruptions: How to keep your core running as smoothly as possible through understaffed situations. (@ Montpelier A)

10) Tim Hunter (UVM/BioTek, retired). Transitioning from a career in academia to industry: Is the grass greener? (@ Montpelier B)

Vendor talk: Singular Genomics. G4 benchtop sequencer: enhance your core lab sequencing capabilities. (@ Montpelier B)

11) Jonathan (Jon) Preall (Cold Spring Harbor Lab). Artificial Intelligence (AI) in cores (ChatGPT and other Bioinformatic Tools. (@ Green Mountain)

Vendor talk: Element Biosciences. Expanding operational flexibility with new AVITI features and products. (@ Green Mountain)

10:15 am: Morning break and Networking (@ Adirondack)

10:30 am Concurrent Breakout Sessions, 1 hr./vendor talk, 10 minutes

12) Multiomics

Stuart Levine (MIT). Multiomics: war stories from the trenches. (@ Green Mountain)

Vendor talk: 10x Genomics. Maximize core resources: 10x innovations improved data quality, workflow flexibility, and continued support. (@ Green Mountain)

13) FAIR Cytometry

Daniel Mielcarz (DartLab/Dartmouth Cancer Center). FAIR Cytometry: Flow Cytometry in a Data-Sharing World. (@ Montpelier A)

Vendor talk: Gator Bio. Evaluating the versatility of Gator® Next Generation BL1 platform for biotherapeutic development and gene therapy. (@ Montpelier A)

14) Mass Spec

Jeremy Balsbaugh (U Conn). Integrating new and emerging analytical applications in mass spectrometry core facilities. (@ Montpelier B)

Vendor talk: Waters Corporation. New tools for MS imaging in core labs. (@ Montpelier B)

15) Administration

Susanna Perkins (UMass) and Andrew Vinard (UMass). Recruiting, Retention & Compensation – in a new landscape. (@ Montpelier C)

11:45 am: LUNCH and Networking Session (@ Montpelier and Adirondack)

12:45 pm: Platinum talk: Revvity (PerkinElmer). The power of Fontus™ automation: Revvity's new liquid handling workstation. (@ Green Mountain)

1:00 pm Roundtable

Emily Guswa (U of Vermont). Advanced Tech Education: workforce development. (@ Green Mountain)

2:00 pm: Concluding Remarks (@ Green Mountain).

NERLSCD 2023 PROGRAM-ABSTRACTS

WEDNESDAY, OCT 18TH

Pre-Meeting Workshops

1:00 pm – 2:30 pm

- **Illumina (Montpelier A): Interactive user group discussion with the local Illumina technical team.**

Abstract: Illumina has new resources that enable genomics core laboratories to reach a wider audience of prospective genomics customers. We've launched a new educational program intended to demystify Next Generation Sequencing to graduate and early career scientists and show the value of core labs in increasing accessibility of genomic methods, all of which is available on our newest tool, iResources. Plus, hear more about how the latest in illumina technology is helping core labs to drive down cost, improve performance, and simplify workflows through XLEAP-SBS chemistry on the NovaSeqX and NextSeq 2000 system, DRAGEN analysis, and library preparation.

- **New England Biolabs (NEB) (Montpelier C): New tools and techniques for your NGS toolbox: the latest additions to the NEBNext family of products for NGS library prep.**

Abstract: Join New England Biolabs for a poster session to hear more about the latest additions to the NEBNext family of products for NGS library prep.

2:30 pm – 4:00 pm

- **QIAGEN (Montpelier A): Advances in sample preparation through NGS & dPCR detection from liquid biopsy samples.**

Abstract: Identification of circulating tumor cells (CTCs) and cell-free RNA (exosomal and non-EV cfRNA) and cfDNA from biofluids is an area of active study for multiple biomarker programs. In this workshop we will highlight the latest instruments and products dedicated to sample isolation, NGS library construction and digital PCR detection of miRNA, coding and non-coding RNA and cfDNA. Join the experts in sample isolation and simple workflows for a beverage and chat about your liquid biopsy programs.

- **Revvity (PerkinElmer) (Montpelier C): Single cell RNA sequencing workshop.**

Abstract: Join Revvity's NERLSCD 2023 single cell RNA sequencing workshop to receive personalized consultation for your single cell RNA-seq projects from our experts and learn from external scientists who have adopted the HIVE CLX scRNAseq technology into their labs. During this workshop you will get hands-on experience with HIVE CLX™ scRNAseq solution developed by Honeycomb Biotechnologies, and the Cellometer® Fluorescent Cell Counter. Our innovative single cell workflow allows

decentralized scRNA-seq with a portable capture device that locks in molecular signals with the HIVE CLX scRNAseq solution and reliably measure the cell concentration and viability with the Cellometer® Fluorescent Cell Counter to prepare cells and isolated nuclei for single cell sequence analysis. With basic lab equipment, samples can be collected at multiple times and locations, then shipped to a core facility for library processing, minimizing batch effects. Register now to learn how you can optimize your scRNA-seq workflow. For research use only. Not for use in diagnostic procedures.

UVM-Larner College of Medicine Core Tours

2:00 pm – 4:00 pm

University of Vermont, Larner College of Medicine-Center for Biomedical Shared Resources (CBSR), Firestone Bldg.-First Floor, 149 Beaumont Avenue, Burlington, VT. Take the Free College Street Shuttle (<https://ridegmt.com/wp-content/uploads/11CollegeStreetShuttle.pdf> ; <https://parkburlington.com/transportation-demand-action-plan/ccta/>). Take bus at the ECHO center and stop at the UVM Medical Center. At the UVM MC there will be signs for the CBSR tour.

Opening reception

6:00 pm – 9:00 pm

At ECHO Leahy Center for Lake Champlain. 1 College St, Burlington, VT. At walking distance from the Hilton Hotel
<https://www.google.com/maps/dir/Hilton+Burlington+Lake+Champlain,+60+Battery+St,+Burlington,+VT+05401/ECHO,+Leahy+Center+for+Lake+Champlain,+College+Street,+Burlington,+VT/@44.4773718,-73.2221892,17z/data=!3m2!4b1!5s0x4cca7afa943fd29f:0xdc5f4f353747c6b0!4m14!4m13!1m5!1m1!1s0x4cca7af0f4a901e7:0x9387c428f4901901!2m2!1d-73.218361!2d44.4780804!1m5!1m1!1s0x4cca7afa9720cbf9:0x8eddf37adf6cb85!2m2!1d-73.2208675!2d44.4766747!3e2?entry=ttu>

THURSDAY, OCT-19TH

9:30 am: Keynote 1

Speaker: Rita Colwell

Oceans, climate, and human health: cholera as a model for global pandemics. (@ Green Mountain)

10:15 am: Platinum talk: Qiagen

Speed up and simplify your RNA and DNA biomarker workflows using NGS and digital PCR. (@ Green Mountain)

Speakers: Samuel J. Rulli, Jr., PhD., Director Global Product Manager, RNAseq Profiling, NGS Assay Technologies.

Abstract: RNA and DNA Biomarker Research projects often fall into a discovery phase using next generations sequencing (NGS) which is used to discover relevant RNA or DNA targets and a verification phase where digital PCR can be used to verify the utility of the discovered biomarkers in a much larger sample size. Here we will introduce new QIAGEN kits which speed up and simplify RNA-seq workflows and a cloud-based software solution to help researchers collaborate between NGS and digital PCR assays

10:30 am: Morning break and Networking (@ Adirondack)

10:45 am (1 hr.): Roundtable

Moderator: Valeria Mezzano-Robinson (NYU Langone) and Nicole Contaxis (NYU Langone)

Guest speakers: Roxana del Rio-Guerra (U of Vermont)

Data management and data sharing: What is the role of Shared Research Resource Facilities/Cores? (@ Green Mountain)

Abstract: The 2023 NIH Data Management and Sharing Policy has brought increased attention to how research data is generated, managed, and published. While this session will provide some background information on the policy itself, it will focus on how data management is implemented at shared resource facilities, highlighting differences across institutions and disciplines. Designed as an interactive session, attendees will have the chance to discuss how they manage data at their institution, their own relationship with the data they generate, and their understanding of opportunities the policy provides for Core Scientists.

11:45 am: Platinum talk: New England Biolab (NEB)

Streamlined for speed: new library prep for DNA & RNA. (@ Green Mountain)

Speaker: Siva Chavadi, PhD. Sr. Field Application Scientist, NGS US-EAST

Abstract: The NEBNext difference is based on our nearly 50 years of enzymology expertise, and that includes NEBNext UltraExpress™, the latest generation of DNA and RNA library prep. With substantially faster and more streamlined workflows, high-quality libraries can be generated from a broad input range with a single protocol for all input amounts, all while generating less plastic waste.

12:00 pm: LUNCH and Networking (@Montpelier and Adirondack)

1:30 pm: Concurrent Breakout sessions, 1 hr./vendor talk 10 minutes

1) Genomics

Moderator: Scott Tighe (U of Vermont)

Implementation of Long Read Sequencing and Data Analysis in Core Facilities. (@ Green Mountain)

Guest speakers: Claire Bailey Reardon (Harvard U), Sara Goodwin (Cold Spring Harbor Lab), Shawn Polson (U. Of Delaware), Bruce Kingham (U. of Delaware)

Abstract: The use of long read sequencers continues to grow at an unprecedented rate in genomic core facilities. These Instruments and techniques largely center around the two most common systems including Oxford Nanopore and Pacific Biosciences but also include some synthetic short read approaches. Not surprisingly, challenges exist at every level of implementing and executing routine long read sequencing including instrument selection, protocols to extract nucleic acids, type of library synthesis, required read depth, approaches to data analysis, and troubleshooting to name a few.

This session will include five regional experts to discuss implementing long reads sequencing and engage in an open panel to discuss any aspects of long read sequencing. The discussion is open to all experience levels and will be a forum to answer any questions by both the panelists and experienced audience.

Vendor talk: PacBio

Game-changing products for high accuracy sequencing. (@ Green Mountain)

Speaker: Minqian Wang, Territory Account Manager – Northern New England, NY.

Abstract: Get the best of both worlds with PacBio's newest long and short-read sequencing systems! Come to learn the PacBio difference in generating top-quality genomes, epigenomes, transcriptomes, metagenomes and more. Discover our kitted solution for single-cell transcriptomics, long-read targeted panels, and metagenomic sequencing and analysis. Think what you can do with near-perfect short reads

2) Flow-Informatics

Moderator: Tim Bushnell (U. of Rochester MC)

Evaluating flow cytometry software. (@ Montpelier A)

Guest speakers: Ryan Brinkman, John Quinn

Abstract: Flow cytometry has become an indispensable tool in biomedical research and clinical diagnostics, facilitating the analysis of single cells and particles in heterogeneous populations. As the field continues to evolve, the role of flow cytometry software in data analysis and interpretation has grown in importance. When considering adopting new software, it is important to evaluate the performance of the package using an objective series of metrics that allow one to compare different packages. Such a framework can be applied to various facets critical for software assessment, including data acquisition, preprocessing, gating strategies, visualization, and data export. In addition, it emphasizes user-friendliness, accuracy, and scalability. Flow cytometry professionals require software that streamlines the analytical process while maintaining high data integrity and reproducibility. This session will provide an open forum for

cytometrists to discuss this topic with two experts in the field of flow cytometry software development, gaining perspective on practices they might adopt in their operations.

Vendor talk: Bio-Techne (Namocell)

Empowering single cell workflow with fast and gentle single cell sorting. (@ Montpellier A)

Speaker: Tracy Liu, PhD. Sr. Product Manager, Cellular Analysis, Bio-Techne.

Abstract: Single cell isolation is an essential step in cell line development and engineering. Meanwhile, single cell resolution is increasingly valued in genomic and cellular analyses in basic, translational, and clinical research. Bio-Techne's Pala Single Cell Dispenser is a simple yet scalable solution that enables fast isolation of target cells in singlets or in bulk while preserving cell viability and integrity. Whether you are printing single cells for clonal isolation or sorting target cells for single cell analyses, the small, microfluidic Pala Single Cell Dispenser is a fast, easy, and reliable tool that provides cells of interest that are optimal for your downstream workflow.

3) Imaging

Moderator: Doug Taatjes

Reproducibility in publishing microscopy imaging data. (@ Montpellier B)

Guest speakers: Caterina Strambio-De-Castillia (UMass Chan Medical School), and Nicole Bouffard (U. of Vermont)

Abstract: This session will introduce recent efforts by microscopy imaging scientists to create community-driven guidelines for publishing microscopy data and analyses in an effort to enhance the rigor, reproducibility, and reliability of published imaging data. The forum will discuss ways to implement these guidelines into microscopy core facilities for the education of their clients.

Vendor talk: NanoString Technologies. (@ Montpellier B).

Spatial Biology from Organs to Organelles Powered by a Cloud-based Analysis Platform

Speaker: Sarah Weigel, Regional Account Manager for Greater New England, NanoString Technologies

Abstract: Unlock the spatial multiomics of your samples with the CosMx Spatial Molecular Imager

During the session, participants will:

- Obtain new ideas, approaches, and learnings about spatial transcriptomics and understand how to apply spatial technologies in their research

- Learn about the whole-transcriptome analysis of archival FFPE tissues and how to analyze 6,000 RNA targets with single-cell resolution

4) Research Facilities

Moderator: Ying-Wai Lam (U. of Vermont).

Regional Analytical Resource Cores. (@ Montpelier C)

Guest speakers: Giuseppe Petrucci (U. of Vermont); Jennifer Liddle (UConn); Papa Nii Asare-Okai (U. of Delaware)

Abstract: This session aims to create opportunities for participants to learn about technologies that are available in analytical core facilities and to form collaborations within the network. We will be featuring several facilities that offer unique expertise and services to the community for conducting research that involves state-of-the-art analytical instrumentation and data analysis via fee-for-service, unique operating models, and collaborations.

Vendor talk: Alamar Biosciences

High-sensitivity proteomics at the push of a button. (@ Montpelier C)

Speaker: Alex Forrest-Hay, VP of Sales, Alamar Biosciences.

Abstract: Alamar Biosciences is powering precision proteomics with automated, high throughput solutions for ultra-high sensitivity protein analysis across a range of multiplex levels. The innovative ARGO™ System provides a fully automated workflow with <30 minutes hands-on time and runtimes of <8 hours from sample to data for single-plex analysis or <16 hours for multiplex analysis. Implementation of the ARGO System and NULISA™ assays allow you to generate robust and reproducible data with the sensitivity and dynamic range to measure important low abundant biomarkers. Off-the-shelf panels enable comprehensive profiling of ~250 biomarkers with the NULISAseq Inflammation Panel or ~150 neurology biomarkers with the NULISAseq CNS Disease Panel. Using the ARGO System, your lab can achieve high-sensitivity proteomic sat the push of a button.

2:45 pm: Afternoon break and Networking (@ Adirondack)

3:00 pm: Keynote 2

Speaker: Bill Parker

Creating prototype devices for novel research applications in the core lab. (@ Green Mountain)

4:00 pm: Platinum talk: Illumina

Enabling core laboratories to expand access to genomics. (@ Green Mountain)

Speaker: Meghan Buckley, Sr. Product Marketing Manager, Illumina.

Abstract: As core lab directors and genomics technology users come together in person to discuss and collaborate, we are excited to participate with an informative workshop covering the latest in technology and product developments from Illumina. In our workshop, we will discuss what's possible with the NovaSeq X, NextSeq 2000, and Illumina Complete Long Reads!

4:15 pm: Afternoon break and Networking (@ Adirondack)

4:30 pm: Concurrent Breakout sessions, 1 hr./vendor talk 10 minutes

5) Spatial Transcriptomics

Moderator: Sridar Chittur (Albany U.)

Spatial Transcriptomics, tales from the core. (@ Green Mountain)

Guest speakers: Nicole Bouffard (U of Vermont), Ioannis Vlachos (Beth Israel Deaconess Medical Center), Fred Kolling (Giesel School of Medicine, Dartmouth)

Abstract: This session will discuss the challenges with running a spatial transcriptomics core in a dynamic arena where the technology is changing rapidly. Pros and cons of each technology and thought processes for their choice will be presented.

This session is sponsored by “**Sampled**”.

6) Facilities

Moderator: Nate Herzog (U. of Vermont)

Facility tools for enabling reproducible research: The Core Marketplace and the Micro Meta App. (@ Montpelier A)

Guest speakers: Caterina Strambio-De-Castillia (UMass Chan Medical School)

Abstract: As funders and journals push for greater reproducibility in research, what resources are available to assist core facilities in this goal? This presentation will demonstrate how the Core Marketplace and the Micro Meta App are two examples of tools using persistent identifiers to assist in accurate citation of facilities and instrumentation in publications.

Vendor talk: Scale Biosciences

Combinatorial indexing for single cell sequencing with CRISPR. (@ Montpelier A)

Speakers: Pace Cranney, Dominic Skinner, Nick Pervolarakis, Jerushah Thomas, Dmitry Pokholok, Sanika Khare, Aimee Beck, Ashley Woodfin, Maggie Nakamoto, Felix Schlesinger.

Abstract: Single-cell sequencing technology has uncovered new biology across a wide range of disciplines; however, cell and sample throughput of experiments has not scaled rapidly due to high costs and complex workflows. To meet this need combinatorial

indexing has been established as a cost-effective method. This method utilizes each cell as a reaction compartment to perform 2-3 rounds of sequential barcoding in a plate-based workflow, eliminating the need for instrumentation and offering a robust, affordable, high-throughput protocol that enhances yield, diversity, and coverage. First, we used the ScaleBio scRNA Kit to profile PBMCs. Briefly 3-levels of barcodes were added to cells via RT, ligation, and PCR amplification before sequencing. Data show high barcode and mapping rates with similar sensitivity to current on-market systems with a throughput of >125,000 cells from a single experiment. Further analysis shows cell types were recovered in expected proportions with clear signal from cell-type specific markers.

Next to demonstrate this kit's ability to capture of non-polyadenylated transcripts, we adapted it to recover guide RNA barcodes from CRISPR screens. We added a barcoded primer targeting the scaffold region of the Cas9 gRNA to the reverse transcription module in addition to a gRNA-specific PCR enrichment downstream. This workflow was tested across human and mouse cell lines and organoids.

Together these data showcase the power of combinatorial indexing technology to increase throughput and decrease cost of single-cell experiments while maintaining strong data quality. The flexibility in experimental design enabled by these workflows, with easy addition of custom reagents and workflow steps, further broadens the scope and impact of data coming from these systems and opens up new opportunities for biological discovery.

7) Administration

Moderator: Susanna Perkins (UMass Chan Medical School)

Cost saving measures in core facilities: options & experiences. (@ Montpelier B)

Guest speakers: Marimar Lopez (Rensselaer Polytechnic Institute); Dominic Therrien (U. de Sherbrooke); Jiju Mathew (UPenn)

Abstract: Core Directors and staff are regularly challenged with fiscal constraints within their Facilities. This Session will provide insight into 3 different Institutions and the particular cost saving measures that they have utilized, and the successes and challenges related to each. After a brief presentation from the 3 Institutions, the discussion will be open to all attendees to share their experiences.

PANELIST TOPICS:

Marimar:

- Lab coats expenses and processes
- Service Contracts and third parties: what works and what does not work (always an option but we have discussed it often)
- How about handling of biohazards by specialized companies?

Dominic:

- We have a human resource core/platform: Two types of employees: hired directly by the core or university part-time staff. The core is taking care of HR tasks. It charges a fee to the user. User could be PI lab or core facilities with specific needs (part time, rush time or specific projects) but can afford a fulltime position.
- Core specific staff member for industry project: A lot of our engineering core provide service to the industry. However, these projects are more demanding and time sensitive. Evaluation of feasibility is complicate, and realization of these projects often takes more time and more resources than first expected. Core lab tends to be overcautious in taking these projects, which make their service less attractive to industry. Industry project is a great source of revenue for the core. Having someone who can answer the industry, do some prospecting, and manage and execute the project in house, will benefit the core lab without affecting the bandwidth.

Jiji:

- Partnering with closely located Institutions
- Reducing Service line offerings

8) Informatics

Moderator: Ramiro Barrantes-Reynolds (U of Vermont).

Reproducibility in Bioinformatics. (@ Montpelier C)

Guest speakers: Christopher Hemme (U of RI), Owen Wilkins (Dartmouth College), George Bell (MIT)

Abstract: Reproducibility in bioinformatics is a first step in ensuring that the results of a study or analysis can be replicated by a different group given the same data and code, or sometimes even by the same group at a different time. As the datasets and analyses become larger and more complex, reproducibility also becomes more challenging. In this panel we will discuss approaches that different groups are taking to ensure or try to reach reproducibility, best practices, challenges encountered, and general sharing of experiences on this topic.

Vendor talk: IDT

Not just oligos...IDT is here to help. (@ Montpelier C)

Speaker: Jayne Simon

Abstract: IDT has a suite of products to help with all your research needs including NGS, CRISPR, SybBio, qPCR, RNAi, and custom oligos. Our xGen product line for NGS offers a complete solution from library preparation through enrichment. With flexible options each step of the way and custom builds available, IDT is your one-stop for Next Generation Sequencing. This presentation will focus on new updates at IDT with a focus on our NGS portfolio.

5:45 pm to 7:15 pm: Vendor show and poster session (@ Adirondack)

7:15 pm - : Dinner on your own.

9:30 pm - : NERLSCD afterdark. Drinks sponsored by Complete Genomics at the Beacon Bar & Lounge/Hilton Hotel.

FRIDAY, OCT-20TH

7:30 am- 12:00 pm REGISTRATION

9:00 am: Concurrent Breakout sessions, 1 hr./vendor talk 10 minutes

9) Moderator: Caroline Shamu (Harvard U)

Labor disruptions: How to keep your core running as smoothly as possible through understaffed situations. (@ Montpelier A)

Guest speakers: Paula Montero Llopis (Harvard Medical School), Claire Hartmann (Harvard U)

Abstract: We will provide some examples of how our cores have dealt with different sorts of labor disruptions, and then, we will move to a discussion with all session attendees.

10) Moderator: Tim Hunter (UVM/BioTek, retired)

Transitioning from a career in academia to industry: Is the grass greener? (@ Montpelier B)

Guest speakers: Jessica Hoffman (UVM/Agilent), Karen Oppenheimer (UVM/ThermoFisher), Dan Vellone (UVM/Nanopore)

Abstract: This interactive breakout session will be a must attend for anyone considering a workforce change from academia to industry. This session will address differences between a career in academics vs industry through the perspectives of core personnel who have experienced this transition. Panelists will share about why they chose to pursue a career in industry, leveraging existing unique core relationships, what opportunities or other considerations that were important in making this change, and the perceived and realized pros and cons experienced in each setting. Panelists will also explore from their own perspective if the “grass is greener” and encourage audience participation to question panelist about any aspect or deliberations regarding this type of transition.

The session outline:

1. Welcome and panelist introductions.
2. Each panelist will provide background information regarding workforce capacity and transition. a. Why they made the change/transition including change in expertise/responsibilities.

b. What preparations/training/education were required to be prepared to be an ideal candidate in desired industry career?

c. What (if any) academic core relationships were leveraged

d. Discuss experienced differences based on a list of talking points that will include: i.

Acclimation strategies: Academic to industry

— ii. Training

— iii. Work setting/ infrastructure

— iv. Culture/ Work environment

— v. Professional Development accessible

— vi. Career Advancement

— vii. Unique Opportunities

— viii. Compensation/benefits

— ix. Employee Recognition

— a. Hoping to have audience drive the specific questions but can be prepared with a list of talking points, such as the ones listed above (i-ix) or others we can generate.

—

3. Is the grass greener? What is “the grass”? And how is “grass” defined?

Vendor talk: Singular Genomics

G4 benchtop sequencer: enhance your core lab sequencing capabilities. (@ Montpellier B)

Speaker: Fred Souret.

Abstract: The G4 Sequencing Platform is a fast, flexible, and cost-effective sequencer. The G4’s 4 flow cells and 4 individual lanes per flow cell allow core labs unparalleled flexibility to design and plan experiments. G4’s latest product, the Max Read flow cell, allows core labs sequencing 10x single cell to process over 2x more samples per day than any other benchtop sequencer at better than Novaseq S4 flow cell pricing.

11) Moderator: Jonathan (Jon) Preall (Cold Spring Harbor Lab)

Artificial Intelligence (AI) in cores (ChatGPT and other Bioinformatic Tools. (@ Green Mountain)

Guest speakers: Ioannis Vlachos (Harvard/Beth Israel) and John Ashton (Rochester U)

Abstract: During this unprecedented technological explosion, A.I.-based tools are evolving daily, often with mixed results. Our panel will discuss their experience evaluating and deploying a variety of AI tools, including popular large language models (LLMs) such as ChatGPT in both day-to-day administrative tasks and as a bioinformatics

“co-pilot”. An open discussion will be greatly welcomed, as institutions may vary greatly in their implementation, sophistication, and policies toward AI technologies.

Vendor talk: Element Biosciences

Expanding operational flexibility with new AVITI features and products. (@ Green Mountain)

Speaker: Chris Higgins, Sr. FAS, Element Biosciences

Abstract: With the AVITI System, Element reimagined DNA sequencing by putting customer needs at the center: High accuracy, low costs, and operational flexibility. Hear how recent and upcoming product releases including the \$200 Genome, Cloud break Chemistry, individually addressable lanes, simplified library prep workflows, a 2x300 cycle kit, and lower throughput flow cells combine to help your lab operate more efficiently and cost effectively, no matter the scale or genomics application your project entails.

10:15 am: Morning break and Networking (@ Adirondack)

10:30 am: Concurrent Breakout Sessions, 1 hr./vendor talk 10 minutes

12) Multiomics

Moderator: Stuart Levine (MIT)

Multiomics: war stories from the trenches. (@ Green Mountain)

Guest speakers: Shahina Maqbool (Albert Einstein COM), George Bell (Whitehead Inst. for Biomed Research) and Claire Reardon (Harvard U)

Abstract: Supporting Integrative analysis and multi-omics is one of the latest catch phrases of research in systems biology. These studies are often among the most complex and expensive but also are frequently highly susceptible to technical challenges and biases as difficult choices may have to be made to enable samples to be cross-compatible. This session will focus on real world issues associated with multi-omic analysis highlighting and sharing both successful experiences and lessons learned.

Vendor talk: 10x Genomics

Maximize core resources: 10x innovations improved data quality, workflow flexibility, and continued support. (@ Green Mountain)

Speaker: Rosha Poudyal, PhD, Sr. Science & Technology Advisor, 10x Genomics

Abstract: Join us to learn how single cell, spatial, and in situ technologies from 10xGenomics can help contribute to lab efficiencies in the Core lab workflow. Uncover molecular insights, dissect cell-type differences, investigate the adaptive immune system, detect novel subtypes and biomarkers, and map the epigenetic landscape cell-by-cell. Review our advanced, probe-based chemistry that expands sample access to

include fresh, PFA-fixed, and FFPE tissues, and simplifies experimental logistics. Enabling deeper insight into cancer, immunology, neuroscience, and developmental biology, 10x Genomics gives researchers the ability to see biology in new ways, driving science together.

13) FAIR Cytometry

Moderator: Daniel Mielcarz (DartLab/Dartmouth Cancer Center).

FAIR Cytometry: Flow Cytometry in a Data-Sharing World. (@ Montpellier A)

Guest speakers: Ryan Brinkmann (Dotmatics); Cindy Danielson (NIH Off of Extramural Research); Amy Hafez (NIH Off Science Policy); Ishwar Chandramouliswaran (NIH Off Data Science Strategy)

Abstract: FAIR data is Findable, Accessible, Interoperable, and Reusable. These general principles along with other, more specific requirements are a standard to which all federally-funded data must conform. This panel discussion will discuss the general requirements and unique challenges facing flow cytometry shared resources in adhering to these new standards. What is the role for shared resources in ensuring user-generated data follows the standards? How long must data be stored by the shared resources? What repositories should be used? These questions and more will be discussed.

Vendor talk: Gator Bio.

Evaluating the versatility of Gator® Next Generation BL1 platform for biotherapeutic development and gene therapy. (@ Montpellier A)

Speaker: Zachary Graha, regional sales manager, Gator Bio.

Abstract: The Gator® next generation BLI platform is a label-free, real-time monitoring system that enables characterization and optimization of therapeutic antibodies, proteins, small molecules, LNPs, and viruses. The Gator® instruments and biosensors offer a wide range of assays for protein-protein interactions and quantitation including epitope binning, kinetics, affinity, and specificity. Here, we present data on these applications that demonstrate the versatility, throughput, and accuracy for accelerating the development of biotherapeutic and gene therapy candidates.

14) Mass Spec

Moderator: Jeremy Balsbaugh (U Conn)

Integrating new and emerging analytical applications in mass spectrometry core facilities. (@ Montpellier B)

Guest speakers: Andrew Magnuson (U of Vermont); Fereshteh Zandkarimi (Columbia U); Xiaoyang Su (Rutgers U)

Abstract: This session will foster discussions centered on challenges and successes in analytical core facilities when implementing brand new technologies and methodologies. This can range from brand new MS instrumentation models, expansion into proteomics or metabolomics for the first time, introduction of brand-new analysis workflows or analytical methods, and/or implementation of mass spectrometry-adjacent analytical technologies. This session will also encourage new scientist connections as MS-centric core facilities continue to grow and expand analysis offerings throughout our region.

Vendor talk: Waters Corporation. New tools for MS imaging in core labs. (@ Montpellier B).

Speaker: Iggy J. Kass, PhD, HRMS Business Development Manager, Waters Corporation.

Abstract: MS Imaging provides scientists with the ability to view the chemical diversity in a sample for both discovery and targeted analysis. While a relatively simple technique it requires a level of skill and frequent practice which fits well in a core lab to make it available to users who would benefit from this type of analysis, but do not use it routinely. Waters recently introduced the Select Series MRT system for in-depth molecular MS imaging, providing Ultra-High Time of Flight mass resolution combined with multiple mechanisms for component visualization; MALDI and DESI. As result of these experiments, it came to light that a rapid, sensitive route for routine targeted imaging was desired and the Xevo TQ-Absolute targeted imaging system with DESI was introduced. Both the Select Series MRT and Xevo TQ-Absolute imaging platform will be described and imaging applications on each platform will be provided.

15) Administration

Moderator: Susanna Perkins (UMass) and Andrew Vinard (UMass)

Recruiting, Retention & Compensation – in a new landscape. (@ Montpellier C)

Guest speakers: Carolyn Gorham (Ass. VC People Strategies, UMASS Chan Med School); Viji Dinakaran (Talent Acquisition Manager, UMASS Chan Medical School); Luellen Fletcher (Ass. Director, Path BioResource, Perelman School of Medicine, UPenn); Shekhar Patil (Sr. Director, Shared Res Resources and Core Admin. Icahn School of Medicine at Mount Sinai)

Abstract: This session will involve discussions with Human Resource Talent Specialists to learn ways that department has pivoted post-Covid to recruit and retain employees. Following the HR discussion will be an overview of the ABRF Salary Survey.

11:45 am: LUNCH and Networking Session (@ Montpellier and Adirondack)

12:45 pm: Platinum talk: Revvity (PerkinElmer).

The power of Fontus™ automation: Revvity's new liquid handling workstation. (@ Green Mountain)

Speaker: Andy Raneri, Sr. Principal Sales Specialist, Revvity.

Abstract: Discover Revvity and Revvity's new solutions that help accelerate workflows in your laboratory including the new Fontus™ Liquid Handler automation which has increased flexibility and performance to solve complex applications. Revvity also offers a wide breadth of NGS library prep automation solutions and Cell based assay solutions. Join our session to learn about Revvity, the new Fontus liquid handler, our 100+ NGS vendor qualified methods and our Explorer G3 fully automated systems for cell-based assays.

1:00 pm Roundtable

Moderator: Emily Guswa (U of Vermont)

Advanced Tech Education: workforce development. (@ Green Mountain)

Guest speakers: Kelley Thomas, Lauren Traister (U of Vermont), Christin Monroe

Abstract: Diverse backgrounds and experiences bring unique insights to problem solving and discovery. However, the STEM workforce does not currently represent the demographics diversity of the United States despite recent gains. How can we engage, empower, and support pre-college and undergraduate students from underrepresented backgrounds to pursue careers in STEM?

Engage with our guest speakers who bring unique experiences and perspectives for developing a diverse STEM workforce. Kelley Thomas and his collaborators bring technology related to regenerative medicine and biotechnology into K-12 classrooms to cultivate interest and skills for the future workforce. Lauren Traister works with teens to develop knowledge, skills, attitudes, and aspirations to be successful in their workforce. Christin Monroe mentors, teaches, and advocates for neurodivergent undergraduates as they prepare to enter the workforce.

2:00 pm: Concluding Remarks. (@ Green Mountain)

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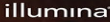


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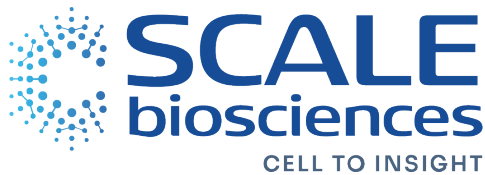
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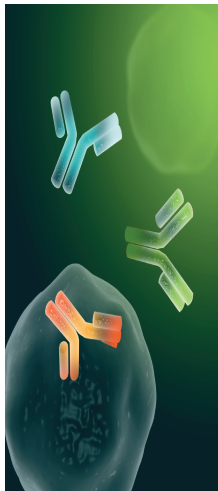
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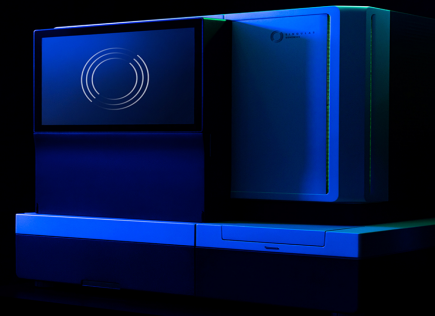
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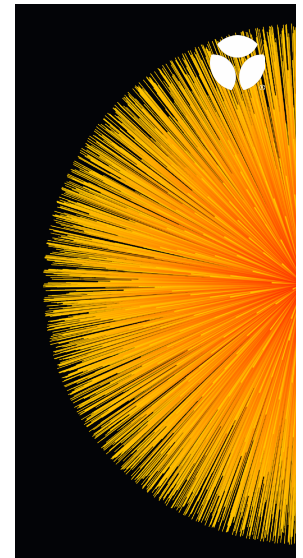


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