AMP Association for Molecular Pathology

AMP 2019 ANNUAL MEETING & EXPO

ANNIVERSARY CELEBRATION

PROGRAM

November 7-9, 2019

Baltimore Convention Center
Baltimore, MD, USA

PGDx™
Personal Genome Diagnostics

FUTURE READY

WE SEE THE FUTURE OF GENOMIC DIAGNOSTICS CLEARLY.

Personal Genome Diagnostics (PGDx) is Empowering the Fight Against Cancer by unlocking actionable information from the genome. We are committed to improving clinical insight, speed of results, and health economics by developing an innovative portfolio of regulated tissue-based and non-invasive liquid biopsy genomic based Next Generation Sequencing (NGS) products for laboratories worldwide.

We are placing the power of proximity in the hands of physicians and lab directors, and putting the power of control back into your patient care ecosystem.

**DRIVEN BY SCIENCE.
INSPIRED BY PATIENTS.
EMPOWERING PHYSICIANS.
COMMITTED TO YOU.**

Want to learn more about our products and partnerships, visit pgdx.com or call (443) 602-8833.

AMP 2019
TABLE OF CONTENTS

AMP Association for Molecular Pathology

WELCOME TO THE 2019

Association for Molecular Pathology Annual Meeting & Expo!

It has been a true pleasure to work alongside the members of the 2019 AMP Annual Meeting Program Committee in putting together this program, marking the 25th Anniversary of our organization. In designing the program for this Silver Anniversary, we were challenged to acknowledge the history of our organization and our specialty, while also reporting on the present, and projecting into the future. Our program is an attempt to concurrently respect our historical traditions and, also, to establish some new ones. I'm very proud of the work that your committee conducted, and of the program that we compiled.

Among the new features we are bringing to the meeting this year are the engagement of meetings with guest societies, Infectious Diseases Society of America (IDSA) and (American College of Medical Genetics and Genomics (ACMG). These organizations are made up of health care specialists, in infectious diseases and human genetics, respectively, whose work has substantial overlap with the work conducted by AMP. This year, each of these organizations will be hosting a 2.5 hour symposia prior to our meeting, these symposia will present issues in their specialties that are shared with ours, and to help foster inter-organizational and cross-specialty relations and cooperation. I offer a hearty welcome to the members of IDSA and ACMG who are joining us this year, and hope that this is a tradition that continues, and expands, in the future.

Another feature that we are bringing to the meeting this year is to engage with AMP committees, to develop sessions of mutual interest to the attendees. Historically, the program has been largely developed through the work of the subdivision representatives - two each from genetics, infectious diseases, informatics, hematopathology, solid tumors, and technical topics. This year, we also engaged with the cross-practice committees to develop sessions. These have brought us several exciting new features such as the Pipeline Showcase, the Business of Molecular Lab Management, the International Quality Assurance Program, and the Future Practice of Molecular Pathology.

We have redesigned some of the meeting formats, with an emphasis on active learning in the workshop sessions, refocusing the "early bird" sessions as targeted talks on specific individual topics, enabled more, and later, late breaking abstracts (case studies) from our trainees, and implemented short educational courses to take place during the days leading up to the main meeting.

However, while these and other aspects of the meeting are new, much will remain familiar. We will, again, have a full day of corporate workshops from our vendors during the day before the meeting. We will, again, be taking a trip to Capitol Hill to meet and talk with members of Congress about public health issues of interest to our specialty, we will, again, learn about practice guidelines in development, we will again learn about exciting new findings at posters and platforms, and we will, again, have hours and hours of fascinating talks from leaders in our field, both from within the organization and from invited experts from other fields.

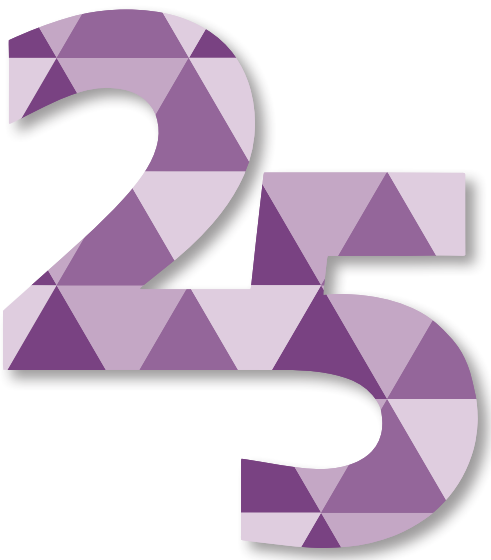
As always, our meeting kicks off in earnest with the Award for Excellence in Molecular Diagnostics Presentation and Lecture. This year's honoree is Dr. Russ Higuchi, a true pioneer in our field, whose many accomplishments date back to (and precede) the origins of the polymerase chain reaction, and include developing the first protocols for the use of PCR in forensic and ancient genetics investigations, for cloning from cDNA, and the invention of real-time PCR with closed tube fluorescence detection, as well as many other innovative uses of DNA as a diagnostic analyte, most recently for improved rapid non-invasive detection of bladder cancers.

I am really excited about this year's meeting, which was the culmination of a tremendous amount of work spanning over a year, that was conducted by a dedicated and talented team of individuals, who have worked hard for very little recognition. I thank the members of our planning committee, Esther Babady, Jennifer Dien-Bard, Raj Emmadi, Mark Ewalt, Rashmi Kanagal, Peter Kang, Matt Lebo, Tina Lockwood, Angshumoy Roy, Fernanda Sabato, Elaine Spector, Renee Webb, and next year's Program Chair, Jane Gibson. Beyond the faculty volunteers, however, we all thank the AMP staff who are the backbone of the entire organization and who absolutely make this (and all our crazy ideas) happen; if you see them around the meeting, please join me, and extend your own thanks to Lucia Barker, Tara Burke, Elisabeth Campbell, Kathleen Carmody, Eriko Clements, Sara Hamilton, Rhonda Jenkins, Jon Korman, Laurie Menser, Andy Noble, Mrudula Pullambhatla, Crystal Quinones, TaNika Switzer, Robyn Temple-Smolkin, Sarah Thibault-Sennett, Michele Zink, and our Executive Director, Mary Williams

From the 2019 Program Committee,

Neal I. Lindeman, MD
2019 Program Committee Chair

AMP 2019
ANNUAL MEETING & EXPO



NOTES

THE LATEST INFORMATION ABOUT BIOMARKER TESTING

ARE YOU UP TO DATE?

GENERAL INFORMATION

VISIT BOOTH **2925** TO LEARN MORE

The sponsor of this ad verifies that they had no input into decision making regarding the selection of educational programs, content, or faculty for this 2019 Annual Meeting.

MERCK

GENERAL INFORMATION

PICKING UP PIK3CA MUTATIONS

Learn about the most common mutation in HR+/HER2- advanced breast cancer (aBC) and how to detect it at **BOOTH 2741**[1-4]

INNOVATION SPOTLIGHT

with Jean Lopategui, MD

Associate Professor of Pathology
Director of Translational Genomics
Program Director of Molecular Genetic Pathology Fellowship
Cedars-Sinai Medical Center
Los Angeles, California

Friday, November 8, 2019
10:00 AM - 10:30 AM
at STAGE 2

Join us as Dr Jean Lopategui discusses PIK3CA mutations in HR+/HER2- aBC and how to detect them.

References: 1. The Cancer Genome Atlas Network. Comprehensive molecular portraits of human breast tumours. *Nature*. 2012;490(7418):61-70. 2. Tolaney S, Toi M, Neven P, et al. Presented at: 2019 American Association for Cancer Research (AACR) Annual Meeting; March 29-April 3, 2019; Atlanta, GA. 3. Di Leo A, Johnston S, Seok Lee K, et al. *Lancet Oncol*. 2018;19(1):87-100. 4. Moynahan ME, Chen D, He W, et al. *Br J Cancer*. 2017;116(6):726-730.

NOVARTIS

Novartis Pharmaceuticals Corporation
East Hanover, New Jersey 07936-1080

10/19 BST-1222219

AMP 2019 EVENTS

Code of Conduct

The Association for Molecular Pathology (AMP) is committed to providing a friendly, comfortable, and welcoming environment for all, regardless of gender, sexual orientation, disability, race, ethnicity, religion, national origin, age, gender identity, or any other demographic group. We expect all attendees, media, speakers, AMP staff and volunteers, venue staff, contractors, guests, and exhibitors to take an active role in providing a safe and positive experience for everyone by conducting themselves in a professional and lawful manner.

Unacceptable behavior can take many forms, including words, signage, or actions. For example, intimidation, unwelcome sexual advances, or abusive or vulgar language. Such behavior from any participant in an AMP activity, attendees, users of online services, media, presenters, AMP staff and volunteers, venue staff, guests, and exhibitors, will not be tolerated.

Anyone asked to stop unacceptable behavior is expected to comply immediately. If a participant is found to have engaged in unacceptable behavior, the AMP Executive Director will determine appropriate action to be taken, if any, which may include expulsion from the AMP activity, without refund, and/or contacting local law enforcement authorities. The Board of Directors may consider the matter for additional action.

While we cannot influence behavior outside of the official AMP event hours, we expect all participants at AMP events and meetings to abide by this Code of Conduct in all venues, including ancillary events and all social gatherings. All participants are responsible for their own conduct. Anyone who is the recipient of unacceptable behavior should feel free to speak up without any fear of retaliation.

- AMP hold its collegial community in high value. Do your part to give everyone you encounter an enjoyable experience so they remember you and the meeting favorably.
- Exercise consideration and respect in your speech and actions.
- Abstain from all demeaning, discriminatory, or harassing behavior and speech.
- Respect the fact that slides and posters may include unpublished work so if a speaker or author requests that slides or posters not be photographed, do not photograph them.
- Do not video record presentations. Holding up your phone or tablet throughout the presentation likely blocks the view of attendees behind you or is distracting. Speakers' slides are available to the attendees after the meeting and recordings of sessions are often made available as well.

AMP 2019 EVENTS CODE OF CONDUCT

- Do not audio record presentations without the express permission of the presenter(s). If you obtain permission, place your recording device, e.g., phone, such that it does not interfere with another attendee.
- Be mindful of your surroundings and of your fellow participants. Alert Security Personnel or call 911 if you notice a dangerous situation or someone in distress.
- Notify AMP Staff of any violation of this Code of Conduct that you experience or observe.

Unacceptable Behaviors at AMP Events Include:

- Intimidating, harassing, abusive, discriminatory, derogatory or demeaning speech or actions
- Harmful or prejudicial verbal or written comments, jokes, or visual images related to gender, sexual orientation, disability, race, ethnicity, religion, national origin, age, gender identity, or any other demographic group
- Use of provocative and/or sexual images, including in presentation slides and exhibit booths
- Deliberate intimidation, stalking, or following
- Harassing photography
- Photographing slides of oral presentations or posters when the presenter/author requests no photography
- Video recording presentations
- Audio recording presentations without the express permission of the presenter(s)
- Undue disruption of scientific sessions or other events
- Unwelcome and uninvited attention or contact
- Physical assault, including unwelcome touch or groping
- Real or implied threat of physical harm
- Real or implied threat of professional or financial damage or harm

What To Do If You Observe or Experience Conduct That Violates this Code:

Please contact the nearest AMP or Security Staff. All reports will be kept confidential to the extent possible while allowing for effective investigation and response. If you believe the situation is an emergency, call 911.

AMP Staff will help participants contact convention center/hotel/venue security or local law enforcement authorities, and otherwise assist those experiencing conduct that violates this Code. We value your participation with AMP, and want your experience to be professionally rewarding and personally enjoyable.

BALTIMORE, MD

Map

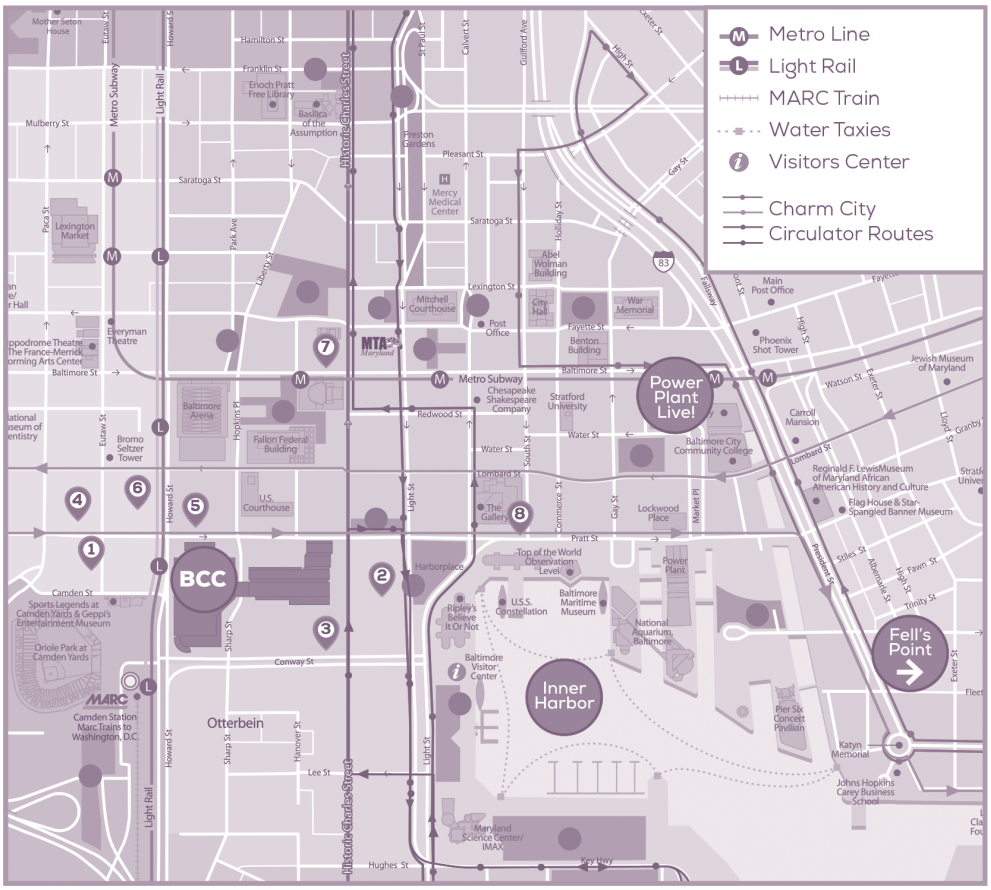
For more maps and information about Baltimore, visit:

baltimore.org

VisitBaltimore™

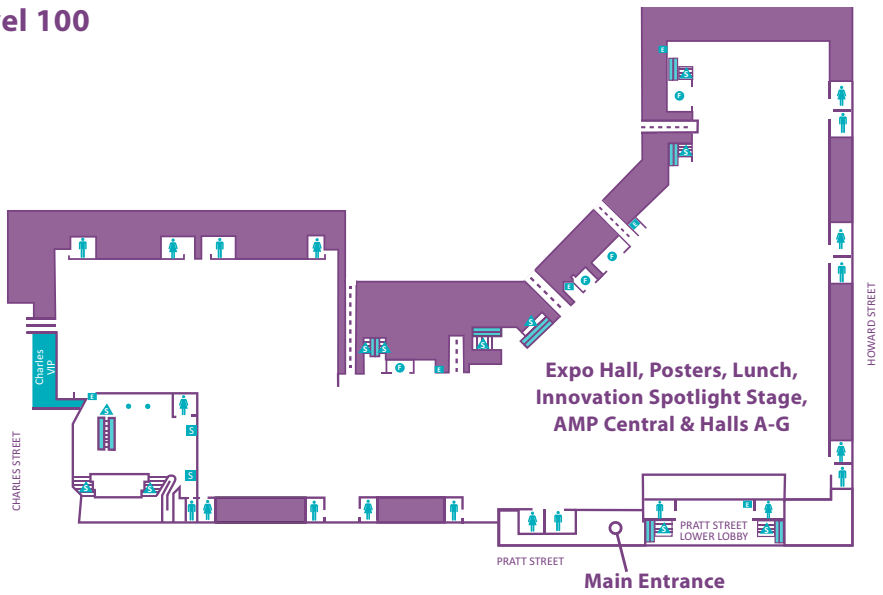
Hotels:

1. **Hilton Baltimore Inner Harbor**
2. **Hyatt Regency Baltimore**
3. **Sheraton Inner Harbor**
4. **Baltimore Marriott Inner Harbor at Camden Yards**
5. **Days Inn Baltimore Inner Harbor**
6. **Holiday Inn Inner Harbor**
7. **Kimpton Hotel Monaco Baltimore**
8. **Renaissance Baltimore Harborplace Hotel**

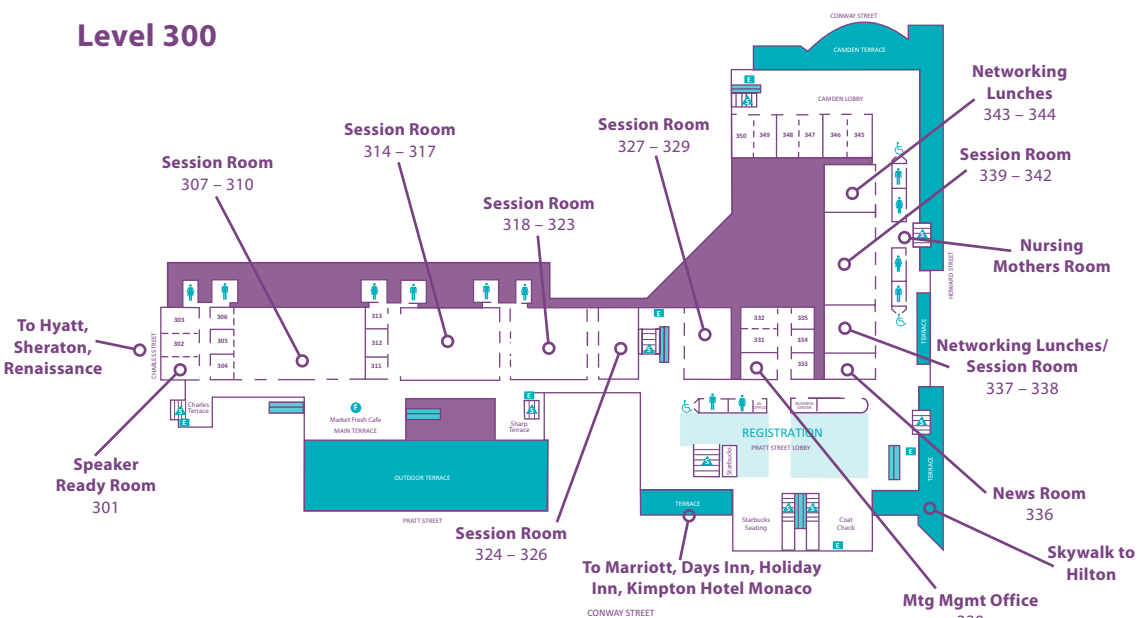


CONVENTION CENTER

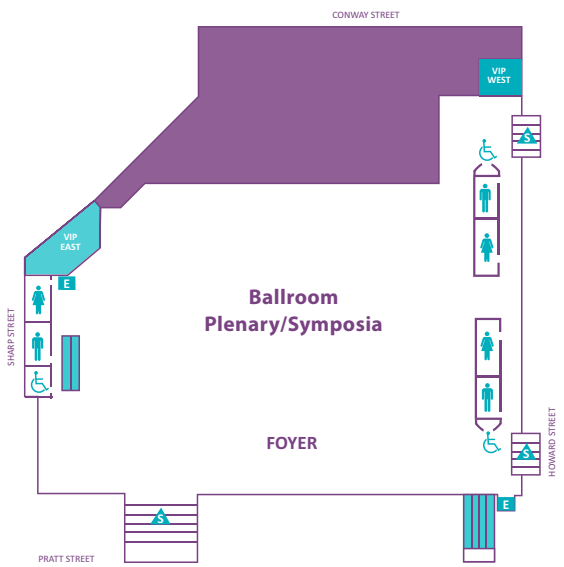
Level 100



Level 300



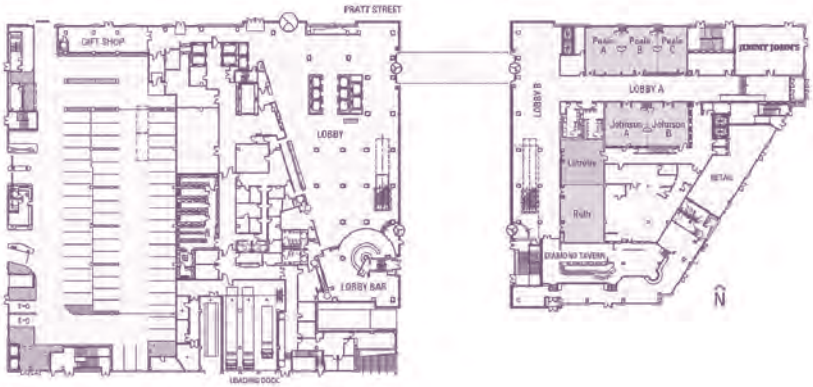
Level 400



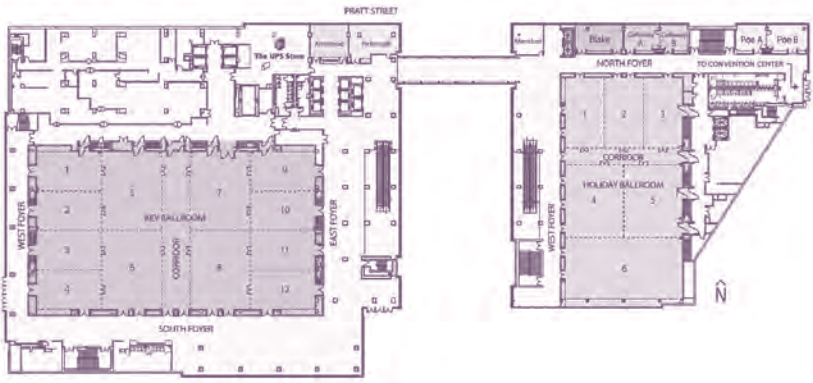
HILTON BALTIMORE

Floorplan, Headquarter Hotel

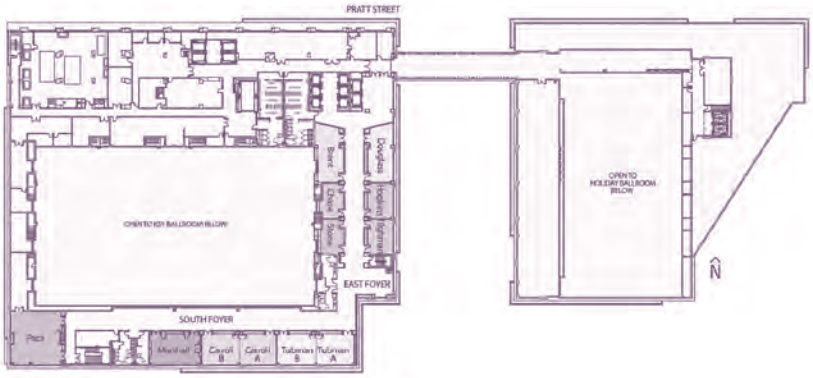
First Floor



Second Floor



Third Floor



HIGHLIGHTS & GENERAL INFORMATION

Attendee/Exhibitor Registration Desk Hours
(Convention Center, Pratt Street Lobby, Level 300)

Tuesday, November 5	11:00am – 6:00pm
Wednesday, November 6	7:00am – 5:00pm
Thursday, November 7	6:45am – 5:00pm
Friday, November 8	6:45am – 5:00pm
Saturday, November 9	6:45am – 2:00pm

Expo Hall Hours
(Convention Center, Exhibit Hall A-G, Level 100)

Thursday, November 7	11:30am – 4:30pm; 5:45pm – 7:00pm (Welcome Reception in the Expo Hall)
Friday, November 8	9:00am – 4:00pm (Appointment only demos 4:00pm – 5:00pm*)
Saturday, November 9	9:00am – 1:30pm (Appointment only demos 8:00am – 9:00am*)

**Appointment only demo times are specifically for exhibitors and their invited guests (Registered Attendees or Official Guests of Exhibitors) to conduct demos in a quieter atmosphere than during regular Expo Hall hours.*

AMP Meeting Paths

Want to create your own Path? AMP Meeting Paths are a convenient way to tailor your meeting experience around the content you most want to see. The 2019 Program Committee has carefully examined the scientific program and identified seven paths that will direct you to sessions based on your favored area of interest.

2019 Meeting Paths Key:

A = Advocacy/Lab Management

C = Cancer/Oncology

ID = Infectious Diseases

IF = Informatics

IC = Inherited Conditions

M = Molecular Methodologies & Technologies

You can select Browse by Path in the Schedule on the Mobile App to find sessions included on your preferred Path.

Special Events

Welcome Reception

Supported by QIAGEN

Please join us for the Welcome Reception in the Expo Hall, immediately following the scientific Program on Thursday, November 7th from 5:45pm – 7:00pm. Help us kick-off another successful Annual Meeting & Expo while networking with your friends and colleagues. We'll also be celebrating AMP's 25th anniversary and *The Journal of Molecular Diagnostics' (JMD)* 20th anniversary, stop by AMP Central for Cake! This event is open to all registered Meeting Attendees.

AMP Trainee Happy Hour

Sponsored by the AMP Jeffrey A. Kant Leadership Fund

Join us for the AMP Trainee Happy Hour on Wednesday, November 6th from 7:00pm – 8:00pm! This is your chance to connect with other AMP trainees over great drinks at a local Baltimore bar. All registered trainees are welcome and will receive a ticket that they may use at Leinenkugel's Beer Garden at Power Plant Live (4 Market Pl, Baltimore, MD 21202), in exchange for a free drink! Your drink ticket will be included on your badge sheet when you check-in for the Annual Meeting & Expo.

AMP Central

Visit AMP's booth in the Expo Hall, centrally located at the center of the hall. AMP Central features unique programming including career networking opportunities and the chance to meet current committee members. AMP Central is the best place to learn about all that AMP does and find out how you can get involved! For details on AMP Central Events, see event listings throughout this program.

Networking Corner/Speed Networking

Sponsored by the Membership Affairs Committee

AMP is a great place to meet, share ideas, and explore new opportunities. Join the us at the Networking Corner to build new connections and network with the AMP community. You might find a new boss, collaborator, employee, troubleshooter, mentor, scientist, enthusiast, inspiration, advocate, motivator, travel guide in a new city, admirer, colleague, or just a new friend. During lunch on Friday (12:30 – 1:00 PM) and Saturday (12:30 – 1:00 PM), this space will feature speed networking sessions. Speed networking is simply a format to encourage greater interaction. The key is to come, start a conversation, then connect and follow up after. All you need to bring is your business cards and a willingness to meet someone new.

Subdivision Open Forums

In the past 25 years, the AMP Subdivisions and multiple AMP volunteers have spearheaded substantial contributions to the field of molecular diagnostics. As we look to the future, AMP leadership would like to invite subdivision members and meeting attendees with an interest in their respective field to attend an open forum session. Please bring your ideas, energy, and enthusiasm to the conversation as we discuss the future of molecular diagnostics within AMP. The Open Forums will be held for each subdivision will be held on Saturday, November 9th from 3:00pm – 3:45pm. Please see the Program Schedule for additional information and room locations.

HIGHLIGHTS & GENERAL INFORMATION

Innovation Spotlight Stages
This year's Innovation Spotlight Stages will continue to provide a unique opportunity for exhibiting companies to showcase products or services, but this year the Stages will also feature cutting-edge AMP produced content. The TWO Innovation Spotlight Stages are located in the main cross aisles on the back and right corners of the Expo Hall. Innovation Spotlight presentations are open to all Meeting Registrants and seating will be on a first come, first served basis. Schedules for this program are available in your meeting bag, on the Mobile App or on signage located outside the seating of each Stage. Please see complete schedule and descriptions in the Expo section of the Program Book, Page 189.

Business & Awards Session
AMP invites all Meeting Attendees to attend the AMP Business & Awards Session on Friday, November 8th at 5:15pm. Come hear how AMP is working hard to help you advance patient care. A number of awards, including the Young Investigator, Technologist and the Jeffrey A. Kant Leadership Awards are presented at this session.

Amazing Molecular Party (25th Anniversary Celebration)
Known as the AMP Social Event, this year the "Amazing Molecular Party" will take place on Friday, November 8th at 7:00pm at the HQ Hotel (Hilton Baltimore). This event is intended to facilitate networking opportunities between trainees, new, and long-standing AMP attendees. There will be mingling, dancing, amateur acts, great food and surprises! Attendees who purchased tickets when registering for the meeting will receive their ticket when they check-in at the registration desk for their name badge. If any tickets are still available for sale, they may be purchased at the Registration Desk.

General Information

Mobile App
The AMP 2019 Mobile App is available for your Android, iPhone and other mobile devices. The AMP Mobile App is a robust tool allowing you to plan your meeting experience in advance and allows you to get instant updates onsite! AMP thanks Asuragen, Bayer Healthcare, Hologic, Karius, LGC, Biosearch Technologies and Novartis for its generous support of the AMP Mobile App. Please go to https://amp19.amp.org/program/mobile-app/ for more information.

Abstracts
A record number of abstracts were submitted this year! Please refer to the Poster section of the Program for more information on the Poster Map, Poster Listings and Author Index. The abstracts have been published in the November 2019 issue of The Journal of Molecular Diagnostics (JMD). This issue is in your meetings bags. They are also available online at https://amp19.amp.org/abstracts-posters/poster-list/.

AMP Ambassadors
Members of the AMP Membership Affairs Committee will be donning big yellow "Ask me About AMP" buttons. Look for them in the hallways and between sessions to learn about AMP membership benefits and opportunities during the meeting for first time attendees and those who are early in their career.

AMP Europe 2020 – Clinical Genomics: Beyond the Somatic Mutation
AMP Europe 2020 will be in Milan, Italy from May 11 - 13, 2020. The meeting will bring together a network of molecular professionals and representatives of the diagnostics industry to educate healthcare practitioners and to advance the value of molecular laboratories in providing high quality patient care around the world. This multi-disciplinary scientific program will showcase molecular diagnostics with clinical applications in oncology (solid tumors, hematopathology), genetics (congenital, heritable), infectious diseases and informatics. For more information and to register for the Congress, please visit here: https://amp-europe-congress.com/.

Attendee Badges
Name badges are required for admittance to all scientific sessions, expo hall, meals and other official meeting events. Badges contain a bar code that holds the attendee's name, address, email. Exhibitors will scan badges to send information after the meeting.

Attire
Attire is business casual for the meeting sessions and receptions, and casual for the Social Event. Remember to dress in layers and wear comfortable walking shoes.

Business Center
ABC Imaging is conveniently located in the Business Center of the Baltimore Convention Center. The Business Center is located in the Pratt Street Lobby adjacent from Room 334. Their team is available to support for any last minute needs! Some of their services include but are not limited to copy & print services, and shipping & receiving. Their standard hours of operation are Monday - Friday from 7:30 am - 6:00pm but can vary based on events occurring at the Convention Center. Please contact them for more information at 410-649-7196.

There is also a FedEx Office located in the Renaissance Baltimore Harbor Place Hotel, which is 2 blocks away from the Convention Center. They are open Monday - Friday from 8:00 am - 7:00pm and can be reached at 410-528-1057.

Charging Station
Stop by and re-charge your electronics at one of the AMP Charging Stations in the Expo Hall. (see floorplan in the "Exhibits" section).

City Information – Baltimore
Baltimore has become one of America's most authentic cities. With the world-famous Inner Harbor; renowned museums and attractions; award-winning restaurants; a locally loved music scene, and hip and historic neighborhoods. We hope that AMP Annual Meeting & Expo attendees and exhibitors will be able to explore and take in all the authenticity Baltimore has to offer. Find more information on local dining, hotels, shopping and other amenities online at: https://baltimore.org/groups/amp-2019.

Consent to Use of Photographic Images/Contact Information
Registration for and attendance at the AMP 2019 Annual Meeting & Expo constitutes the registrant's agreement with the AMP's use and distribution (both now and in the future) of the registrant or attendee's image or voice in photographs, videotapes, electronic reproductions, audiotapes of such events and activities, and inclusion of their address in the registrant mail list (email addresses are not distributed).

HIGHLIGHTS & GENERAL INFORMATION

Continuing Education

The AMP 2019 Annual Meeting & Expo has been planned and implemented in accordance with the Essential Areas and policies of the Accreditation Council for Continuing Medical Education Amedco LLC and the Association for Molecular Pathology. Amedco LLC is accredited by the ACCME to provide continuing medical education (CME) for physicians, and through a joint providership with the American Society for Clinical Pathology (ASCP) to provide continuing medical laboratory education (CMLE) for non-physicians. Refer to the "Continuing Education" section for more information.

Dining Options

Baltimore has a wide range of food options available for meeting attendees near the Convention Center. Find more information on local dining online at https://baltimore.org/dining-nightlife. Please see down below for meals included in attendee registration.

First Aid & Medical Emergencies

For medical emergencies, please dial 410-649-7055 to be instantly connected to the Security Department. Attendees are also able to go to any house phone and dial 7055 to be directly connected to Public Safety. If the injury is life threatening, call 911 immediately. The Convention Center address is 1 W Pratt St, Baltimore, MD 21201. Call the Security Division after the 911 call to ensure they coordinate with the first responders to minimize response time. Automated External Defibrillator (AED) units are located throughout the Convention Center. The AED's are available for use and are marked "Automatic Defibrillator". There are always EMTs on-site during the day and there are multiple medical centers in close proximity to the property.

Guest of Presenter Badges

If a registered attendee would like a family member or friend to see his/her invited talk or poster presentation, the registered attendee may request a session guest badge at the AMP Registration Desk. The session guest badge must be returned to the Registration Desk after the session requested. Guests should be accompanied at all times and are not permitted at breaks/meals.

Guest of Exhibitor Badges

Each exhibiting company receives non-personalized guest badges for use during the event. Exhibitors are responsible for coordinating, issuing, and providing badges to their guests. All guests of exhibitors must be accompanied by a registered member of the exhibit staff and are permitted access to the Expo Hall, only. Badges must be worn at all times.

International Exhibitors

AMP is Global! With members from more than 56 countries and meeting attendees from around the world, AMP has newly formed the International Affairs Committee. The AMP Annual Meeting & Expo is the gathering place for molecular diagnostic professionals from around the globe. AMP exhibitors are no exception, representing more than 7 countries, many of our exhibitors have traveled far to share their products and services with us. Look for the globe icon in the program listing to identify these exhibitors and stop by to say hello.

Internet

Complimentary Wireless Internet is available in all of the lobby spaces of the Convention Center. Please search for the "Free BCC WiFi" network and follow the prompts to connect to this free service. (Not available in the Expo Hall).

Lost & Found

The Lost & Found is located at the AMP Registration Desk. Please speak to an AMP Staff member regarding a lost item or to turn in a found item.

Luggage & Coat Check Hours

A luggage and coat check area will be made available for all attendees. Attendees utilizing this service do so at their own risk. AMP will not be responsible for any missing or stolen personal items from this area or for items that are not retrieved after the luggage check closes.

Location: *Pratt Street Lobby, Level 300.*	
Wednesday, November 6	7:30am – 5:30pm
Thursday, November 7	6:30am – 7:30pm
Friday, November 8	6:30am – 6:30pm
Saturday, November 9	6:30am – 5:30pm

Meals (Continental Breakfast and Lunch)

Continental Breakfast and Lunch are provided for registered meeting attendees, only, and are included in the price of meeting registration. Exhibitors are encouraged to grab lunch onsite in the concession stands in the Expo Hall or at one of the variety of local venues just outside the convention center.

	Continental Breakfast Times	Lunch Times*
Thursday, November 7	6:45am – 8:00am	11:30am – 12:45pm
Friday, November 8	6:45am – 8:00am	12:15pm – 1:30pm
Saturday, November 9	6:45am – 8:00am	12:15pm – 1:30pm

**Please go to the end of the "Highlights & General Information" section for full descriptions of lunch options.*

HIGHLIGHTS & GENERAL INFORMATION

News Room

The News Room is available for all qualified print, online, and broadcast news media outlets. Visit https://amp19.amp.org/media1/media-information/ for more information or contact Andy Noble (nobel@amp.org or 415-722-2129). Location and hours of operation for the News Room are as follows:

AMP News Room: Convention Center, Room 336, Level 300.	
Thursday, November 7	8:00am – 4:30pm
Friday, November 8	8:00am – 4:30pm
Saturday, November 9	8:00am – 12:00pm

Nursing Mothers

A Nursing Mothers Room is located across from Room 341 in the convention center and available for Annual Meeting attendees. Seating and outlets will be available in the rooms.

Parking

Parking is available in several garages near the Baltimore Convention Center. You can see a full listing of locations and costs online at: https://spothero.com/baltimore/baltimore-convention-center-parking. You can also ask for information at the Information Desks at the Convention Center.

Photography/Recording

Please be respectful of the presenters and your colleagues. Do not record presentations without the speaker's permission. Do not take photographs of posters or presentations slides if presenters have indicated no photography. AMP reserves the right to dismiss individuals from sessions for violation of AMP's Code of Conduct.

Poster Tube Storage

Bins for poster tubes will be available throughout the poster sections. Poster Tube Storage will NOT be staffed and is not secured. If you would like to leave your poster tube, please clearly mark it with your name and place it in one of the bins. AMP is not responsible for any lost, stolen or damaged posters or poster tubes.

Ribbon Bar

Back by popular demand! Stop by the RIBBON BAR located in the Registration Area to pick-up applicable ribbon(s) for your meeting badge, i.e., Committee, Speaker, Awardee, Trainee, First Time Attendee and others.

Speaker Presentations

The AMP 2019 Speaker Presentations will be made available to all Registered Meeting Attendees and AMP Members through March 2020. The Presentations will also be available to AMP Members in the Digital Library. Detailed instructions will be sent to all registered meeting attendees in December.

Speaker Ready Room

If you are speaking at a scientific session and did not upload your presentation in advance of the meeting, you will need to visit the speaker ready room before your session to provide a copy of your presentation. The speaker ready room is located at the **Convention Center, Room 301, Level 300**. All presentations will be collected in the speaker ready room, and your presentation will be preloaded onto the computer in your session room. Please visit the speaker ready room at least one hour prior to the start of your session. Technicians will be available to receive your presentation during the hours listed below. Presentations will not be loaded directly onto the computers in the session room, so it is essential that you stop by the speaker ready room. You will be able to review and/or make changes to your presentation before providing it to the technicians.

Speaker Ready Room Hours	
Wednesday, November 6	12:00pm - 5:00pm
Thursday, November 7	6:30am - 5:00pm
Friday, November 8	6:30am - 5:00pm
Saturday, November 9	6:30am - 5:00pm

Lunch Options

General Lunches are open to all AMP 2019 Annual Meeting & Expo registered attendees. The General Lunches will be held in the Expo Hall (**Convention Center, Exhibit Hall A-G, Level 100**) and can be accessed in the designated areas on the Exhibit Floor.

Networking Lunches are open to all AMP 2019 Annual Meeting & Expo registered attendees* They do not require payment or pre-registration. Simply show up at the appropriate networking lunch as noted below. Please note that seating is limited and available on a first come, first served basis. Networking lunches close when room capacity is filled. Please have your badge scanned as you enter the networking luncheons. This helps AMP measure outcomes and facilitate future planning.

**Some lunches are for specific groups of members, only – see descriptions below…*

Thursday, November 7

New to AMP? First Time at the Annual Meeting? – New Member and First Timers Lunch
(Hosted by the Membership Affairs Committee)
Time: 11:30am – 12:45pm
Location: Rooms 337-338, Level 300

Description: New to AMP? First Time at the Annual Meeting? Join us for lunch! This event is an opportunity to network with other first time attendees and new AMP Members. Current members of the Membership Affairs Committee will be on hand to answer questions and help you kick off a great experience at this year's AMP meeting!

HIGHLIGHTS & GENERAL INFORMATION

International Members' Luncheon
(Hosted by the International Affairs Committee)
Time: 11:30am – 12:45pm
Location: Room 343-344, Level 300
Speaker: Roberta Sitnik, PhD
Moderator: Renata Coudry, MD, PhD

Description: Hosted by AMP's International Affairs Committee, this luncheon is an opportunity for meeting attendees who reside and work outside of North America to gather, network, and discuss topics of mutual concern and interest. This year's topic is Certification in Molecular Pathology Outside the USA. Please join your fellow international colleagues at this special, free luncheon event.

Friday, November 8

Training & Education Networking Luncheon
(Hosted by the Training & Education Committee)
Time: 12:15pm – 1:30pm
Location: Rooms 337-338, Level 300
Moderators: Brittany Coffman, MD & Mara Williams, MS

Description: Trainees, junior faculty and technologists: SEIZE this opportunity to speak to and network with some of the best and most prominent players in the molecular pathology field! WIN valuable textbooks in the annual textbook give-away! EAT free food! JOIN US for this unique and valuable event!

NOTES

AMP Association for Molecular Pathology

AWARD RECIPIENT

AMP AWARD FOR EXCELLENCE

in Molecular Diagnostics 2019

Russell Higuchi, PhD

Cepheid, Sunnyvale, CA, USA

AMP Association for Molecular Pathology

AWARD RECIPIENT

JEFFREY A. KANT LEADERSHIP AWARD 2019

For Exceptional Leadership in Advancing the Mission and Goals of the Association for Molecular Pathology

Karl V. Voelkerding, MD

ARUP Laboratories, Inc
Salt Lake City, UT, USA

AMP Association for Molecular Pathology

AWARD RECIPIENT

AMP MERITORIOUS SERVICE AWARD 2019

Rami Mahfouz, MD, MPH, IFCAP

American University of Beirut
Medical Center Beirut, Lebanon

AMP Association for Molecular Pathology

AWARD RECIPIENTS

TRAVEL AWARDS 2019

AMP Technologist Travel Awards

Caitlin Dougherty, *Children's Hospital of Philadelphia, Philadelphia, PA, USA*

Lama Hamadeh, *American University of Beirut, Beirut, Lebanon*

Ashley Shean, *Sentara Norfolk General Hospital, Norfolk, VA USA*

International Trainee Travel Awards

Mamta Gurav, *MSc, Tata Memorial Hospital, Mumbai, India*

Elan Hahn, *MD, University of Toronto, Ontario, Canada*

Vamshi Krishna Thamtam, *MD, Tata Memorial Hospital, Kolkata, India*

AMP 2019
Officers and Committee Members

Board of Directors

President	Victoria M. Pratt, PhD
President-Elect; Awards and Strategic Opportunities Committee Chair	Karen Weck, MD
Past President and Nominating Committee Chair	Kojo S. J. Elenitoba-Johnson, MD
Secretary-Treasurer and Finance Committee Chair	Daniel E. Sabath, MD, PhD
Clinical Practice Committee Chair	Dan Jones, MD, PhD
Economic Affairs Committee Chair	Samuel K. Caughron, MD
International Affairs Committee Chair	Rami Mahfouz, MD, MPH
Membership Affairs Committee Chair	Midhat S. Farooqi, MD, PhD
Professional Relations Committee Chair	Jordan Laser, MD
Program Committee Chair	Neal Lindeman, MD
Publication & Communication Committee Chair	Paul G. Rothberg, PhD
Training & Education Committee Chair	Cecilia C.S. Yeung, MD
Genetics Subdivision Chair	Thomas W. Prior, PhD
Hematopathology Subdivision Chair	Annette S. Kim, MD, PhD
Infectious Diseases Subdivision Chair	Frederick S. Nolte, PhD
Informatics Subdivision Chair	Somak Roy, MD
Solid Tumors Subdivision Chair	Roger D. Klein, MD, JD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

Executive Committee

President	Victoria M. Pratt, PhD
President-Elect	Karen Weck, MD
Past President	Kojo S. J. Elenitoba-Johnson, MD
Secretary-Treasurer	Daniel E. Sabath, MD, PhD
Subdivision Chair (Hematopathology)	Annette S. Kim, MD, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

Awards Committee

Chair	Karen Weck, MD
Member	Helen Fernandes, PhD
Member	David R. Hillyard, MD
Member	Thomas W. Prior, PhD
Member	Vivianna Van Deerlin, MD, PhD
President	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

Clinical Practice Committee

Chair	Daniel Jones, MD, PhD
Genetics Subdivision Representative	Jianling Ji, MD
Genetics Subdivision Representative	Pinar Bayrak-Toydemir, MD, PhD
Hematopathology Subdivision Representative	Noah A. Brown, MD
Hematopathology Subdivision Representative	Marian Harris, MD, PhD
Infectious Diseases Subdivision Representative	Kenneth L. Muldrew, MD, MPH
Infectious Diseases Subdivision Representative	Daniel N. Cohen, MD, PhD
Informatics Subdivision Representative	Justin Zook, PhD
Informatics Subdivision Representative	Annette Leon Meredith, PhD
Solid Tumors Subdivision Representative	Pranil Chandra, DO
Solid Tumors Subdivision Representative	Jonathan Earle, MD
Junior Member	Megan B. Wachsmann, MD
Junior Member	Celeste Eno, PhD
President	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

AMP 2019 OFFICERS AND COMMITTEE MEMBERS

Economic Affairs Committee

Chair	Samuel K. Caughron, MD
Vice Chair, New Codes and Pricing	Anthony N. Sireci, MD, MSc
Vice Chair, Coverage	Pranil Chandra, DO
Member	Jennifer Dien Bard, PHD
Member	Rajyasree Emmadi, MD
Member	Andrea Ferreira-Gonzalez, PhD
Member	R. Tanner Hagelstrom, PhD, MBA
Member	Matthew Hiemenz, MD
Member	Susan J. Hsiao, MD
Member	Lloyd Hutchinson, PhD
Member	Loren Joseph, MD
Member (Ex Officio – PRC Chair)	Jordan Laser, MD
Member	Elaine Lyon, PhD
Member	Federico Monzon, MD
Member	Jay L. Patel, MD
Member	Richard D. Press, MD, PhD
Member	Aparna Rajadhyaksha, MD
Member	Katherine Tynan, PhD
Member	Oana Rosca, MD
Junior Member	Salvatore Priore, MD, PhD
Advisor	Aaron D. Bossler, MD, PhD
Advisor	Jan A. Nowak, MD, PhD
President Elect	Karen Weck, MD
President	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

Finance Committee

Chair	Daniel E. Sabath, MD, PhD
President	Victoria M. Pratt, PhD
President-Elect	Karen Weck, MD
Past President	Kojo S. J. Elenitoba-Johnson, MD
Member	Sharathkumar Bhagavathi, MD
Member	Steven A. Schichman, MD, PhD
Member	Xiao-Ming Yin, MD, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

International Affairs Committee

Chair, Rep to Membership Affairs, AUB Affiliate Coordinator	Rami Mahfouz, MD, MPH
Member	Adewunmi Oluseye Adeoye, MD
Member, Representative to Professional Relations	David E. Barton, PhD
Member, Brazil Affiliate Coordinator	Renata A. Coudry, MD, PhD
Member, India Affiliate Coordinator	Bibhu R. Das, PhD
Member	Andrew P. Fellowes, PhD
Member, Korea Affiliate Coordinator	Jin Kyung Lee, MD, PhD
Member	Benedict Yan, MBBS
Member, Representative to Training & Education	Roberta Sitnik, PhD
Member, Hong Kong Affiliate Coordinator	Lei Po (Chris) Wong, PhD
Member	Denis F. York, PhD
Germany Affiliate Coordinator	Silke Lassman, PhD
Italy Affiliate Coordinator	Massimiliano M. Corsi Romanelli, MD, PhD
Advisor	Helen Fernandes, PhD
Advisor	Jin-Yeong Han, MD, PhD
President	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

Membership Affairs Committee

Chair	Midhat S. Farooqi, MD, PhD
Member	Betsy A. Bove, PhD
Member	Yi Ding, MD, PhD
Member	Lisa M. Haley, MS
Member	Cristiane Ida, MD
Member	Giovanni Insuasti-Beltran, MD
Member, Representative to Training & Education	Cynthia L. Jackson, PhD
Member	Irene Newsham, PhD
Member	Wanda Reygaert, PhD
Member	Angshumoy Roy, MD, PhD
Member	Yaolin Zhou, MD
Junior Member	Talent Theparee, MD
International Affairs Liaison	Rami Mahfouz, MD
President	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

AMP 2019 OFFICERS AND COMMITTEE MEMBERS

Nominating Committee

Chair	Kojo S. J. Elenitoba-Johnson, MD
Genetics Subdivision Representative	Bert Gold, PhD
Genetics Subdivision Representative	Qiulu Pan, MD, PhD
Hematopathology Subdivision Representative	David Viswanatha, MD
Hematopathology Subdivision Representative	Keyur Patel, MD, PhD
Infectious Diseases Subdivision Representative	Amanda Harrington, PhD
Infectious Diseases Subdivision Representative	Blake W. Buchan, PhD
Informatics Subdivision Representative	Carlos J. Suarez, MD
Informatics Subdivision Representative	Nefize Sertac Kip, MD, PhD
Solid Tumors Subdivision Representative	Shelby Melton, MD
Solid Tumors Subdivision Representative	Anna Yemelyanova, MD
Ex Officio	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

Professional Relations Committee

Chair	Jordan Laser, MD
Vice-Chair	Eric Q. Konnick, MD, MS
Member	Linnea Baudhuin, PhD
Member (Ex Officio – EAC Chair)	Samuel K. Caughron, MD
Member	Jill Hagenkord, MD
Member	Robert Klees, PhD
Member	Roger D. Klein, MD, JD
Member	Amy Lo, MD
Member	Elaine Lyon, PhD
Member	Jill Murrell, PhD
Member	George J. Netto, MD
Member	Nirali Patel, MD
Member	David Viswanatha, MD
Member	Barbara Zehnbauer, PhD
Junior Member	Betty Chung, DO, MPH
Junior Member	Jason N. Rosenbaum, MD
International Affairs Liasion	David E. Barton, PhD
AMP Representative to FASEB Science Policy Committee (Ex Officio)	Betsy A. Bove, PhD
President	Victoria M. Pratt, PhD
President-Elect	Karen Weck, MD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

Program Committee

Chair	Neal Lindeman, MD
Chair-Elect	Jane S. Gibson, PhD
Genetics Representative	Elaine B Spector, PhD
Genetics Representative	Peter Kang, MD, MS
Hematopathlogy Representative	Rashmi Kanagal Shamanna, MD
Hematopathlogy Representative	Mark D. Ewalt, MD
Infectious Diseases Representative	Jennifer Dien Bard, PhD
Infectious Diseases Representative	Esther Babady, PhD
Informatics Representative	Matthew Lebo, PhD
Informatics Representative	Angshumoy Roy, MD, PhD
Solid Tumors Representative	Christina Lockwood, PhD
Solid Tumors Representative	Rajyasree (Raj) Emmadi, MD
Technical Topics Representative	Fernanda Sabato, MS
Technical Topics Representative	Renee Webb, BS
President	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

Publication & Communication Committee

Chair	Paul G. Rothberg, PhD
JMD Editor-in-Chief	Barbara A. Zehnbauer, PhD
Test Directory Co-Editor	Nefize Sertac Kip, MD, PhD
Test Directory Co-Editor	Annette Leon Meredith, PhD
Member	Mary C. Lowery-Nordberg, PhD
Member	Dahui Qin, MD, PhD
Member	Mohamadou Sene, BS, MB(ASCP)
Member	Shalini Verma, MD
Member	Shaochun Bai, PhD
JMD Managing Editor	Emily Essex
JMD Scientific Editor	Chhavi Chauhan, PhD
President	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

AMP 2019 OFFICERS AND COMMITTEE MEMBERS

Strategic Opportunities Committee

Chair	Karen Weck, MD
Member	Michael Hadjisavas, PhD
Member	Annette S. Kim, MD, PhD
Member	Roger D. Klein, MD, JD
Member	Robert L. Nussbaum, MD
Member	Ester Stein, BS, MBA
Advisor	Jill Hagenkord, MD
Advisor	Terri E. Ozegovich, BS, MBA
Advisor	Christine K. Ward, PhD
President	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

Training & Education Committee

Chair	Cecilia C.S. Yeung, MD
Genetics Subdivision Representative	Yassmine Akkari, PhD
Genetics Subdivision Representative	Alanna Church, MD
Hematopathology Subdivision Representative	Rashmi S. Goswami, MD, PhD
Hematopathology Subdivision Representative	Kristin Hunt Karner, MD
Infectious Diseases Subdivision Representative	Preeti Pancholi, PhD
Infectious Diseases Subdivision Representative	Erin Graf, PhD
Informatics Subdivision Representative	Joshua F. Coleman, MD
Informatics Subdivision Representative	Sabah Kadri, PhD
Solid Tumors Subdivision Representative	Susan J. Hsiao, MD, PhD
Solid Tumors Subdivision Representative	Christian Kunder, MD, PhD
Junior Member	Brittany Coffman, MD
Junior Member	Cinthya Zepeda Mendoza, PhD
Medical Technologist Member	Mara Williams, MS
Medical Technologist Member	Barbara Anderson, MS
Membership Affairs Liaison	Cynthia Jackson, PhD
International Affairs Liaison	Roberta Sitnik, PhD
President	Victoria M. Pratt, PhD
Executive Director	Mary Steele Williams, MNA, MT(ASCP)SM, CAE

SUBDIVISION
Leadership

Genetics Subdivision Leadership Committee

Thomas W. Prior, PhD, Chair
Yassmine Akkari, PhD
Pinar Bayrak-Toydemir, MD, PhD
Alanna Church, MD
Bert Gold, PhD
Jianling Ji, MD, MD
Hyunseok P. Kang, MD
Qiulu Pan, MD PhD
Elaine B. Spector, PhD

Hematopathology Subdivision Leadership Committee

Annette S. Kim, MD, PhD, Chair
Noah A. Brown, MD
Mark D. Ewalt, MD
Rashmi S. Goswami, MD, PhD
Marian Harris, MD PhD
Rashmi Kanagal-Shamanna, MD
Kristin Hunt Karner, MD
Keyur Patel, MD, PhD
David Viswanatha, MD

Infectious Diseases Subdivision Leadership Committee

Frederick S. Nolte, PhD, Chair
Esther Babady, PhD
Blake W. Buchan, PhD
Daniel N. Cohen, MD, PhD
Jennifer Dien Bard, PhD
Amanda Harrington, PhD
Kenneth L. Muldrew, MD
Preeti Pancholi, PhD
Erin Graf, PhD

Informatics Subdivision Leadership Committee

Somak Roy, MD, Chair
Joshua F. Coleman, MD
Sabah Kadri, PhD
Matthew Lebo, PhD
Annette Leon Meredith, PhD
Angshumoy Roy, MD, PhD
Nefize Sertac Kip, MD, PhD
Carlos J. Suarez, MD
Justin Zook, PhD

Solid Tumors Subdivision Leadership Committee

Roger D. Klein, MD, JD, Chair
Pranil Chandra, DO
Jonathan Earle, MD
Rajyasree Emmadi, MD
Susan J. Hsiao, MD
Christian Kunder, MD, PhD
Shelby Melton, MD
Christina Lockwood, PhD
Anna Yemelyanova, MD

AMP WORKING GROUPS
and Task Forces

Bioinformatics in silico Validation Working Group

Eric J. Duncavage, MD, Chair
Monica de Baca, MD
Joshua F. Coleman, MD
Sabah Kadri, PhD
Annette L. Meredith, PhD
Carlos Jose Suarez, MD
Mark J. Routbort, MD, PhD
Chad M. Vanderbilt, MD
Somak Roy, MD
Justin Zook, PhD

CLIA Modernization Working Group

Andrea Ferreira-Gonzalez, PhD
Robert F. Klees, PhD
Roger D. Klein, MD, JD
Eric Q. Konnick, MD, MS
Jordan Laser, MD
Roberta Madej, PhD
Federico A. Monzon, MD
Victoria M. Pratt, PhD
Barbara A. Zehnbauer, PhD

Copy Number Variants (CNV) Working Group

Birgit Funke, PhD
Madhuri R. Hegde, PhD, Chair
Elaine Lyon, PhD
Carolyn Sue Richards, PhD

EAC 101 Working Group

Dara L. Aisner, MD, PhD, Chair
Anthony N. Sireci, MD, MS, Chair
Samuel K. Caughron, MD
Mathew Hiemenz, MD
Loren Joseph, MD
Jay L. Patel, MD
Oana C. Rosca, MD

Genomics Education for Primary Care Residents Working Group

Laura J. Tafe, MD, Chair
Maria E. Arcila, MD
Devon Chabot-Richards, MD
Preeti Pancholi, PhD
Anthony Snow, MD
Yassmine Akkari, PhD
(T&E Committee Representative)

JMD Joint Journal Oversight Committee

Ron M. Przygodzki, MD, Chair
Paul G. Rothberg, PhD

Laboratory Benefit Managers Task Force

Samuel K. Caughron, MD
Jill Hagenkord, MD
Susan Hsaio, MD, PhD
Lloyd Hutchinson, PhD
Loren Joseph, MD
Roger D. Klein, MD, JD
Jordan Laser, MD
Aparna Rajadhyaksha, MD
Katherine Tynan, PhD
David Viswanatha, MD

Liquid Biopsy Applications Working Group

Christina Lockwood, PhD, Chair
Laetitia Borsu, MD
Milena Cankovic, PhD
Jonathan Earle, MD
Christopher Gocke, MD
Meera Hameed, MD
Jean R. Lopategui, MD
Jason D. Merker, MD, PhD
Geoffrey R. Oxnard, MD
Jacquelyn Reuther, PhD
Kandelaria Rumilla, MD

MGP Fellow Training in Genomics Task Force

Mark D. Ewalt, MD, Co-Lead
Jason N. Rosenbaum, MD, Co-Lead
Kristy R. Crooks, PhD
Jeffrey R. Gagan, MD, PhD
Anthony N. Snow, MD
David Wu, MD, PhD

MGP Program Directors' Council

Allison Cushman-Vokoun, MD, PhD, Chair
Keyur Patel, MD, PhD, Chair-Elect
Shuko Y. Harada, MD, Past-Chair
Joshua F. Coleman, MD
(Training & Education Committee Representative)

Molecular MRD Monitoring in AML Working Group

Keyur P. Patel, MD, PhD, Chair
Noah A. Brown, MD
Todd Druley, MD, PhD
Rashmi S. Goswami, MD, PhD
Marian Harris, MD, PhD
Duane Hassane, PhD
Daniel Jones, MD, PhD
Annette S. Kim, MD, PhD
Brian Parkin, MD
Harrison K. Tsai, MD, PhD
Christopher Watt, MD, PhD
David Wu, Md, PhD

AMP WORKING GROUPS AND TASK FORCES

New Frontiers in Infectious Diseases Multiplex Testing Working Group

Michael Lewinski, PhD, Chair
Kevin Alby, PhD
Esther Babady, PhD
Susan Butler-Wu, PhD
Jennifer Dien Bard, PhD
Alex Greninger, MD, PhD
Kimberly Hanson, MD
Samia Naccache, PhD
Duane Newton, PhD
Frederick Nolte, PhD

NGS Utility of T/B Cell Clonality Working Group

David Viswanatha, MD, Chair
Maria Arcila, MD
Devon Chabot-Richards, MD
Timothy C. Greiner, MD
Joseph D. Khoury, MD
Habibe Kurt, MD
Keyur Patel, MD, PhD
David Wu, MD, PhD

NGS Germline Variant Confirmation Working Group

Kristy Crooks, PhD, Chair
Kelly Hagman
Stephen E. Lincoln
Diana Mandelker, MD, PhD
Avni Santani, PhD
Ryan Schmidt, MD, PhD

PAMA Task Force

Samuel K. Caughron, MD
Pranil Chandra, DO
Betty Chung, DO, MPH, MA
Rajyasree Emmadi, MD
Robert Klees, PhD
Roger D. Klein, MD, JD
Eric Konnick, MD, MS
Jordan Laser, MD
Amy Lo, MD
Elaine Lyon, PhD
Federico Monzon, MD
Jay L. Patel, MD
Salvatore Priore, MD, PhD
Jason N. Rosenbaum, MD
Anthony N. Sireci, MD, MSc
Ester Stein, MBA

Professional Reimbursement Task Force

Betsy Bove, PhD
Aaron D. Bossler, MD, PhD
Pranil Chandra, DO
Samuel K. Caughron, MD
Jennifer Dien Bard, PhD
R. Tanner Hagelstrom, PhD, MBA
Matthew Hiemenz, MD
Roger D. Klein, MD, JD
Jordan Laser, MD
Elaine Lyon, PhD
Jan A Nowak, MD, PhD
Aparna Rajadhyaksha, MD
Jason Rosenbaum, MD
Ester Stein, MBA

SAM Content Editing Group

Sophie Arbefeville, MD
Adrienne Bambach, PhD
Cory J. Broehm, MD
Alan F. Brown, MD
Catherine E. Cottrell, PhD
Yi Ding, MD, PhD
Ron He, MD
Cristiane Ida, MD
Kristin H. Karner, MD
Cheryl Mather, MD
Honey V. Reddi, PhD
Christopher Sande, MD
Pamela J. Snyder
Vernell Williamson, PhD

Standardization of Pharmacogenetic Alleles (PGx) Working Group

Victoria M. Pratt, PhD, Chair
Larisa Cavallari, PhD
Andria del Tredici, PhD
Houda Hachad, PharmD
Yuan Ji, PhD
Lisa Kalman, PhD
Reynold Ly, PhD
Ann Moyer, MD, PhD
Stuart A. Scott, PhD
Karen Weck, MD
Michelle Whirl-Carrillo, PhD

Targeting DNA Repair Pathways: Current and Future Implications of PARP Inhibitors Working Group

Lynette Sholl, MD, Content Chair
Diana Mandelker, MD, PhD
Tracy Stockley, PhD

Tumor Mutational Burden: Diagnostic Innovations and Clinical Implications Working Group

Jonathan Nowak, MD, PhD, Content Chair
Laura J. Tafe, MD
Albrecht Stenzinger, MD

Tumor Mutational Burden Working Group

Larissa V. Furtado, MD, Chair
Carlo Bifulco, MD
Mark Boguski, MD, PhD
Daniel Dolderer, MD
Jeffrey Gregg, MD
Susan J. Hsiao, MD
Benjamin R. Kipp, PhD
Neal Lindeman, MD
Jonathan A. Nowak, MD, PhD
Solange Peters, MD, PhD
Lauren Ritterhouse, MD, PhD
Jeremy P. Segal, MD, PhD
Antonia Sepulveda, MD, PhD
Ahmet Zehir, PhD

AMP WORKING GROUPS AND TASK FORCES

Variant Interpretation Test Across Labs (VITAL) Working Group

Elaine Lyon, PhD, Chair
Sherri Bale, PhD
Julie Gastier-Foster, PhD
Madhuri Hegde, PhD
Glenn E. Palomaki, PhD
Carolyn Sue Richards, PhD

Variant Interpretation Test Across Labs (VITAL) Somatic Working Group

Marilyn M. Li, MD, PhD, Chair
Catherine Cottrell, PhD
Matthew Ferber, PhD
Somak Roy, MD
Scott A. Turner, PhD
Cindy Vnencak-Jones, PhD
Kai Wang, PhD

Whole Exome Sequencing Standards Working Group

Rong Mao, MD, Chair
Monica J. Basehore, PhD
Pinar Bayrak-Toydemir, MD, PhD
Birgit Funke, PhD
Jianling Ji, MD
Megan B. Wachsmann, MD

AMP Association for Molecular Pathology

AMP EUROPE 2020

Clinical Genomics: Beyond the Somatic Mutation

CONTINUING EDUCATION

Milan, Italy

May 11–13, 2020

NH Milano Congress Centre

www.amp-europe-congress.com

CONTINUING EDUCATION

SAVE THE DATE

AMP 2020
ANNUAL MEETING & EXPO

November 17–21, 2020

November 17
Short Course Day

November 18
Corporate Workshop Day

November 19–21
Scientific Program

Vancouver Convention Centre
Vancouver, British Columbia, Canada

AMP Association for Molecular Pathology

CONTINUING EDUCATION
Information

Disclosure of Conflict of Interest

The following table of disclosure information is provided to learners and contains the relevant financial relationships that each individual in a position to control the content disclosed to Amedco. All of these relationships were treated as a conflict of interest, and have been resolved. (C7 SCS 6.1--6.2, 6.5) All individuals in a position to control the content of CE are listed in the program book. If their name is not listed below, they disclosed that they had no financial relationships with a commercial interest.

Organizers – 2019 Program Committee Disclosures:

- Jennifer Dien Bard – Consultant to BioFire
- Peter Kang – Employee of Myriad Women's Health

Organizers – 2017 Awards Committee Disclosures (AMP Award for Excellence in Molecular Diagnostics:

- Kojo Elenitoba-Johnson – Co-founder of GENOMENON
- Margaret Gulley – Research Grant Site Principal Investigator to Illumina; Consultant to Beacon LBS
- Marc Ladanyi – Research Grant Site Principal Investigator to LOXO Pharmaceuticals
- Barbara Zehnbauer – Consultant to Amgen

Invited Speakers of CME Scientific Sessions Disclosures:

- Gabriel Bien-Wilner – Employee of Palmetto GBA
- Karissa Culbreath – Research Grant Site Principal Investigator with Copan Diagnostics
- Lisa Edelman – Employee of Sema4
- Nicole Faulkner – Employee of Invitae
- Birgit Funke – Employee of Veritas Genetics
- Susan Hancock – Employee of Myriad Women's Health
- John Iafrate – Stock Shareholder of ArcherDx
- Marcin Imielinski – Consultant to Novartis Venture Fund
- Amy Leber – Research Grant Site Principal Investigator and Scientific/Medical Advisory Board Member to BioFire; Research Grant Site Principal Investigator to Qiagen; Research Grant Site Principal Investigator to Diasorin
- Nathan Ledeboer – Corporate Board Member to CosmosID; Scientific/Medical Advisory Board Member to Karius
- Anthony Letai – Scientific/Medical Advisory Board Member to Vivid Biosciences
- Dale Muzzey – Employee of Myriad Genetics
- Rick Nolte – Research Grant Site Principal Investigator to GenMark Dx; Speakers Bureau Member with Abbott; Consultant to BioFire; Speakers Bureau Member with Roche
- Victoria Pratt – Consultant to Translational Software; Scientific/Medical Advisory Board Member with Veritas Genetics; Consultant to Glaxo; Scientific/Medical Advisory Board Member to Avalon Healthcare
- Rosana Risques – Research Grant Site Principal Investigator to TwinStrand Biosciences
- Robert Schlaberg – Employee, Corporate Board Member, Patent Holder and Stock Holder with IDbyDNA

CONTINUING EDUCATION INFORMATION

- Patricia Simner – Research Grant Site Principal Investigator to Check-Points, BV
- Jan Smout – Employee of MCR Holland
- Matija Snuderl – Honoraria and Travel Funds from Illumina
- Olena Vaske – Employee of ImmunityBio; Stock Holder with NantHealth
- Brian Walker – Research Grant Site Principal Investigator with Celgene
- Carl Wittwer – Research Grant Overall Principal Investigator and Patent Holder with BioFire; Research Grant Overall Principal Investigator with Canon Virginia; Consultant to ARUP; Associate Editor, Clinical Chemistry to AACC

Abstract Author Disclosures:
Only the abstracts listed below are included as CME content of the AMP 2019 Annual Meeting and Expo and will be defended in oral platform presentations. The other abstracts submitted to the AMP 2019 Annual Meeting and Expo that are published in The Journal of Molecular Diagnostics are not included as a CME activity.

- GENETICS: G008; G010; G014; G023; G034; G036
- HEMATOPATHOLOGY: H020; H033; H034; H039; H021; H027
- INFECTIOUS DISEASES: ID003; ID015; ID018; ID019; ID020; ID043
- INFORMATICS: I004; I013; I020; I031; I036; 1040
- SOLID TUMORS: ST009; ST010; ST015; ST094; ST121; ST132
- TECHNICAL TOPICS: TT005; TT011; TT061; TT066; TT071; TT072

Physicians
In support of improving patient care, this activity has been planned and implemented by Amedco LLC and the Association for Molecular Pathology. Amedco LLC is jointly accredited by the Accreditation Council for Continuing Medical Education (ACCME), the Accreditation Council for Pharmacy Education (ACPE), and the American Nurses Credentialing Center (ANCC), to provide continuing education for the healthcare team.

Credit Designation Statement
Amedco LLC designates this enduring activity for a maximum of **19.75 AMA PRA Category 1 Credits™**. Physicians should claim only the credit commensurate with the extent of their participation in the activity.

CMLE
This activity has been planned and implemented in accordance with the Amedco and joint providership of the American Society for Clinical Pathology (ASCP) and the Association for Molecular Pathology (AMP). ASCP CMLE credit hours are acceptable for the ASCP Board of Certification Maintenance Program (CMP).

American Board of Pathology Self-Assessment Credit
SAM satisfactory completion: Learners must pass the MOC post-test with a score of 80% or higher and complete an evaluation form to receive a certificate of completion. Your chosen sessions must be attended in their entirety. Partial credit of individual sessions is not available. If you are seeking continuing education credit for a specialty not listed below, it is your responsibility to contact your licensing/certification board to determine course eligibility for your licensing/certification requirement.

This course is valid for up to 19.75 of SA-CME Self-Assessment credits (SAMs). Learners should self-submit these credits to their boards.

CONTINUING EDUCATION INFORMATION

PLEASE NOTE: Sessions that are not eligible for Continuing Medical Education (CME):

The meeting program states those events which are not a Continuing Medical Education activity with the designation "NOT CME."

The following events/sessions are not eligible for CME:

- Social events and meals listed in the meeting program.
- Visiting exhibits because of standards of the ACCME that are designed to prevent commercial bias.
- Viewing posters in the Exhibit Hall because the posters are in the line of sight of commercial exhibits.

ONLINE Continuing Education (CE) Application and Meeting Evaluation

Instructions on how to claim continuing education credit will be sent to all attendees by e-mail following the Annual Meeting & Expo.

Applications for CME and CMLE credits will be submitted ONLINE. Keep track of your credit by completing the Credit Tracker found on the tab divider for this section. Complete only for the sessions that you attended, then transfer your information to the online form.

IMPORTANT: The deadline to claim CME/CMLE is Tuesday, December 31, 2019

NOTE: Meeting participants may receive both CME and SAM credit, but it is important that applicants understand that **both types of credit cannot be claimed for the same content** and the total number of credits claimed cannot exceed 19.75. Applicants verify that they will not claim SAM credit on any content (e.g., sessions/workshops/symposia) for which CME credit has been - or is being - claimed and vice-versa.

Please contact AMP via email (AMPEducation@amp.org) if you have any questions regarding Continuing Education.

Certificate of Attendance

We value your comments and feedback on the AMP 2019 Annual Meeting & Expo regardless of whether you apply for CE credit. If you do not apply for CE, please submit your Meeting Evaluation no later than December 31, 2019. Instructions will be provided in the post-meeting e-mail. You will receive a Certificate of Attendance upon completion.

NOTES

PROGRAM-AT-A-GLANCE

Announcing TruSight™ Oncology 500 ctDNA and TruSight Oncology 500 High-Throughput assays

We're excited to announce our new TruSight Oncology 500 ctDNA and TruSight Oncology 500 High-Throughput assays (available Q1 2020). We've enabled our new assays to run on the high-throughput NovaSeq™ 6000 sequencing system, giving you the flexibility of analyzing blood and tissue samples on a single, consolidated system. By evolving our solutions for oncology, we are setting a new standard for testing in the lab.

Visit us at booth 2341 to learn more about TruSight Oncology 500.

Pre-orders available at www.illumina.com/TSO500NovaSeq

illumina.com

For Research Use Only. Not for use in diagnostic procedures.

illumina®

HOLOGIC®

Infinite Power Together

PROGRAM-AT-A-GLANCE

Consolidate your molecular testing today on a platform that offers scalability and growth for tomorrow.

ADD ON **PANTHER** FUSION®

ADD ON **PANTHER**® PLUS*

ADD ON **PANTHER**® LINK*

ADD ON **PANTHER**® TRAX*

WOMEN'S HEALTH AND INFECTIOUS DISEASE ASSAY MENU

CT/NG
Mycoplasma genitalium
Trichomonas vaginalis
Bacterial vaginosis
Candida vaginitis/*Trichomonas vaginalis*
HSV 1 & 2
HPV
HPV 16 18/45
Group B Strep
Zika Virus

HIV-1 Quant
HIV-1 Qual Claim*†
HCV Quant Dx
HBV Quant
CMV*
Flu A/B/RSV
Paraflu
AdV/hMPV/RV
Bordetella*
GI Panel*

PANTHER®

* In development and not for sale.
† Seeking dual claim for the HIV-1 Quant assay.

Visit us at Booth 2621

The Aptima Zika Virus assay:
- This test has not been FDA cleared or approved;
- This test has been authorized by FDA under an EUA for use by authorized laboratories;
- This test has been authorized only for the detection of RNA from Zika virus and diagnosis of Zika virus infection, not for any other viruses or pathogens; and
- This test is only authorized for the duration of the declaration that circumstances exist justifying the authorization of the emergency use of in vitro diagnostic tests for detection of Zika virus and/or diagnosis of Zika virus infection undersection 564(b)(1) of the Act, 21 U.S.C.§ 360bbb-3(b)(1), unless the authorization is terminated or revoked sooner.

PROGRAM-AT-A-GLANCE

Chart

		Thursday, 11/07/19	Friday, 11/08/19	Saturday, 11/09/19
MORNING	06:45-08:00	Breakfast	Breakfast	Breakfast
	07:00-07:30	Targeted Topics	Targeted Topics	Targeted Topics
	07:30-08:00			
	08:00-08:30	Break	Break	Break
	08:30-09:00	Opening Remarks Award for Excellence Lecture	Symposia Sessions	Symposia Sessions
	09:00-09:30			
	09:30-10:00	Break	Visit the Exhibits, AMP Central & Posters	Visit the Exhibits, AMP Central & Posters (Odd-numbered Posters)
	10:00-10:30	Symposia Sessions		
	10:30-11:00		Breakout Sessions	Breakout Sessions
	11:00-11:30			
	11:30-12:00	Lunch	Lunch	Lunch
AFTERNOON	12:00-12:30			
	12:30-01:00	Breakout Sessions	Breakout Sessions	Breakout Sessions
	01:00-01:30			
	01:30-02:00			
	02:00-02:30	Visit the Exhibits, AMP Central & Posters (Award Judging & General Viewing)	Visit the Exhibits, AMP Central & Posters (Even-numbered Posters)	Break AMP Subdivision Open Forums
	02:30-03:00			
	03:00-03:30			
	03:30-04:00	Breakout Sessions	Plenary Session	Break Plenary Session
	04:00-04:30			
	04:30-05:00	Break	Break	Closing Remarks
	05:00-05:30	Plenary Session	Business Meeting & Award Session	
	05:30-06:00			
	06:00-06:30	Welcome Reception (Supported by QIAGEN)		
	06:30-07:00			
	07:00-07:30		Amazing Molecular Party	
	07:30-08:00			
	08:00-08:30			
	08:30-09:00			

MEETING-AT-A-GLANCE

Listing

Tuesday, November 5, 2019		
8:00 am – 5:00 pm	**Advocacy Day** *(Separate Registration)*	*Offsite*
8:00 am – 4:30 pm	**AMP Reference Materials Forum**	*Hilton, Holiday Ballroom 1-2*
12:00 pm – 5:00 pm	**Guest Society Symposia & Pre-Meeting Workshops** *(Separate Registration)*	*Hilton, Holiday Ballroom 4-5*
11:00 am – 6:00 pm	**Attendee, Speaker, and Exhibitor Registration and Check-In**	*Pratt Street Lobby, Level 300*
6:30 pm – 8:30 pm	**Board of Directors Dinner** *(Invitation Only)*	*Offsite*
Wednesday, November 6, 2019		
7:00 am – 5:00 pm	**Attendee, Speaker, and Exhibitor Registration and Check-In**	*Pratt Street Lobby, Level 300*
7:30 am – 11:30 am	**Board of Directors Meeting** *(Invitation Only)*	*Hilton, Ruth Room*
8:00 am – 5:00 pm	**Corporate Workshop Day** *(No Registration Required!)*	*Various Rooms, Level 300*
8:30 am – 3:45 pm	**Molecular Pathology Outreach Course (MPOC)** *(Separate Registration)*	*Hilton, Holiday Ballroom 1-2*
1:00 pm – 6:00 pm	**Committee Meetings** *(Invitation Only)*	*Hilton, Various Rooms*
6:00 pm – 7:00 pm	**Volunteer Appreciation Reception** *(Invitation Only)*	*Hilton, Peale Room*
7:00 pm – 8:00 pm	**Trainee Happy Hour**	*Leinenkugel's Beer Garden , see Page 13 for details*
Thursday, November 7, 2019		
6:30 am – 8:00 am	**Poster Set-Up**	*Exhibit Hall A-G, Level 100*
6:45 am – 5:00 pm	**Attendee, Speaker, and Exhibitor Registration and Check-In**	*Pratt Street Lobby, Level 300*
11:30 am – 4:30 pm 5:45 pm – 7:00 pm	**Expo Hall Open** *(Note: the Expo Hall will be closed from 4:30pm – 5:45pm)*	*Exhibit Hall A-G, Level 100*

Thursday, November 7, 2019

6:45 am – 8:00 am **Continental Breakfast**

Location: Session Room Foyers, Level 300

7:00 am – 8:00 am **Targeted Topics**

◆**Artificial Intelligence and Diagnostics Microbiology: Friend or Foe?**

Location: Rooms 339-342, Level 300 **CE Credit:** 1 **Path:** Infectious Diseases

Moderators: *Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA and Paul Luethy, University of Maryland School of Medicine, Baltimore, MD, USA*

Use of Machine Learning Algorithms to Support Clinical Microbiology Culture Interpretation
Karissa Culbreath, PhD, TriCore Reference Laboratories, Albuquerque, NM, USA

Detection of Outbreaks and Unusual Pathogen using AI and Machine Learning
Amy Leber, PhD, Nationwide Childrens Hospital, Columbus, OH, USA

◆**Case Studies in Genetics**

Location: Rooms 324-326, Level 300 **CE Credit:** 1 **Path:** Infectious Diseases

Moderators: *Elaine Spector, PhD, University of Colorado School of Medicine, Aurora, CO, USA and Yassmine Akkari, PhD, Legacy Health, Portland, OR, USA*

Ultra-hypermutated Pediatric Glioblastoma of Lynch Syndrome Mimicking Constitutional Mismatch Repair Deficiency Syndrome
Chen Yang, MD, PhD, Virginia Commonwealth University, Richmond, VA, USA

A Case of T-PLL with EZH2 Mutation; EZH2 the Sword or the Shield?
Panieh Terraf, PhD, Harvard Medical School - Brigham and Women's Hospital, Boston, MA, USA

Exome Reanalysis in a Patient with a Somatic CN-LOH in 17p and TP53 Mutation, and a Germline DNAJC21 Biallelic Mutation Associated with Myelodysplastic Susceptibility
Elan Hahn, MD, University of Toronto, Toronto, Ontario, Canada

Somatic Mosaic IDH1 Mutation in a Case of Maffucci Syndrome
Diana Bryk, MD, New York Presbyterian - Columbia, New York, NY, USA

◆**Case Studies in Hematopathology**

Location: Rooms 327-329, Level 300 **CE Credit:** 1 **Path:** Cancer/Oncology

Moderators: *Mark D. Ewalt, MD, University of Colorado School of Medicine, Aurora, CO, USA and Kristin Hunt Karner, MD, ARUP Laboratories, Salt Lake City, UT, USA*

A Surprising Finding in Primary Cutaneous CD8-positive Aggressive Epidermotropic Cytotoxic T-cell Lymphoma
Mark Evans, MD, University of California, Irvine, Orange, CA, USA

"Clonal Selection Following FLT3 Tyrosine Kinase Inhibitor Treatment for Acute Myeloid Leukemia"
Adam Fisch, Brigham and Women's Hospital, Boston, MA, USA

Identification of a Cryptic ABL1 Rearrangement in a Refractory Acute Myeloid Leukemia Patient with Diploid Karyotype by Conventional Cytogenetics
Arash Ronaghy, MD, PhD, MD Anderson Cancer Center, Houston, TX, USA

Muddy Waters: A Report of Granulocytes Infusion Confounding Next-Generation Sequencing Interpretation
Tareq Qdaisat, MD, University of Nebraska Medical Center, Omaha, NE, USA

MEETING AT-A-GLANCE LISTING

◆**Case Studies in Solid Tumors**
Location: Rooms 318-323, Level 300 **CE Credit:** 1 **Path:** Cancer/Oncology

Moderators: *Christina Lockwood, PhD, University of Washington, Seattle, WA, USA and Christian Kunder, MD, PhD, Stanford University, Stanford, CA, USA*

Compound EGFR and BRAF variants in NSCLC against the backdrop of suspected MEN2A
Jeremy Adler, MD, Pennsylvania Hospital, UPHS, Philadelphia, PA, USA

Expanded Next Generation Sequencing Panel Detects A Rare EGFR Kinase Domain Duplication In A Patient with Metastatic Lung Cancer
Jong Kim, MD, Cedars-Sinai Medical Center, Los Angeles, CA, USA

Pitfalls in Identification of Mismatch Repair Deficiency: An Unusual Pulmonary Intimal Sarcoma.
Wanying Zhang, MD, New York Presbyterian Hospital, New York, NY, USA

EGFR-Mutated Lung Adenocarcinoma with Early Resistance to Osimertinib
Brennan Decker, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA

8:00 am – 8:15 am Break

8:15 am – 8:30 am Opening Remarks

◆**Opening Remarks**
Location: Ballroom, Level 400

Neal Lindeman, MD, Brigham & Women's Hospital, Cambridge, MA, USA

8:30 am – 9:45 am Award Lecture

◆**Award for Excellence Lecture**
Location: Ballroom, Level 400 **CE Credit:** 1.25 **Path:** Special Session

Moderators: *Neal Lindeman, MD, Brigham & Women's Hospital, Cambridge, MA, USA (2019 Program Chair) and Victoria M. Pratt, PhD, Indiana University School of Medicine, Indianapolis, IN, USA (AMP President)*

Efficient Use of the Available DNA – A Career
Russell Higuchi, PhD, Cepheid, Sunnyvale, CA, USA

9:45 am – 10:00 am Coffee Break
Location: Ballroom Foyer, Level 400

10:00 am – 11:30 am Symposia Sessions

◆**Criminal Investigations & Forensics**
Location: Rooms 309-310, Level 300 **CE Credit:** 1.5 **Path:** Inherited Conditions; Molecular Methodologies & Technologies

Moderators: *Elaine Spector, PhD, University of Colorado School of Medicine, Aurora, CO, USA and Peter Kang, MD, Promis Diagnostics, Studio City, CA, USA*

Rapid DNA: From Research to Field
Amanda Sozer, PhD, SNA International, Washington, D.C., USA

Forensic DNA Testing at the Crossroads of Science, Law, and Policy
Frederick Bieber, PhD, Harvard Medical School, Boston, MA, USA

Basics of Genetic Genealogy and Its Impact on Forensic Investigation
Howard Cash, Gene Codes Corporation, Ann Arbor, MI, USA

◆**CRISPR-CAS: Applications for Diagnostics and Therapeutics of Human diseases**
Location: Ballroom, Level 400 **CE Credit:** 1.5 **Path:** Infectious Diseases; Molecular Methodologies & Technologies

Moderators: *Fernanda Sabato, MS, Virginia Commonwealth Univ/MCV Clinical Support Center, Richmond, VA, USA and Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

Getting More from your MiSeq with DASH and FLASH
Emily D. Crawford, PhD, Chan Zuckerberg Biohub, San Francsico, CA, USA

Assessing Unintended Off-Target Mutations Caused by Cas9 and Other Gene Editing Enzymes
Vikram Pattanayak, MD, PhD, Massachusetts General Hospital, Boston, MA, USA

◆**Genetics of Sensitivity and Resistance to Non-Chemotherapy Agents**
Location: Rooms 314-317, Level 300 **CE Credit:** 1.5 **Path:** Cancer/Oncology

Moderators: *Mark D. Ewalt, MD, University of Colorado School of Medicine, Aurora, CO, USA and Rashmi Kanagal Shamanna, MD, The University of Texas MD Anderson Cancer Center, Houston, TX, USA*

Choosing Patient Therapy with Dynamic BH3 Profiling
Anthony Letai, MD, PhD, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, USA

Diverse Mechanisms of Acquired Resistance to CAR T Cell Immunotherapy
Andrei Thomas-Tikhonenko, PhD, Children's Hospital of Philadelphia, Philadelphia, PA, USA

11:30 am – 12:45 pm General Lunch - Visit Expo Hall and View Posters

Location: Exhibit Hall A-G, Level 100

Networking Lunches: Please see lunch descriptions in the "Highlights & General Information" section of the Program Book, Pages 19-20.

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

12:45 pm – 2:00 pm Breakout Sessions

◆**Biobanking and 3D-Organoid Technology**
Location: Rooms 339-342, Level 300 **CE Credit:** 1.25 **Path:** Advocacy/Lab Management; Molecular Methodologies & Technologies; Cancer/Oncology

Moderators: *Fernanda Sabato, MS, Virginia Commonwealth Univ/MCV Clinical Support Center, Richmond, VA, USA and Peter Kang, MD, Promis Diagnostics, Studio City, CA, USA*

Perspective on Establishing a Biorepository for Clinical and Research Use
Kristy Crooks, PhD, University of Colorado, Aurora, CO, USA

Profiling the DNA Damage Repair Capacity of High Grade Serous Ovarian Tumors using Patient-Derived Organoids
Sarah Hill, MD, PhD, Dana-Farber Cancer Institute, Boston, MA, USA

MEETING AT-A-GLANCE LISTING

◆**Diagnostic Stewardship for Molecular Testing**
Location: Rooms 327-329, Level 300 **CE Credit:** 1.25 **Path:** Infectious Diseases; Molecular Methodologies & Technologies

Moderators: *Jennifer Dien Bard, PhD, Childrens Hospital Los Angeles, Los Angeles, CA, USA and Erin McElvania, NorthShore University HealthSystem, Evanston, IL, USA*

Diagnostic Stewardship for Molecular Testing
Kimberle Chapin, MD, Brown Biology and Medicine, Providence, RI, USA

The Art of Navigating Molecular Infectious Disease Test Results: From Ordering To Application In the Clinical Setting
Sejal Morjaria, MD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

◆**Is Bigger Always Better? Targeted versus Genome Oncology Tests**
Location: Rooms 309-310, Level 300 **CE Credit:** 1.25 **Path:** Cancer/Oncology

Moderators: *Christina Lockwood, PhD, University of Washington, Seattle, WA, USA and Ryan Schmidt, MD, PhD, Children's Hospital Los Angeles, Los Angeles, CA, USA*

Big Data and Little Patients: Targeted Sequencing for Pediatric Brain Tumors
Sarah Leary, MD, MS, Seattle Children's Hospital, University of Washington and Fred Hutchinson Cancer Research Center, Seattle, WA, USA

Bigger is Better: More Cancer Genes in More Patients
Wendy Chung, MD PhD, Columbia University, New York, NY, USA

◆**Reimbursement: It's Never too Late to Start Getting Paid**
Location: Rooms 307-308, Level 300 **CE Credit:** 1.25 **Path:** Advocacy/Lab Management

Moderators: *Rajyasree Emmadi, MD, University of Illinois, Chicago, IL, USA and Samuel Caughron, MD, MAWD Pathology Group, Lenexa, KS, USA*

Reimbursement: It's Never too Late to Start Getting Paid
Anthony Sireci, MD, Loxo Oncology, Stamford, CT, USA

Reimbursement: It's Never too Late to Start Getting Paid
Aaron D. Bossler, MD, PhD, University of Iowa, Iowa City, IO, USA

Demystifying Molecular testing coverage and policies: MolDX and Medicare
Gabriel Bien-Willner, MD, PhD, Palmetto GBA, TX, USA

◆**State of Pharmacogenetics**
Location: Rooms 314-317, Level 300 **CE Credit:** 1.25 **Path:** Advocacy/Lab Management; Cancer/Oncology; Inherited Conditions

Moderators: *Elaine Spector, PhD, University of Colorado School of Medicine, Aurora, CO, USA and Matthew Lebo, PhD, Brigham & Women's Hospital, Cambridge, MA, USA and Tamara Roman, The University of North Carolina at Chapel Hill, Durham, NC, USA*

Clinical Implementation of Pharmacogenomics
Philip E. Empey, PharmD, PhD, University of Pittsburgh/UPMC, Pittsburgh, PA, USA

What's New in Pharmacogenetics?
Victoria M. Pratt, PhD, Indiana University School of Medicine, Indianapolis, IN, USA

2:00 pm – 3:45 pm **Coffee Break - Visit Expo Hall and View Posters**

Location: Exhibit Hall A-G, Level 100

AMP Central Activities: Technologist Mixer

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

3:45 pm – 4:30 pm **Breakout Sessions**

◆**AMP CPC's ID Multiplex Working Group: Update & Open Comment Forum**
Location: Rooms 314-317, Level 300 **CE Credit:** 0.75 **Path:** Infectious Diseases

AMP CPC's ID Multiplex Working Group: Update & Open Comment Forum
Michael Lewinski, PhD, Roche Molecular Systems, Inc., Pleasanton, CA, USA

◆**AMP CPC's In Silico Reference Materials Working Group: Update & Open Comment Forum**
Location: Rooms 309-310, Level 300 **CE Credit:** 0.75 **Path:** Advocacy/Lab Management; Infectious Diseases; Informatics

AMP CPC's In Silico Reference Materials Working Group: Update & Open Comment Forum
Eric J. Duncavage, MD, Washington University, Saint Louis, MO, USA; Justin M. Zook, PhD, National Inst of Standards & Tech, Gaithersburg, MD, USA

◆**AMP CPC's T & B Cell Clonality Working Group: Update & Open Comment Forum**
Location: Rooms 318-323, Level 300 **CE Credit:** 0.75 **Path:** Cancer/Oncology

AMP CPC's T & B Cell Clonality Working Group: Update & Open Comment Forum
David S. Viswanatha, MD, Mayo Clinic and Foundation, Rochester, MN, USA

◆**AMP CPC's Tumor Mutational Burden Working Group: Update & Open Comment Forum**
Location: Rooms 307-308, Level 300 **CE Credit:** 0.75 **Path:** Cancer/Oncology

AMP CPC's Tumor Mutational Burden Working Group: Update & Open Comment Forum
Larissa V. Furtado, MD, St. Jude Children's Research Hospital, Memphis, TN, USA

◆**The first 25 years of AMP: Our Society's Groundbreaking Past and Future Opportunities**
Location: Rooms 327-329, Level 300 **CE Credit:** 0.75 **Path:** Special Session; Molecular Methodologies & Technologies

Moderator: *Margaret L. Gulley, MD, Univ of North Carolina-Chapel Hill Sch Medicine, Chapel Hill, NC, USA*

Standing of Molecular within the Pathology/Lab Profession
Karen L. Kaul, MD, PhD, NorthShore University Health System, Evanston, IL, USA

Evolving Technologies and Automation
Karl Voelkerding, MD, University of Utah School of Medicine, Salt Lake City, UT, USA

Panel Discussion
Federico A. Monzon, MD, Castle Biosciences, Friendswood, TX, USA; Aaron D. Bossler, MD, PhD, University of Iowa, Iowa City, IO, USA; Yaolin Zhou, MD, Univ of Oklahoma Health Sciences Center, Oklahoma City, OK, USA; Helen Fernandes, PhD, Columbia University Medical Center, Wayne, NJ, USA

MEETING AT-A-GLANCE LISTING

4:30 pm – 4:45 pm **Break**

4:45 pm – 5:45 pm **Plenary Session**

- **Polygenic Risk Scores: Translating Research Advances into the Clinical Domain**

Location: Ballroom, Level 400 **CE Credit:** 1 **Path:** Informatics

Moderators: *Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA and Matthew Lebo, PhD, Brigham & Women's Hospital, Cambridge, MA, USA*

Using Polygenic Risk Scores (PRS) for Breast Cancer to Inform Screening: Model Fit, Calibration, and Utility

Peter Kraft, PhD, Harvard T.H. Chan School of Public Health, Boston, MA, USA

5:45 pm – 7:00 pm **Welcome Reception** *(Supported by QIAGEN)*

Location: Exhibit Hall A-G, Level 100

AMP Central Activities: Celebrate AMP's New Vision

Friday, November 8, 2019

6:45 am – 5:00 pm **Attendee, Speaker, and Exhibitor Registration and Check-In**

Location: Pratt Street Lobby, Level 300

6:45 am – 8:00 am **Continental Breakfast**

Location: Session Room Foyers, Level 300

9:00 am – 4:00 pm **Expo Hall Open**

Location: Exhibit Hall A-G, Level 100

7:00 am – 8:00 am **Targeted Topics**

- **Behind the Curtain: Developing Clinical Knowledgebase Systems**

Location: Rooms 309-310, Level 300 **CE Credit:** 1 **Path:** Informatics

Moderators: *Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA and Andrea Sboner, PhD, Weill Cornell Medicine, New York, NY, USA*

Behind the Curtain: Developing Clinical Knowledgebase Systems

Malachi Griffith, PhD, Washington University School of Medicine, St. Louis, MO, USA

- **Blood Bank & HLA**

Location: Rooms 318-323, Level 300 **CE Credit:** 1 **Path:** Inherited Conditions

Moderators: *Peter Kang, MD, Promis Diagnostics, Studio City, CA, USA and Craig Soderquist, Columbia University Medical Center, New York, NY, USA*

Blood Group Genotyping from High Density Arrays to Whole Genomes

Bill Lane, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA

◆**Case Studies in Hematopathology**
Location: Rooms 324-326, Level 300 **CE Credit:** 1 **Path:** Cancer/Oncology

Moderators: *Rashmi Kanagal Shamanna, MD, The University of Texas MD Anderson Cancer Center, Houston, TX, USA and Rashmi Goswami, MD, PhD, University of Toronto, Canada*

B-lymphoblastic Leukemia with ZNF384 Gene Rearrangement
Shweta Bhavsar, MBBs, MD, University of Pittsburgh Medical Center, Pittsburgh, PA, USA

Molecular Diagnosis of MDS in a Non-Diagnostic Bone Marrow Specimen
Jeffrey SoRelle, MD, University of Texas Southwestern Medical Center, Dallas, TX, USA

The Role of Lymphoma Sequencing Panel in the Diagnosis of Pediatric-Type Follicular Lymphoma
Guang Yang, MD, PhD, University of Pennsylvania, Philadelphia, PA, USA

5q- in a Patient with Chronic Myelogenous Leukemia in Accelerated Phase
James Corines, DO, SUNY Upstate Medical University, Syracuse, NY, USA

◆**How to Validate Rare Findings**
Location: Rooms 314-317, Level 300 **CE Credit:** 1 **Path:** Cancer/Oncology

Moderators: *Christina Lockwood, PhD, University of Washington, Seattle, WA, USA and Adam Fisch, Brigham and Women's Hospital, Boston, MA, USA*

How to Validate Rare Findings - Focus on Novel Fusions
John Iafrate, MD PhD, Massachusetts General Hospital, Boston, MA, USA

Did I Find the Right Needle in the Haystack? Sensitivity and Specificity Challenges Revealed by Ultra-accurate NGS
Rosana Risques, PhD, UW Pathology, Seattle, WA, USA

◆**Novel Mechanisms of Acquired Resistance to Targeted Therapies in Cancer**
Location: Rooms 327-329, Level 300 **CE Credit:** 1 **Path:** Cancer/Oncology

Moderator: *Shelby Melton, MD, VA North Texas Health Care System, Dallas, TX, USA*

Novel Mechanisms of Acquired Resistance to Targeted Therapies in Cancer
Fei Dong, MD, Brigham and Women's Hospital, Boston, MA, USA

8:00 am – 8:15 am Break

8:15 am – 9:45 am Symposia Sessions

◆**Carrier Screening: The Good, The Bad, and The Ugly**
Location: Rooms 314-317, Level 300 **CE Credit:** 1.5 **Path:** Inherited Conditions

Moderators: *Elaine Spector, PhD, University of Colorado School of Medicine, Aurora, CO, USA and Peter Kang, MD, Promis Diagnostics, Studio City, CA, USA*

The Limitations and Consequences of Ethnicity-specific Guidelines for Carrier Screening
Dale Muzzey, PhD, Myriad Women's Health, Inc., South San Francisco, CA, USA

Current Complexities and Future Directions of Expanded Carrier Screening
Nicole Faulkner, PhD, FACMGG, Invitae Corporation, San Francisco, CA, USA

Technological Advances and Detections Rates: Demystifying the Influence of Ethnicity on Carrier Detection and Residual Risk
Lisa Edelmann, PhD, Sema4, New York, NY, USA

MEETING AT-A-GLANCE LISTING

◆**Emerging Technology for Circulating Tumor Cells, Beyond Counting/ctDNA Alternative Fluids**
Location: Ballroom, Level 400 **CE Credit:** 1.5 **Path:** Cancer/Oncology; Molecular Methodologies & Technologies

Moderators: *Fernanda Sabato, MS, Virginia Commonwealth Univ/MCV Clinical Support Center, Richmond, VA, USA and Christina Lockwood, PhD, University of Washington, Seattle, WA, USA*

Advances in Liquid Biopsy: Isolation, Analysis and Expansion of CTCs
Sunitha Nagrath, PhD, University of Michigan, Ann Arbor, MI, USA

Microfluidic Platforms for the Efficient Isolation of Circulating Leukemia Cells and Circulating Plasma Cells
Steven A. Soper, PhD, The University of Kansas, Lawrence, KS, USA

◆**Structural Variation Detection in Human Disease**
Location: Rooms 309-310, Level 300 **CE Credit:** 1.5 **Path:** Informatics

Moderators: *Matthew Lebo, PhD, Brigham & Women's Hospital, Cambridge, MA, USA and Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA*

Patterns of Complex Structural Variation across Thousands of Cancer Whole Genomes
Marcin Imielinski, MD, PhD, Weill Cornell Medical College, Brooklyn, NY, USA

Identification and Characterization of Cryptic Structural Variation in Human Genomes
Ryan Mills, PhD, University of Michigan, Ann Arbor, MI, USA

9:45 am – 10:45 am Coffee Break - Visit Expo Hall and View Posters

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

10:45 am – 12:15 pm Breakout Sessions

◆**Hands-on Workshop: Variant Interpretation & Classification**
Location: Rooms 318-323, Level 300 **CE Credit:** 1.5 **Path:** Informatics; Inherited Conditions

Moderators: *Matthew Lebo, PhD, Brigham & Women's Hospital, Cambridge, MA, USA and Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA*

Hands-on Workshop: Variant Interpretation & Classification
Mark Routbort, MD, PhD, University of Texas MD Anderson Cancer Center, Houston, TX, USA

◆**Metagenomics in Prime Time**
Location: Rooms 314-317, Level 300 **CE Credit:** 1.5 **Path:** Infectious Diseases

Moderators: *Jennifer Dien Bard, PhD, Childrens Hospital Los Angeles, Los Angeles, CA, USA and Nathan Ledeboer, PhD, Medical College of Wisconsin, Milwaukee, WI, USA*

Panel Discussion
Robert Schlaberg, MD, MPH, IDbyDNA, Salt Lake City, UT, USA; Charles Chiu, MD, PhD, University of California, San Francisco, San Francisco, CA, USA; Erin Graf, PhD, Mayo Clinic Hospital, Arizona, Phoenix, AZ, USA; Patricia Simner, MSc, PhD, Johns Hopkins University School of Medicine, Baltimore, MD, USA

◆**Picking a LIMS System**
Location: Rooms 327-329, Level 300 **CE Credit:** 1.5 **Path:** Advocacy/Lab Management; Informatics

Moderators: *Renee Webb, BS, Texas Children's Hospital, Houston, TX, USA and Scott Turner, VCU, Richmond, VA, USA*

Do-It-Yourself Molecular LIMS
Long P. Le, MD, PhD, Massachusetts General Hospital, Charlestown, MA, USA

Picking a LIMS System
Kristina Cusmano-Ozog, MD, Children's National, Palo Alto, CA, USA

Development of a Laboratory Information System to Support Clinical NGS Testing
Michael Kluk, MD, PhD, Weill Cornell Medicine, New York, NY, USA

◆**Process Validation and Quality Assurance Around the World**
Location: Rooms 339-342, Level 300 **CE Credit:** 1.5 **Path:** Advocacy/Lab Management

Moderator: *Marilyn Li, MD, Children's Hospital of Philadelphia, Philadelphia, PA, USA*

ESP Molecular Pathology WG: Diagnosis and Clinical Research Reproducibility
Giorgio Stanta, MD, PhD, University of Trieste, Duino-Aurisina, Friuli-Venezia Giulia, Italy

Quality Assessment Experience in Brazil
Roberta Sitnik, MSc, PhD, Departamento de Patologia Clínica e Anatomia Patológica, São Paulo, Brazil

◆**Updates on Emerging Technologies**
Location: Rooms 309-310, Level 300 **CE Credit:** 1.5 **Path:** Molecular Methodologies & Technologies

Moderators: *Fernanda Sabato, MS, Virginia Commonwealth Univ/MCV Clinical Support Center, Richmond, VA, USA and Ying Zou, Johns Hopkins University, Baltimore, MD, USA*

Nanopore Sequencing Comes of Age
Miten Jain, PhD, University of California Santa Cruz, Santa Cruz, CA, USA

Extreme Molecular Diagnostics
Carl Wittwer, MD, PhD, University of Utah, Salt Lake City, UT, USA

12:15 pm – 1:30 pm General Lunch - Visit Expo Hall and View Posters

Location: Exhibit Hall A-G, Level 100

Networking Lunches: Please see lunch descriptions in the "Highlights & General Information" section of the Program Book, Pages 19-20.

AMP Central Activities: Education Showcase

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

Speed Networking: Please visit the Networking Corner in the Expo Hall from 12:30pm - 1:00pm. Open to all registered attendees.

MEETING AT-A-GLANCE LISTING

1:30 pm – 2:45 pm Breakout Sessions

◆**Cell-free DNA testing for Autosomal Dominant disorders**
Location: Rooms 309-310, Level 300 **CE Credit:** 1.25 **Path:** Inherited Conditions

Moderators: *Peter Kang, MD, Promis Diagnostics, Studio City, CA, USA and Annette Leon, Color Genomics, Burlingame, CA, USA*

Non-invasive Prenatal Sequencing for Multiple Mendelian Monogenic Disorders using Circulating Cell-free Fetal DNA
Shashikant Kulkarni, PhD, FACMG, Baylor College of Medicine, Houston, TX, USA

Prenatal Diagnosis: The Next Generation
Mark I. Evans, MD, Comprehensive Genetics & Icahn School of Medicine Mt. Sinai, New York, NY, USA

◆**New Players in Reimbursement: Laboratory Benefit Managers *(Sponsored by the AMP Economic Affairs Committee)***
Location: Rooms 339-342, Level 300 **CE Credit:** 1.25 **Path:** Advocacy/Lab Management

Moderator: *Samuel Caughron, MD, MAWD Pathology Group, Lenexa, KS, USA*

Panel Discussion
Geoffrey Baird, MD, PhD, University of Washington, Seattle, WA, USA; Trish Brown, MS, LCGC, Illumina, Inc., San Diego, CA, USA; Heather Agostinelli, Xifin, Inc., San Diego, CA, USA

◆**Point Counterpoint: Who Owns Molecular Infectious Disease Testing?**
Location: Rooms 324-326, Level 300 **CE Credit:** 1.25 **Path:** Advocacy/Lab Management; Infectious Diseases

Moderators: *Jennifer Dien Bard, PhD, Childrens Hospital Los Angeles, Los Angeles, CA, USA and Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

Point Counterpoint: Who Owns Molecular Infectious Disease Testing?
Nathan Ledeboer, PhD, Medical College of Wisconsin, Milwaukee, WI, USA; Frederick S. Nolte, PhD, Medical Univ of South Carolina, Charleston, SC, USA

◆**Practical Approaches to Centralizing (or Decentralizing) Molecular Testing**
Location: Rooms 307-308, Level 300 **CE Credit:** 1.25 **Path:** Advocacy/Lab Management

Moderators: *Renee Webb, BS, Texas Children's Hospital, Houston, TX, USA and Michael Alberti, Washington University, Saint Louis, MO, USA*

Centralized Testing in Molecular Pathology via Lean Laboratory Design
John W. Longshore, PhD, Carolinas Pathology Group, Charlotte, NC, USA

Molecular Laboratory Organization: the University of Washington Experience
Daniel E. Sabath, MD, PhD, University of Washington School of Medicine, Seattle, WA, USA

◆**Updates in Myeloma Genomics**
Location: Rooms 318-323, Level 300 **CE Credit:** 1.25 **Path:** Cancer/Oncology

Moderators: *Mark D. Ewalt, MD, University of Colorado School of Medicine, Aurora, CO, USA and Jesse Cox, University of Nebraska Medical Center, Omaha, NE, USA*

Advances in Multiple Myeloma Genomics
Brian A. Walker, BSc, PhD, University of Arkansas for Medical Sciences, Little Rock, AR, USA

Molecular Monitoring of Myeloma
Nikhil Munshi, MD, Dana-Farber Cancer Institute, Boston, MA, USA

2:45 pm – 4:00 pm **Coffee Break - Visit Expo Hall and View Posters**

Location: Exhibit Hall A-G, Level 100

Posters: Even-numbered posters attended from 2:45pm - 3:45pm.

AMP Central Activities: Get Involved with AMP! AMP Committee "Meet & Greet" Event

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

4:00 pm – 5:00 pm **Plenary Session**

- **Climate Change & Global Surveillance**

Location: Ballroom, Level 400 **CE Credit:** 1 **Path:** Infectious Diseases

Moderators: *Jennifer Dien Bard, PhD, Childrens Hospital Los Angeles, Los Angeles, CA, USA and Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

Climate Change & Global Surveillance

Arturo Casadevall, MD, PhD, Johns Hopkins, Baltimore, MD, USA

5:00 pm – 5:15 pm **Break**

5:15 pm – 6:30 pm **Business Session**

- **Business Meeting and Awards Session *(Open to All Registered Attendees)***

Location: Rooms 314-317, Level 300 **CE Credit:** Not CME/CMLE **Path:** Special Session

7:00 pm – 10:30 pm **Social Event**

- **Amazing Molecular Party (25th Anniversary Celebration), *(Separate Registration)***

Location: Hilton, Key Ballroom 1-6

Saturday, November 9, 2019

6:45 am – 2:00 pm **Attendee, Speaker, and Exhibitor Registration and Check-In**

Location: Pratt Street Lobby, Level 300

6:45 am – 8:00 am **Continental Breakfast**

Location: Session Room Foyers, Level 300

9:00 am – 1:30 pm **Expo Hall Open**

Location: Exhibit Hall A-G, Level 100

12:30 pm – 1:30 pm **Poster Removal**

Location: Exhibit Hall A-G, Level 100

MEETING AT-A-GLANCE LISTING

7:00 am – 8:00 am Targeted Topics

◆A Review of FGFR Related Inherited Disorders

Location: Rooms 318-323, Level 300 **CE Credit:** 1 **Path:** Inherited Conditions

Moderators: *Elaine Spector, PhD, University of Colorado School of Medicine, Aurora, CO, USA and Jianling Ji, MD, MS, Children's Hospital of Los Angeles, South Pasadena, CA, USA*

The Skeletal Dysplasias; the Long and Short of It

Deborah Krakow, FACMG, UCLA School of Medicine, Los Angeles, CA, USA

◆Case Studies in Solid Tumors

Location: Rooms 324-326, Level 300 **CE Credit:** 1 **Path:** Cancer/Oncology

Moderators: *Rajyasree Emmadi, MD, University of Illinois, Chicago, IL, USA and Susan Hsiao, MD, Columbia University, New York, NY*

An Interesting Case Involving a CIC-NUTM1 Rearranged Epitheliod Tumor

Latrice Landry, PhD, MMSc, MS, Dana Farber Cancer Institute/ Brigham and Women's Hospital, Boston, MA, USA

Detection of Rare Fusion using Foundation One and Oncomine Tests: A Male in his 20's with an Aggressive Orbital Tumor

Terri Jones, MD, University of Pittsburgh Medical Center, Pittsburgh, PA, USA

A Case of Cutaneous Lymphoma with PCM1-JAK2 Rearrangement

Talent Theparee, MD, Stanford Healthcare, Stanford, CA, USA

Microsatellites: Instability in an Apparently Stable World

Patrick Leach, BS, TriCore Reference Laboratories, Albuquerque, NM, USA

◆Genetics & Immunity In Bone Marrow Failure Syndromes

Location: Rooms 307-308, Level 300 **CE Credit:** 1 **Path:** Cancer/Oncology

Moderators: *Rashmi Kanagal Shamanna, MD, The University of Texas MD Anderson Cancer Center, Houston, TX, USA and Phillip Michaels, University Health Network, Toronto, Ontario, Canada*

Genetic Pathways of Myeloid Transformation in Bone Marrow Failure Syndromes

Coleman Lindsley, MD, PhD, Dana-Farber Cancer Institute, Boston, MA, USA

◆Integrating Genomics into the EHR

Location: Rooms 327-329, Level 300 **CE Credit:** 1 **Path:** Advocacy/Lab Management; Informatics

Moderator: *Matthew Lebo, PhD, Brigham & Women's Hospital, Cambridge, MA, USA*

Barriers to Integrating Genomics More Fully into the EHR

Brian H. Shirts, MD, PhD, University of Washington, Seattle, WA, USA

◆Liquid Biopsy in Infection and Cancer

Location: Rooms 314-317, Level 300 **CE Credit:** 1 **Path:** Infectious Diseases; Molecular Methodologies & Technologies

Moderators: *Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA and Tabetha Sundin, Sentara Healthcare, Norfolk, VA, USA*

Opportunities and Challenges of Fungal Cell-Free DNA Testing for Diagnosis of Invasive Fungal Infection

Niaz Banaei, MD, Stanford University, Stanford, CA, USA

Detecting HPV Circulating Tumor DNA by Liquid Biopsy
Daniel Higginson, MD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

◆**Methylation Analysis Technologies**
Location: Rooms 309-310, Level 300 **CE Credit:** 1 **Path:** Molecular Methodologies & Technologies

Moderators: *Renee Webb, BS, Texas Children's Hospital, Houston, TX, USA and Jianhua Zhao, Genosity Inc, Dresher, PA, USA*

DNA Methylation and Machine Learning in Molecular Pathology for Diagnosis and Clinical Management
Matija Snuderl, MD, NYU Langone Medical Center, New York, NY, USA

Oncogene Activation by Pan-Cancer DNA Hypermethylation
Wei Li, PhD, Baylor College of Medicine, Houston, TX, USA

8:00 am – 8:15 am Break

8:15 am – 9:45 am Symposia Sessions

◆**Incidental Findings from Somatic Testing/Cancer Predispositions**
Location: Ballroom, Level 400 **CE Credit:** 1.5 **Path:** Cancer/Oncology; Inherited Conditions

Moderators: *Peter Kang, MD, Promis Diagnostics, Studio City, CA, USA and Christina Lockwood, PhD, University of Washington, Seattle, WA, USA*

Approaches to Returning Germline Results in an Era of Agnostic Cancer Predisposition Testing
Michael F. Walsh, MD, Memorial Sloan Kettering Cancer Center, New York City, NY, USA

The Evolving Landscape of Clinical Genomic Testing: Elective Genome Sequencing
Birgit Funke, Dr, Veritas Genetics, Newton, MA, USA

What to Expect When You Find the Unexpected: Pregnancy and Incidental Findings in Noninvasive Prenatal Screening
Susan Hancock, MS, Myriad Women's Health, Salt Lake City, UT, USA

◆**Precision Medicine in Infectious Disease**
Location: Rooms 314-317, Level 300 **CE Credit:** 1.5 **Path:** Infectious Diseases

Moderators: *Jennifer Dien Bard, PhD, Childrens Hospital Los Angeles, Los Angeles, CA, USA and Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

Genotypic Antiretroviral Resistance Testing
Benjamin Pinsky, MD, PhD, Stanford University School of Medicine, Palo Alto, CA, USA

Bacteriome and Mycobiome Imbalance and Design of Precision Medicine and Nutrition
Mahmoud A. Ghannoum, PhD, EMBA, FIDSA, FAAM, Case Western Reserve University and University Hospitals Cleveland Medical Center, Shaker Heights, OH, USA

◆**Standards and Applications of RNA-seq in Cancer**
Location: Rooms 309-310, Level 300 **CE Credit:** 1.5 **Path:** Cancer/Oncology; Informatics

Moderators: *Matthew Lebo, PhD, Brigham & Women's Hospital, Cambridge, MA, USA and Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA*

MEETING AT-A-GLANCE LISTING

RNA-seq for the Detection of Gene Fusions and Other Alterations in Cancer
Kevin C. Halling, MD, PhD, Mayo Clinic, Rochester, MN, USA

Applications of RNA-Seq in Cancer
Olena Vaske, PhD, FCCMG, University of California Santa Cruz, Santa Cruz, CA, USA

9:45 am – 10:45 am Coffee Break - Visit Expo Hall and View Posters

Location: Exhibit Hall A-G, Level 100

Posters: Odd-numbered posters attended from 9:45am - 10:45am.

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

10:45 am – 12:15 pm Breakout Sessions

◆**Featured Selections from the Journal of Molecular Diagnostics in 2019**
Location: Rooms 339-342, Level 300 **CE Credit:** 1.5 **Path:** Infectious Diseases

Moderator: *Barbara Zehnbauer, PhD, Emory School of Medicine, Atlanta, GA, USA*

Featured Selections from the Journal of Molecular Diagnostics in 2019
James Versalovic, MD, PhD, Texas Children's Hospital, Houston, TX, USA; Kevin C. Halling, MD, PhD, Mayo Clinic, Rochester, MN, USA; Stephen Lincoln, Invitae, San Francisco, CA, USA

◆**Future of Molecular Pathology**
Location: Rooms 327-329, Level 300 **CE Credit:** 1.5 **Path:** Special Session

Moderator: *Victoria M. Pratt, PhD, Indiana University School of Medicine, Indianapolis, IN, USA*

Panel Discussion
Gabriel Bien-Willner, MD, PhD, Palmetto GBA, TX, USA; Samuel K. Caughron, MD, MAWD Pathology Group, Lenexa, KS, USA; Karen L. Kaul, MD, PhD, NorthShore University Health System, Evanston, IL, USA; Federico A. Monzon, MD, Castle Biosciences, Friendswood, TX, USA; Timothy Stenzel, MD PhD FACMG FCAP, FDA, Rockville, MD, USA

◆**Tumor Mutation Burden, Clinical Utility/Efficacy and Harmonization Project**
Location: Rooms 314-317, Level 300 **CE Credit:** 1.25 **Path:** Cancer/Oncology

Moderators: *Fernanda Sabato, MS, Virginia Commonwealth Univ/MCV Clinical Support Center, Richmond, VA, USA and Melody Zhang, Stanford University School of Medicine, Palo Alto, CA, USA*

Tumor Mutational Burden (TMB): Harmonization and Future Application
Jeff Allen, PhD, Friends for Cancer Research, Washington, D.C., USA

TMB: The Case for Understanding and Harmonizing Complex Biomarkers
Albrecht Stenzinger, MD, University Hospital Heidelberg, Heidelberg, Germany

◆**Hands-on Workshop: Informatic Tools in Metagenomics**
Location: Rooms 337-338, Level 300 **CE Credit:** 1.5 **Path:** Informatics; Infectious Diseases

Moderators: *Matthew Lebo, PhD, Brigham & Women's Hospital, Cambridge, MA, USA and Sabah Kadri, PhD, Lurie Children's Hospital of Chicago, Chicago, IL, USA*

Hands-on Workshop: Informatic Tools in Metagenomics
Alexander L. Greninger, MD, PhD, MS, MPhil, University of Washington, Seattle, WA, USA; Samia Naccache, PhD, LabCorp, Seattle, Seattle, WA, USA

◆**Pipeline Showcase**

Location: Rooms 309-310, Level 300 **CE Credit:** 1.5 **Path:** Informatics

Moderators: *Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA and Somak Roy, MD, University of Pittsburgh Medical Center, Pittsburgh, PA, USA*

Pipeline Showcase

Jeremy Segal, MD, PhD, University of Chicago, Chicago, IL, USA and Ahmet Zehir, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

◆**Whole Genome Sequencing for Bacterial Strain Typing & Genomic Surveillance**

Location: Rooms 314-317, Level 300 **CE Credit:** 1.5 **Path:** Infectious Diseases; Molecular Methodologies & Technologies

Moderators: *Renee Webb, BS, Texas Children's Hospital, Houston, TX, USA and Alexandra Bryson, PhD, D(ABMM), VCU, Health, Richmond, VA, USA*

Real-time Clinical Applications for Whole Genome Sequencing of Bacteria

Brad Cookson, MD, PhD, University of Washington, Seattle, WA, USA

Bacterial Strain Typing in the Age of Whole Genome Sequencing: Promises and Pitfalls

Richard Goering, PhD, Creighton University School of Medicine, OMAHA, NE, USA

12:15 pm – 1:30 am General Lunch - Visit Expo Hall, and View Posters

Location: Exhibit Hall A-G, Level 100

AMP Central Activities: "Meet & Greet" with the JMD Editor-in-Chief

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

Speed Networking: Please visit the Networking Corner in the Expo Hall from 12:30pm – 1:00pm. Open to all registered attendees.

1:30 pm – 2:45 pm Breakout Sessions

◆**Platform Presentations of Selected Genetics Abstracts**

Location: Rooms 339-342, Level 300 **CE Credit:** 1.25 **Path:** Cancer/Oncology; Informatics; Inherited Conditions

Moderators: *Peter Kang, MD, Promis Diagnostics, Studio City, CA, USA and Wei Xie, Baylor College of Medicine, Houston, TX, USA*

G008 - Germline RAD51B Loss-of-function Variants Confer Susceptibility to Hereditary Breast and Ovarian Cancers and Result in

Diana Mandelker, MD, PhD, Memorial Sloan Kettering Cancer Center, NEW YORK, NY, USA

G014 - A Framework of Critical Considerations in Interpretation of NGS Based Tests for Germline Disorders - On Behalf of CLSI Document Development Committee (DDC) on Nucleic Acid Sequencing (MM09)

Avni Santani, PhD, Children's Hospital of Philadelphia, Philadelphia, PA, USA

G023 - Integrated Germline and Somatic Analysis Identifies Actionable Cancer Predisposing Germline Mutations in 9,734 Patients with Advanced Cancers

Liying Zhang, MD, PhD, Memorial Slone Kettering Cancer Center, New York, NY, USA

G036 - Significance Associated with Phenotype (SAP) Score – A Method for Ranking Genes and Genomic Regions Based on Sample Phenotype

Jianling Ji, MD, MS, Children's Hospital of Los Angeles, South Pasadena, CA, USA

MEETING AT-A-GLANCE LISTING

G010 - A Method to Missense Madness: Improving Clinical Variant Interpretation with a Pathway-Focused Functional Assay
Sarah E. Brnich, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

◆**Platform Presentations of Selected Hematopathology Abstracts**
Location: Rooms 307-308, Level 300 **CE Credit:** 1.25 **Path:** Cancer/Oncology; Informatics; Molecular Methodologies & Technologies

Moderators: *Rashmi Kanagal Shamanna, MD, The University of Texas MD Anderson Cancer Center, Houston, TX, USA and Mengli Zhu, Memorial Slone Kettering Cancer Center, New York, NY, USA*

H034 - Identification of Neoplastic Clonal T-cell Sequences in Unrelated Healthy Individuals: Limitations of High Throughput TRG Sequencing for Minimal Residual Disease (MRD) Analysis
Siddhartha Sen, MD, PhD, Duke University Medical Center, Durham, NC, USA

H039 - Measurable Residual Disease Monitoring for Patients with Acute Myeloid Leukemia Following Hematopoietic Cell Transplantation Using Error Corrected Hybrid Capture Next Generation Sequencing
Vidya Balagopal, PhD, University of Chicago, Chicago, IL, USA

H021 - IGH Locus Assessment using Hybrid-capture, a Proof-of-concept Study
Etienne Mahe, MD, MSc, FRCPC, FCAP, University of Calgary, Calgary, Alberta, Canada

H027 - Convergence on Genomic Abrogation of the DNA Damage Response Pathway in CLL is Observed in Patients with Loss of18p
Waihay Wong, Brigham and Women's Hospital and Harvard Medical School, Boston, MA, USA

H020 - IDH1 p.S280F Mutation is Potentially a Novel Mechanism of Resistance to Ivosidenib Therapy in an IDH1 Positive Acute Myeloid Leukemia
Zoltan N. Oltvai, MD, University of Pittsburgh, Pittsburgh, PA, USA

◆**Platform Presentations of Selected Infectious Diseases Abstracts**
Location: Rooms 318-323, Level 300 **CE Credit:** 1.25 **Path:** Infectious Diseases; Molecular Methodologies & Technologies

Moderators: *Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA and Erin McElvania, NorthShore University HealthSystem, Evanston, IL, USA*

ID019 - Mycoplasma Genitalium Assay Results from High and Low Risk Populations: Implications for Sexually Transmitted Infection Panel Menu
Kimberle Chapin, MD, Brown Biology and Medicine, Providence, RI, USA

ID018 - Cell-free RNA is More Sensitive than DNA for the Detection of Pediatric Bacterial Sepsis via Shotgun Metagenomic Sequencing
Caitlin Dougherty, The Children's Hospital of Philadelphia, Philadelphia, PA, USA

ID020 - Clinical and Histologic Features of Patients Tested Using the BioFire FilmArray Gastrointestinal Panel
Jonathan Mowers, MD, PhD, Michigan Medicine, Ann Arbor, MI, USA

ID043 - Investigation of Amplicon Sequencing Technology in Diagnosis of Drug Resistant Tuberculosis by Testing FFPE Specimens
Nanying Che, PhD, Departement of Pathology, Beijing Chest Hospitial, Medical Capital University, Beijing, Beijing, China

ID003 - Microbial Cell-free DNA Sequencing for Multiplexed Detection and Quantitation of Cytomegalovirus, Epstein-Barr Virus, and BK Virus

Timothy Blauwkamp, PhD, Karius, Inc., Redwood City, CA, USA

◆Platform Presentations of Selected Informatics Abstracts

Location: Rooms 324-326, Level 300 **CE Credit:** 1.25 **Path:** Cancer/Oncology; Informatics

Moderators: *Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA and Jianling Huang, Johns Hopkins University School of Medicine, Wynnewood, PA, USA*

I031 - Platform-agnostic Deployment of Bioinformatics Pipelines for Clinical NGS Assays using Containers, Infrastructure Orchestration, and Workflow Manager
Sabah Kadri, PhD, Lurie Children's Hospital of Chicago, Chicago, IL, USA

I013 - Benchmarks for Difficult-to-Sequence Genes and Structural Variants
Justin M. Zook, PhD, National Inst of Standards & Tech, Gaithersburg, MD, USA

I040 - Machine Learning Applications for Patient Testing: Computational Assessment of MSI by NGS in the Clinical Laboratory
Gregory Omerza, PhD, The Jackson Laboratory, Farmington, CT, USA

I020 - Mixed Reality for a Precision Medicine Laboratory: the Future is Now!
Andrea Sboner, PhD, Weill Cornell Medicine, New York, NY, USA

I004 - Impact of Next Generation Sequencing Panel Composition on Tumor Mutation Burden Calculation – In Silico Comparison of Frequently Utilized Panels
Nicholas Bevins, MD PhD, University of California at San Diego, San Diego, CA, USA

◆Platform Presentations of Selected Solid Tumors Abstracts

Location: Rooms 309-310, Level 300 **CE Credit:** 1.25 **Path:** Cancer/Oncology; Molecular Methodologies & Technologies

Moderators: *Rajyasree Emmadi, MD, University of Illinois, Chicago, IL, USA and Alanna Church, Boston Children's Hospital, Boston, MA, USA*

ST132 - The Impact of Clinical Molecular Testing and Precision Medicine in Thyroid Cancer
Dora Dias-Santagata, PhD, FACMG, Massachusetts General Hospital - Harvard Medical School, Boston, MA, USA

ST009 - Improved Detection of MET Exon 14 Skipping Mutations in Lung Adenocarcinoma with Combined DNA/RNA Testing and Refined Analysis Methods
David Manthei, MD, PhD, University of Michigan, Department of Pathology, Ann Arbor, MI, USA

ST010 - Detection of Point Mutations in Paediatric Low Grade Glioma (PLGG) and Diffuse Intrinsic Pontine Glioma (DIPG) Patients: Validation of a Novel Liquid Biopsy Assay
Monique Johnson, Masters of Science, The Hospital for Sick Children, Toronto, Ontario, Canada

ST015 - Clonal Hematopoiesis Mutations in Plasma cfDNA RAS/BRAF Genotyping of Metastatic Colorectal Cancer
Fei Huang, Zhongshan Hospital, Fudan University, Shanghai, Shanghai, China

ST094 - STK11 Loss of Function Variants Mediate Immune Evasion in NSCLC via Dysregulation of the FAK/Hippo Signaling Axis and Subsequent Alterations in Tumor-Intrinsic Cytokine Expression
Liam Donnelly, MD, University of Vermont Medical Center, Burlington, VT, USA

MEETING AT-A-GLANCE LISTING

◆**Platform Presentations of Selected Technical Topics Abstracts**
Location: Rooms 327-329, Level 300 **CE Credit:** 1.25 **Path:** Cancer/Oncology; Informatics; Molecular Methodologies & Technologies

Moderators: *Fernanda Sabato, MS, Virginia Commonwealth Univ/MCV Clinical Support Center, Richmond, VA, USA and Shi Yang, Boston University Medical Center, Boston, MA, USA*

TT011 - A Comprehensive Assessment of Onco-panel Sequencing across Multiple Laboratories and Technologies

Joshua Xu, FDA's National Center for Toxicological Research (NCTR), Jefferson, AR, USA

TT066 - Variants Reported by Tumor-Only Clinical Oncology NGS Testing Are Frequently Found in the Germline of Pediatric Patients
Azhar Saeed, MD, MSc, University of Kansas Medical Center, Kansas City, KS, USA

TT071 - EXaCT-2: Augmented Whole Exome Sequencing Optimized for Clinical Testing in Oncology
Duane C. Hassane, PhD, Weill Cornell Medicine, New York, NY, USA

TT072 - Dissimilarity Score (DisScore): Identifying Potential Discordance between Anatomic Pathology and Mutation Landscape in the Evaluation of Clinical Sequencing as Part of a Molecular Tumor Board
Grzegorz T. Gurda, MD, PhD, Gundersen Health System, La Crosse, WI, USA

TT055 - Digital Methylation Specific Multiplex Ligation-Dependent Probe Amplification: A Novel MLPA Based Technique for Assessing Promoter Methylation Status in Cancer
Jan Smout, MSc, MRC Holland, Amsterdam, Netherlands

◆**The Future of the AMP v. Myriad Decision: Exploring potential impacts on multigene panel testing and patient care *(Sponsored by the AMP Professional Relations Committee)***
Location: Rooms 314-317, Level 300 **CE Credit:** 1.25 **Path:** Advocacy/Lab Management

Moderator: *Roger Klein, MD, JD, Consulting, Cleveland, OH, USA*

Panel Discussion
Charles Duan, JD, The R Street Institute, Washington, DC, USA; Robert Nussbaum, MD, Invitae, San Francisco, CA, USA; Sandra Park, JD, American Civil Liberties Union, New York, NY, USA; Hans Sauer, JD, Biotechnology Innovation Organization, Washington, DC, USA

2:45 pm – 3:00 pm **Break**

3:00 pm – 3:45 pm **AMP Subdivision Open Forums**

◆**Genetics Subdivision Open Forum**
Location: Rooms 339-342, Level 300 **CE Credit:** 0.75 **Path:** Inherited Conditions

Moderator: *Elaine Spector, PhD, University of Colorado School of Medicine, Aurora, CO, USA*

◆**Hematopathology Subdivision Open Forum**
Location: Rooms 307-308, Level 300 **CE Credit:** 0.75 **Path:** Cancer/Oncology

Moderator: *Annette Kim, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA*

◆**Infectious Diseases Subdivision Open Forum**
Location: Rooms 318-323, Level 300 **CE Credit:** 0.75 **Path:** Infectious Diseases

Moderator: *Frederick S. Nolte, PhD, Medical Univ of South Carolina, Charleston, SC, USA*

◆**Informatics Subdivision Open Forum**

Location: Rooms 324-326, Level 300 **CE Credit:** 0.75 **Path:** Informatics

Moderator: *Somak Roy, MD, University of Pittsburgh Medical Center, Pittsburgh, PA, USA*

◆**Solid Tumors Subdivision Open Forum**
Location: Rooms 309-310, Level 300 **CE Credit:** 0.75 **Path:** Cancer/Oncology

Moderator: *Roger Klein, MD, JD, Roger D. Klein, MD JD, Beachwood, OH, USA*

3:45 pm – 4:00 pm **Break**

4:00 pm – 5:00 pm **Plenary Session**

◆**Liquid Biopsies for MRD/Opportunities & Pitfalls in Monitoring AML Patients**
Location: Rooms 314-317, Level 300 **CE Credit:** 1 **Path:** Cancer/Oncology

Moderators: *Mark D. Ewalt, MD, University of Colorado School of Medicine, Aurora, CO, USA and Rashmi Kanagal Shamanna, MD, The University of Texas MD Anderson Cancer Center, Houston, TX, USA*

MRD in AML - Promises, Problems and Perspectives
Christian Thiede, MD, University of Technics, Dresden, Germany

5:00 pm – 5:15 pm **Closing Remarks**

◆**Closing Remarks**
Location: Rooms 314-317, Level 300

Neal Lindeman, MD, Brigham & Women's Hospital, Cambridge, MA, USA (2019 Program Chair) and Jane Gibson, PhD, University of Central Florida College of Medicine, Orlando, FL, USA (2020 Program Chair)

NOTES

AMP CENTRAL

Visit the AMP Central Booth in the Exhibit Hall! You can...

Meet Someone New
The Technologist Mixer, hosted by the Training & Education Committee, is a great way for Technologists to network and meet other attendees who share their interests.

Explore AMP Education
Learn about AMP's wide array of educational offerings and tools to help expand your knowledge base at the Education Showcase hosted by the Training & Education Committee.

Get Involved with AMP!
On Friday afternoon, AMP committee representatives will be available to answer questions about the important work they do and how you can get more involved.

Nominate Yourself or a Colleague
Stop by any time to view open committee positions and submit nominations for candidates ready to advance the field and take the next step in their career. (Self-nominations are encouraged!)

View/Post Job & Fellowship Opportunities
Find your next job or right candidate during the meeting!

Celebrate AMP and *JMD* History
To celebrate our 25th anniversary and *The Journal of Molecular Diagnostics'* (*JMD*) 20th anniversary, we will be sharing photos and memories throughout the meeting at AMP Central.

SCHEDULE OF EVENTS

Thursday, Nov. 7
2:00pm – 3:45pm
Technologist Mixer

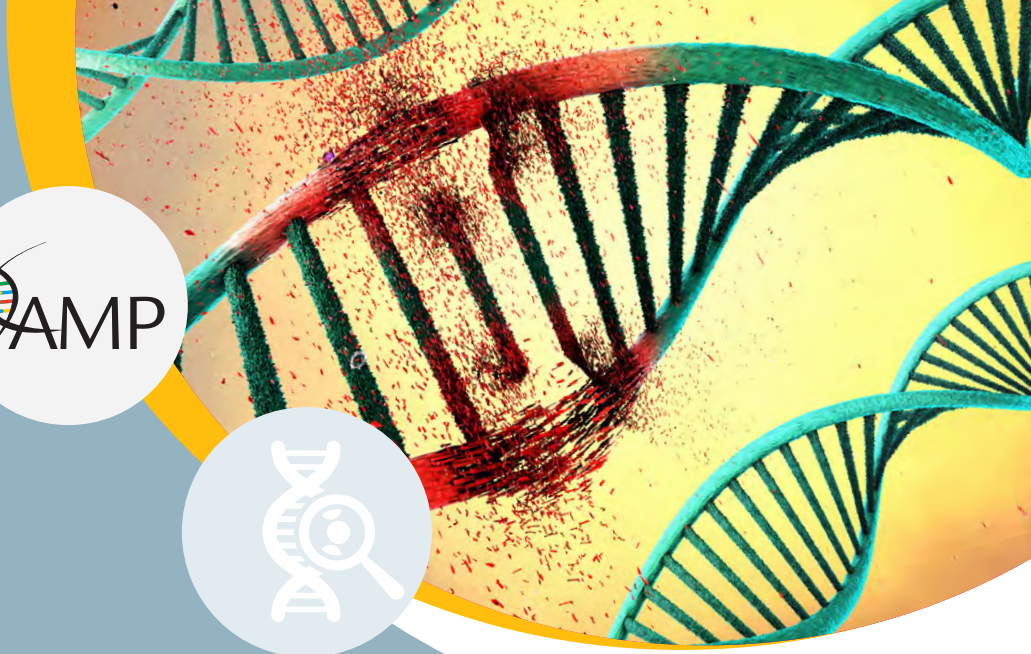
5:45pm – 7:00pm
Celebrate AMP's New Vision

Friday, Nov. 8
12:15pm – 1:30pm
Education Showcase

2:45pm – 4:00pm
Get Involved with AMP! AMP Committee "Meet & Greet" event

Saturday, Nov. 9
12:15pm – 1:30pm
"Meet & Greet" with the *JMD* Editor-in-Chief

AMP Central is the place to be if you're a member or attendee interested in learning more about all that AMP has to offer!



THURSDAY PROGRAM

Targeting DNA Repair Pathways:

CURRENT AND FUTURE IMPLICATIONS OF PARP INHIBITORS

Join us for this free online learning experience where AMP subject matter experts organize the most current research and clinical information into an up-to-date and useful three-part webcast series on PARP inhibitors and Homologous Recombination Deficiency (HRD) testing. These presentations will include recent research, laboratory testing considerations, and implications for patients and their caregivers; including oncologists, genetic counselors and primary care clinicians.

Supported by educational grants provided by AstraZeneca and Merck

INCLUDED IN THE SERIES

Understanding the *BRCA*-Dependent DNA Repair Axis for Assessing Cancer Risk and Therapeutic Intervention
Speaker: Ryan Jensen, PhD

Identifying Mutational Signatures of Homologous Recombination Deficiency to Predict PARPi Response.
Speaker: Peter Park, PhD

PARP Inhibitors in the Clinic: The Implications of Genetic Testing for Treatment Selection and Germline Counseling
Speakers: Katherine Nathanson, MD; Payal Shah, MD

VIEW THE SERIES ONLINE:
www.amp.org/PARPi

THURSDAY PROGRAM

November 7, 2019

6:45 am – 8:00 am

Continental Breakfast

Location: Session Room Foyers, Level 300

7:00 am – 8:00 am

Targeted Topics

◆**Artificial Intelligence and Diagnostics Microbiology: Friend or Foe?**
Location: Rooms 339-342, Level 300
CE Credit: 1
Path: Infectious Diseases

Use of Machine Learning Algorithms to Support Clinical Microbiology Culture Interpretation
Karissa Culbreath, PhD, TriCore Reference Laboratories, Albuquerque, NM, USA

Detection of Outbreaks and Unusual Pathogen using AI and Machine Learning
Amy Leber, PhD, Nationwide Childrens Hospital, Columbus, OH, USA

Session Description: The future is now? From pre-analytical to post-analytical there are many opportunities to deploy artificial intelligence in the clinical microbiology laboratory. The question is, are we really ready for it? This session will describe the basic concepts of artificial intelligence and its use in the clinical microbiology laboratory.

Session Objectives:
- Describe applications of artificial intelligence and machine learning in interpretation of digital images in microbiology.
- Describe applications of artificial intelligence and machine learning in predicting the presence of infections and guiding laboratory testing.

◆**Case Studies in Genetics**
Location: Rooms 324-326, Level 300
CE Credit: 1
Path: Infectious Diseases

Ultra-hypermutated Pediatric Glioblastoma of Lynch Syndrome Mimicking Constitutional Mismatch Repair Deficiency Syndrome
Chen Yang, MD, PhD, Virginia Commonwealth University, Richmond, VA, USA

A Case of T-PLL with EZH2 Mutation; EZH2 the Sword or the Shield?
Panieh Terraf, PhD, Harvard Medical School - Brigham and Women's Hospital, Boston, MA, USA

Exome Reanalysis in a Patient with a Somatic CN-LOH in 17p and TP53 Mutation, and a Germline DNAJC21 Biallelic Mutation Associated with Myelodysplastic Susceptibility
Elan Hahn, MD, University of Toronto, Toronto, Ontario, Canada

Somatic Mosaic IDH1 Mutation in a Case of Maffucci Syndrome
Diana Bryk, MD, New York Presbyterian - Columbia, New York, NY, USA

Session Description: Challenging Case Studies are presented by trainees or technologists. They will discuss the case's clinical history, molecular analysis, interesting features, and the proposed diagnosis. Other molecular testing methods, if applicable, will be included in the presentation, including biopsies, gross/microscopic pathology, immunohistochemistry/flow cytometry, and cytogenetic findings.

Session Objectives:
- Describe the context of a challenging clinical case.
- Discuss the molecular pathology techniques used in the diagnosis of the case.
- Propose a final diagnosis based upon findings and diagnostic evidence.

THURSDAY PROGRAM

◆**Case Studies in Hematopathology**
Location: Rooms 327-329, Level 300
CE Credit: 1
Path: Cancer/Oncology

A Surprising Finding in Primary Cutaneous CD8-positive Aggressive Epidermotropic Cytotoxic T-cell Lymphoma
Mark Evans, MD, University of California, Irvine, Orange, CA, USA

"Clonal Selection Following FLT3 Tyrosine Kinase Inhibitor Treatment for Acute Myeloid Leukemia"
Adam Fisch, Brigham and Women's Hospital, Boston, MA, USA

Identification of a Cryptic ABL1 Rearrangement in a Refractory Acute Myeloid Leukemia Patient with Diploid Karyotype by Conventional Cytogenetics
Arash Ronaghy, MD, PhD, MD Anderson Cancer Center, Houston, TX, USA

Muddy Waters: A Report of Granulocytes Infusion Confounding Next-Generation Sequencing Interpretation
Tareq Qdaisat, MD, University of Nebraska Medical Center, Omaha, NE, USA

Session Description: Challenging Case Studies are presented by trainees or technologists. They will discuss the case's clinical history, molecular analysis, interesting features, and the proposed diagnosis. Other molecular testing methods, if applicable, will be included in the presentation, including biopsies, gross/microscopic pathology, immunohistochemistry/flow cytometry, and cytogenetic findings.

Session Objectives:
- Describe the context of a challenging clinical case.
- Discuss the molecular pathology techniques used in the diagnosis of the case.
- Propose a final diagnosis based upon findings and diagnostic evidence.

◆**Case Studies in Solid Tumors**
Location: Rooms 318-323, Level 300
CE Credit: 1
Path: Cancer/Oncology

Compound EGFR and BRAF variants in NSCLC against the backdrop of suspected MEN2A
Jeremy Adler, MD, Pennsylvania Hospital, UPHS, Philadelphia, PA, USA

Expanded Next Generation Sequencing Panel Detects A Rare EGFR Kinase Domain Duplication In A Patient with Metastatic Lung Cancer
Jong Kim, MD, Cedars-Sinai Medical Center, Los Angeles, CA, USA

Pitfalls in Identification of Mismatch Repair Deficiency: An Unusual Pulmonary Intimal Sarcoma
Wanying Zhang, MD, New York Presbyterian Hospital, New York, NY, USA

EGFR-Mutated Lung Adenocarcinoma with Early Resistance to Osimertinib
Brennan Decker, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA

Session Description: Challenging Case Studies are presented by trainees or technologists. They will discuss the case's clinical history, molecular analysis, interesting features, and the proposed diagnosis. Other molecular testing methods, if applicable, will be included in the presentation, including biopsies, gross/microscopic pathology, immunohistochemistry/flow cytometry, and cytogenetic findings.

Session Objectives:
- Describe the context of a challenging clinical case.
- Discuss the molecular pathology techniques used in the diagnosis of the case.
- Propose a final diagnosis based upon findings and diagnostic evidence.

8:00 am – 8:15 am

Break

THURSDAY PROGRAM

8:15 am – 8:30 am

Opening Remarks

Location: Ballroom, Level 400
CE Credit: Not CME/CMLE
Path: Opening Remarks

Opening Remarks
Neal Lindeman, MD, Brigham & Women's Hospital, Cambridge, MA, USA

8:30 am – 9:45 am

Award Lecture

◆**Award for Excellence Lecture**
Location: Ballroom, Level 400
CE Credit: 1.25
Path: Special Session

Efficient Use of the Available DNA – A Career
Russell Higuchi, PhD, Cepheid, Sunnyvale, CA, USA

Session Description: Making the most out of the least has long been a requirement for the practical application of molecular biology. The technology arc of my career- from recombinant DNA to Ancient DNA to PCR to forensic DNA to pathogen detection to Next-Generation Sequencing – has been anchored in this consistent need to deal with samples with limited nucleic acid content. In describing this arc, I will present a personal journey that shows, with respect to getting the most information from our samples, how far we've come over the course of my career. I will also describe the early, heady days of PCR and the invention of real-time PCR, the application of real-time PCR to real-world problems (including those of the developing world) and my recent work on making PCR faster on existing instruments.

Session Objectives:
- Describe the history of sensitive DNA detection and sequence identification.
- Provide a review of the principles of real-time PCR detection and quantification.
- Look forward to better, faster and cheaper molecular diagnostic tools.

9:45 am – 10:00 am

Coffee Break

10:00 am – 11:30 am

Symposia Sessions

◆**Criminal Investigations & Forensics**
Location: Rooms 309-310, Level 300
CE Credit: 1.5
Path: Inherited Conditions; Molecular Methodologies & Technologies

Rapid DNA: From Research to Field
Amanda Sozer, PhD, SNA International, Washington, D.C., USA

Forensic DNA Testing at the Crossroads of Science, Law, and Policy
Frederick Bieber, PhD, Harvard Medical School, Boston, MA, USA

Basics of Genetic Genealogy and Its Impact on Forensic Investigation
Howard Cash, Gene Codes Corporation, Ann Arbor, MI, USA

Session Description: "Recreational genealogy" has been aggressively marketed in recent years, sometimes by commercial companies that sequence and analyze DNA for a below-cost price to participants, and then further analyze and aggregate data for license to third party researchers. We know from history that genetic information can and has been abused. This is one reason why uses of law enforcement's DNA databases has been carefully limited by the laws that created them. However, these protections are less potent than they were only a few years ago; Public and private genealogy databases are not controlled by the same legislation, policies and case law. Recent developments in use of STR analysis and DNA sequencing methods for human identification in both humanitarian efforts following mass fatalities, human trafficking and for identification of perpetrators of violent crime will be reviewed. Combining DNA results with genealogical data has led to identification of suspects in scores of criminal investigations in the past 18 months. This new field of genealogics demonstrates the

THURSDAY PROGRAM

power of these new methods and at the same time raises both policy and privacy questions which will be addressed.

Session Objectives:

- Understand the role of STR analysis and DNA sequencing for humanitarian identification efforts, mass fatalities and forensic investigations.
- Understand how to evaluate some of the main scientific, legal, and policy implications of using DNA sequencing in forensic medicine.
- Understand the application of DNA technology to forensics and the identification of suspects involved in crimes.

◆**CRISPR-CAS: Applications for Diagnostics and Therapeutics of Human diseases**
Location: Ballroom, Level 400
CE Credit: 1.5
Path: Infectious Diseases; Molecular Methodologies & Technologies

Getting More from your MiSeq with DASH and FLASH
Emily D. Crawford, PhD, Chan Zuckerberg Biohub, San Francsico, CA, USA

Assessing Unintended Off-Target Mutations Caused by Cas9 and Other Gene Editing Enzymes
Vikram Pattanayak, MD, PhD, Massachusetts General Hospital, Boston, MA, USA

Session Description: The rapid developing of CRISPR/Cas mediated gene-editing technologies is an immensely powerful research tool with remarkable promise to revolutionize the future therapy for genetic diseases, cancer, and sensitive nucleic acid detection, diagnosis of infectious diseases and beyond. Despite the increasing maturity of CRISPR-Cas9 technology, its safety and efficiency are important concerns requiring comprehensive studies. Clinical translation of the CRISPR-Cas9 system is hampered by off-target alterations. In infectious disease diagnosis, metagenomic Next Generation Sequencing (mNGS) has emerged as a promising technology for global detection of pathogens in clinical samples. However, standard methods are often not sensitive enough to detect critical sequences like those responsible for antimicrobial resistance. Novel approaches (DASH and FLASH) based on the programmability of the CRISPR/Cas9 system to increase coverage of desired organisms and genes can result in increased assay sensitivity.

Session Objectives:

- Describe the basic functions of the CRISPR/Cas9 system.
- Discuss the benefits and limitations of metagenomic Next Generation Sequencing (mNGS) for infectious disease diagnostics.
- Discuss the application of CRISPR technology as a diagnostic tool for infectious diseases.

◆**Genetics of Sensitivity and Resistance to Non-Chemotherapy Agents**
Location: Rooms 314-317, Level 300
CE Credit: 1.5
Path: Cancer/Oncology

Choosing Patient Therapy with Dynamic BH3 Profiling
Anthony Letai, MD, PhD, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, USA

Diverse Mechanisms of Acquired Resistance to CAR T Cell Immunotherapy
Andrei Thomas-Tikhonenko, PhD, Children's Hospital of Philadelphia, Philadelphia, PA, USA

Session Description: Novel non-chemotherapeutic agents have revolutionized treatment of hematological malignancies, especially in clinical settings where therapeutic options are limited. This is evidenced by accelerated FDA approval of BCL2 inhibitor, and ever expanding field of immuno-therapeutics using checkpoint inhibitors and CAR-T cells. As we gain more knowledge, molecular laboratories will play a crucial role in identification on biomarkers of sensitivity and resistance to these agents for optimal implementation of precision medicine. This session will discuss the latest updates on the clinical utility, mechanisms of resistance, and innovative state-of-the-art strategies to assess responses in leukemia.

THURSDAY PROGRAM

Session Objectives:
- Describe the sensitivity and resistance patterns to immune check point inhibitors in AML and MDS.
- Understand the potential utility of dynamic BH3 profiling as a functional precision medicine tool.
- Understand the mechanisms of resistance to CD19-directed immunotherapies in B-lymphoblastic leukemias.

11:30 am – 12:45 pm

General Lunch - Visit Expo Hall and View Posters

Location: Exhibit Hall A-G, Level 100

Networking Lunches: Please see lunch descriptions in the "Highlights & General Information" section of the Program Book, Pages 19-20.

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

12:45 pm – 2:00 pm

Breakout Sessions

◆**Biobanking and 3D-Organoid Technology**
Location: Rooms 339-342, Level 300
CE Credit: 1.25
Path: Advocacy/Lab Management; Molecular Methodologies & Technologies; Cancer/Oncology

Perspective on Establishing a Biorepository for Clinical and Research Use
Kristy Crooks, PhD, University of Colorado, Aurora, CO, USA

Profiling the DNA Damage Repair Capacity of High Grade Serous Ovarian Tumors using Patient-Derived Organoids
Sarah Hill, MD, PhD, Dana-Farber Cancer Institute, Boston, MA, USA

Session Description: Recent cost reduction in genetic testing and advances in analytics have enabled the successful establishment of several large-scale biorepositories collecting samples linked to phenotype and health data. Health systems, universities, and private organizations are increasingly investing in biobanking as a means to foster research, develop commercial partnerships, reduce healthcare costs, and improve brand visibility. Additionally, organizations are leveraging biobank resources to return clinical genetic test results to participants. This session will explore the advantages and pitfalls common to emerging biobank initiatives in the context of regulatory requirements, research endeavors, and personalized medicine.

Session Objectives:
- Describe the potential of 3D-organoids technology for clinical applications in infectious diseases, genetic diseases, tumor modeling and biobanking.
- Review the importance and clinical utility of biobanks.
- Discuss the regulatory aspects of maintaining a CLIA certified biobank and the return of results in a clinical setting.

◆**Diagnostic Stewardship for Molecular Testing**
Location: Rooms 327-329, Level 300
CE Credit: 1.25
Path: Infectious Diseases; Molecular Methodologies & Technologies

Diagnostic Stewardship for Molecular Testing
Kimberle Chapin, MD, Brown Biology and Medicine, Providence, RI, USA

The Art of Navigating Molecular Infectious Disease Test Results: From Ordering To Application In the Clinical Setting
Sejal Morjaria, MD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

Session Description: The increased availability of rapid molecular infectious disease diagnostics has significantly improved the potential for clinical laboratories to impact patient outcomes. Appropriate and optimal use of these new tests require communication and partnership between clinical microbiologists and clinicians. In the session, two speakers, a microbiologist and infectious disease clinician will discuss various approaches to diagnostic stewardship in a case format

THURSDAY PROGRAM

Session Objectives:
- Define the concept of diagnostic stewardship.
- List key stakeholders in establishing diagnostic stewardship.
- Describe approaches to establishing diagnostic stewardship.

◆**Is Bigger Always Better? Targeted versus Genome Oncology Tests**
Location: Rooms 309-310, Level 300
CE Credit: 1.25
Path: Cancer/Oncology

Big Data and Little Patients: Targeted Sequencing for Pediatric Brain Tumors
Sarah Leary, MD, MS, Seattle Children's Hospital, University of Washington and Fred Hutchinson Cancer Research Center, Seattle, WA, USA

Bigger is Better: More Cancer Genes in More Patients
Wendy Chung, MD PhD, Columbia University, New York, NY, USA

Session Description: Precision oncology is increasing relying on genetic testing and laboratories frequently develop targeted tests that include hundreds of cancer-related genes. This session will highlight the relative advantages and limitations of targeted (selected gene panel) vs. comprehensive (exome and genome) genetic testing. This session will be presented as a "point-counterpoint" with each speaker focusing on the opportunities of genetic tests in molecular oncology using specific clinical applications such as pediatric brain cancer as illustrative case examples. The presentations will be followed by a panel discussion and Q&A session.

Session Objectives:
- Discuss the benefits of next-generation sequencing in oncology.
- Recognize the need for both targeted and comprehensive tests.
- Describe advantages of targeted testing in pediatric oncology.

◆**Reimbursement: It's Never too Late to Start Getting Paid**
Location: Rooms 307-308, Level 300
CE Credit: 1.25
Path: Advocacy/Lab Management

Reimbursement: It's Never too Late to Start Getting Paid
Anthony Sireci, MD, Loxo Oncology, Stamford, CT, USA

Reimbursement: It's Never too Late to Start Getting Paid
Aaron D. Bossler, MD, PhD, University of Iowa, Iowa City, IO, USA

Demystifying Molecular testing coverage and policies: MolDX and Medicare
Gabriel Bien-Willner, MD, PhD, Palmetto GBA, TX, USA

Session Description: Understanding the processes for coding, pricing and coverage determination is at the heart of getting reimbursed for the clinical molecular procedures we perform. This panel will review those processes and hear insights from a Medical Director for the Palmetto Medicare Administrative Contractor to help members understand the intent and breadth of the molecular procedure codes, understand how coverage policies and procedures affect determination of payment or nonpayment including the National Coverage Determination for NGS testing, and discuss the pricing process and the impact of PAMA on laboratory pricing. The three presentations will be followed by a panel discussion and Q&A session.

Session Objectives:
- Understand current test coding and define tier 1 molecular pathology CPT codes.
- Understand how coverage polices determine payment or nonpayment.
- Understand and describe the impact of PAMA on laboratory pricing.

THURSDAY PROGRAM

◆**State of Pharmacogenetics**
Location: Rooms 314-317, Level 300
CE Credit: 1.25
Path: Advocacy/Lab Management; Cancer/Oncology; Inherited Conditions

Clinical Implementation of Pharmacogenomics
Philip E. Empey, PharmD, PhD, University of Pittsburgh/UPMC, Pittsburgh, PA, USA

What's New in Pharmacogenetics?
Victoria M. Pratt, PhD, Indiana University School of Medicine, Indianapolis, IN, USA

Session Description: Many healthcare professionals (e.g., laboratorians, physicians, physician assistants, pharmacists, nurses and genetic counselors) believe pharmacogenomics (PGx) is essential to personalized medicine; however, many still lack confidence prescribing, dosing, interacting with other healthcare professionals and counseling patients with regard to PGx. This session will explore the current evidence, regulatory, reimbursement and best practice recommendations in PGx testing. Keys to successful implementation and emerging large pharmacogenomics initiatives will be discussed with a focus on contemporary issues in the field.

Session Objectives:
- Recognize the availability of evidence-based PGx resources to inform prescribing.
- Describe the key characteristics of PGx alleles that are recommended for inclusion in clinical testing panels by the AMP.
- Understand successful implementation approaches and barriers to increased PGx clinical testing.

2:00 pm – 3:45 pm

Coffee Break - Visit Expo Hall and View Posters

Location: Exhibit Hall A-G, Level 100

AMP Central Activities: Technologist Mixer

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

3:45 pm – 4:30 pm

Breakout Sessions

◆**AMP CPC's ID Multiplex Working Group: Update & Open Comment Forum**
Location: Rooms 314-317, Level 300
CE Credit: 0.75
Path: Infectious Diseases

AMP CPC's ID Multiplex Working Group: Update & Open Comment Forum
Michael Lewinski, PhD, Roche Molecular Systems, Inc., Pleasanton, CA, USA

Session Description: Recognizing the challenges of multiplexed clinical testing for infectious diseases, AMP has convened a multistakeholder working group with representatives from the American Society for Microbiology, Infectious Diseases Society of America, and Pan American Society for Clinical Virology to develop a best practices guidance document. This session will discuss the development of the consensus document and provide an opportunity for engagement with the working group to provide feedback on existing challenges.

Session Objectives:
- Discuss the AMP-led collaborative initiative regarding multiplexed clinical testing for infectious diseases.
- Discuss current multiplexed clinical testing for infectious diseases techniques and utilization.
- Discuss potential strategies to address multiplexed clinical testing for infectious diseases, test optimization, and accuracy.
- Describe potential methods to continue improvement and quality control of multiplexed clinical testing for infectious diseases.

◆**AMP CPC's In Silico Reference Materials Working Group: Update & Open Comment Forum**
Location: Rooms 309-310, Level 300
CE Credit: 0.75
Path: Advocacy/Lab Management; Infectious Diseases; Informatics

AMP CPC's In Silico Reference Materials Working Group: Update & Open Comment Forum

THURSDAY PROGRAM

Eric J. Duncavage, MD, Washington University, Saint Louis, MO, USA; Justin M. Zook, PhD, National Inst of Standards & Tech, Gaithersburg, MD, USA

Session Descriptions: In order to evaluate the current utilization of and recommend best practices regarding the use of in silico reference materials in clinical laboratories, AMP has convened a multistakeholder working group with representatives from the Association for Pathology Informatics and College of American Pathologists to develop a best practices guidance document. This session will discuss the development of the consensus document and provide an opportunity for engagement with the working group to provide feedback on existing challenges.

Session Objectives:

- Discuss the AMP-led collaborative initiative regarding utilization of in silico reference material in clinical settings.
- Discuss in silico reference materials and utilization based on AMP survey results.
- Discuss potential strategies to address utilization of in silico reference material in clinical testing, test optimization, and accuracy.
- Describe potential methods to continue improvement and quality control.

◆**AMP CPC's T & B Cell Clonality Working Group: Update & Open Comment Forum**
Location: Rooms 318-323, Level 300
CE Credit: 0.75
Path: Cancer/Oncology

AMP CPC's T & B Cell Clonality Working Group: Update & Open Comment Forum
David S. Viswanatha, MD, Mayo Clinic and Foundation, Rochester, MN, USA

Session Description: Recognizing the challenges of clinical T & B cell clonality testing, AMP has convened a multistakeholder working group with representatives from the American Society of Hematology, College of American Pathologists, and Society for Hematopathology to develop a best practices guideline document. This session will discuss the development of the consensus guideline document and provide an opportunity for engagement with the working group to provide feedback on existing challenges.

Session Objectives:

- Discuss the AMP-led collaborative initiative regarding clinical T & B cell clonality testing.
- Discuss current T & B cell clonality testing techniques and utilization.
- Discuss potential strategies to address T & B cell clonality testing, test optimization, and accuracy.
- Describe potential methods to continue improvement and quality control of T & B cell clonality testing.

◆**AMP CPC's Tumor Mutational Burden Working Group: Update & Open Comment Forum**
Location: Rooms 307-308, Level 300
CE Credit: 0.75
Path: Cancer/Oncology

AMP CPC's Tumor Mutational Burden Working Group: Update & Open Comment Forum
Larissa V. Furtado, MD, St. Jude Children's Research Hospital, Memphis, TN, USA

Session Description: Recognizing the challenges of clinical tumor mutational burden testing, AMP has convened a multistakeholder working group with representatives from the American Society for Clinical Oncology, College of American Pathologists, and Society for Immunotherapy of Cancer to develop a best practices guidance document. This session will discuss the development of the consensus document and provide an opportunity for engagement with the working group to provide feedback on existing challenges.

Session Objectives:

- Discuss the AMP-led collaborative initiative regarding clinical tumor mutational burden testing.
- Discuss current TMB techniques and utilization based on AMP survey results.
- Discuss potential strategies to address TMB testing, test optimization, and accuracy.
- Describe potential methods to continue improvement and quality control of TMB testing.

THURSDAY PROGRAM

◆**The first 25 years of AMP: Our Society's Groundbreaking Past and Future Opportunities**
Location: Rooms 327-329, Level 300
CE Credit: 0.75
Path: Special Session; Molecular Methodologies & Technologies

Standing of Molecular within the Pathology/Lab Profession
Karen L. Kaul, MD, PhD, NorthShore University Health System, Evanston, IL, USA

Evolving Technologies and Automation
Karl Voelkerding, MD, University of Utah School of Medicine, Salt Lake City, UT, USA

Panel Discussion
Federico A. Monzon, MD, Castle Biosciences, Friendswood, TX, USA; Aaron D. Bossler, MD, PhD, University of Iowa, Iowa City, IO, USA; Yaolin Zhou, MD, Univ of Oklahoma Health Sciences Center, Oklahoma City, OK, USA; Helen Fernandes, PhD, Columbia University Medical Center, Wayne, NJ, USA

Session Description: This session summarizes the remarkable progress that our AMP community has made together over the society's first 25 years. The inspiring stories we share highlight opportunities to advance your career and to promote scientific and medical progress through collaborative AMP initiatives.

Session Objectives:
- Review the impact AMP has had on medical professionals and patients.
- Share stories illustrating our contributions and future opportunities.

4:30 pm – 4:45 pm

Break

4:45 pm – 5:45 pm

Plenary Session

◆**Polygenic Risk Scores: Translating Research Advances into the Clinical Domain**
Location: Ballroom, Level 400
CE Credit: 1
Path: Informatics

Using Polygenic Risk Scores (PRS) for Breast Cancer to Inform Screening: Model Fit, Calibration, and Utility
Peter Kraft, PhD, Harvard T.H. Chan School of Public Health, Boston, MA, USA

Session Description: At this session, the definition, motivation, and development of polygenic risk scores (PRS) for breast cancer will be presented. The session will also discuss the importance of risk model calibration and the context-specific evaluation of clinical utility (balancing benefits and risks of generating and using genetic risk information in the clinic). Although the session will be focused on breast cancer screening, several general issues in the development and evaluation of PRS for other diseases in other contexts will also be highlighted.

Session Objectives:
- Upon completion, participants will be able to understand the concept and calculation of PRS.
- Upon completion, participants will be able to understand both clinical validity (how it is calibrated) and clinical utility (impact on clinical care) of PRS.
- Upon completion, participants will understand the state of the science regarding PRS for breast cancer and their potential use in risk-stratified screening programs.

5:45 pm – 7:00 pm

Welcome Reception *(Supported by QIAGEN)*

Location: Exhibit Hall A-G, Level 100
CE Credit: Not CME/CMLE
Path: Reception

Session Description: Please join us for the Welcome Reception and help to kick-off another successful Annual Meeting & Expo while networking with your friends and colleagues in the Expo Hall. This event is open to all Registered Meeting Attendees. We'll also be celebrating AMP's 25th anniversary and *The Journal of Molecular Diagnostics' (JMD)* 20th anniversary, stop by AMP Central for Cake! Supported by QIAGEN.

AMP Central Activities: Celebrate AMP's New Vision

NOTES

Join AMP

AMP's **2,500+ MEMBERS** enjoy easy access to information and individuals who support them in their careers. As members of the worldwide community of experts in molecular medicine and diagnostics, AMP members rely on AMP for education, advocacy, and innovation to improve the practice of molecular medicine.

MEMBER BENEFITS INCLUDE:

- Subscription to ***The Journal of Molecular Diagnostics***
- NEW! Discounted page charges for corresponding authors of accepted articles when publishing in ***The Journal of Molecular Diagnostics***
- **Public Affairs and Advocacy** — AMP is a champion for the molecular medicine at all levels of government and regulation
- Access to peers via **CHAMP** — the AMP membership online community
- Reduced rates for the **AMP Annual Meeting, AMP Europe,** the **AMP Global Congress,** and other educational offerings
- Complimentary access to select **Educational Offerings** on AMP's online learning platform, **AMP***ED*
  (search "Free4Members" at educate.amp.org)
- NEW! Free CME/CE on select educational offerings
- Exclusive access to the **AMP Online Membership Directory**
- Networking opportunities - online and at in-person events
- Eligibility to apply for **AMP Awards**
- Opportunity to serve on an AMP Committee or Working Group

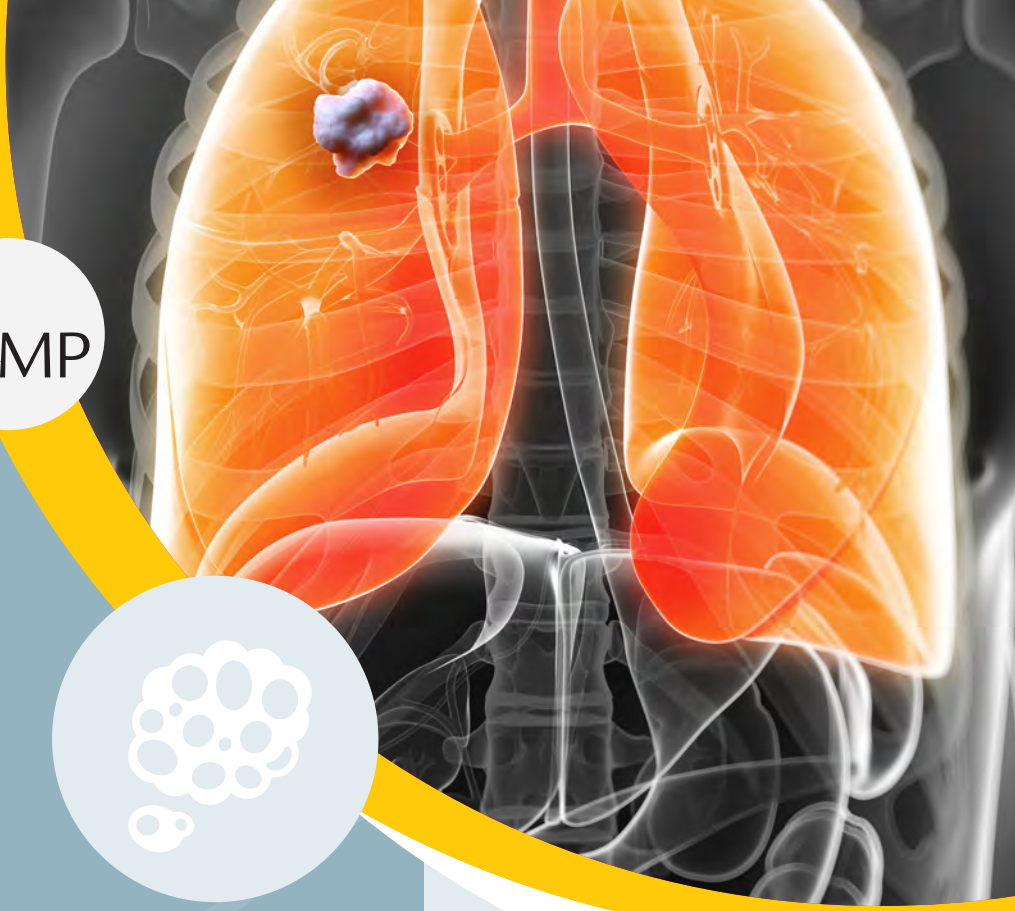
WWW.AMP.ORG/JOIN

"Collegial collaboration is why I joined. ***AMP members*** are the best in the field internationally. There's an expert an arm's length away on any assay you're interested in adopting."

— Betsy A. Bove, PhD
Vice President of Laboratory Regulation Compliance, Genomind, Inc.

FRIDAY PROGRAM

FRIDAY PROGRAM



Advancing Patient Care in NSCLC:

BREAKING DOWN BARRIERS

Join us for this free online learning experience aimed at breaking down barriers to testing and treatment in Non-Small Cell Lung Cancer (NSCLC). In this five-part series world-renowned experts explore best practices in test ordering, sample collection, and test interpretation with the goal of improving patient care.

INCLUDED IN THE SERIES

- **New AMP Molecular Test Guidelines for the Diagnosis and Treatment of Lung Cancer**
- **Best Practices in NSCLC Small Specimen Collection for Clinicians**
- **Best Practices in Small Specimen Management for Laboratory Professionals**
- **Liquid Biopsies – Promises and Pitfalls**
- **Best Practices in Test Ordering**
  This presentation includes a companion reference card to which clinicians and laboratory professionals can refer to in the clinic.

Supported by an educational grant provided by AstraZeneca

www.amp.org/NSCLC

FRIDAY PROGRAM

November 8, 2019

6:45 am – 8:00 am

Continental Breakfast

Location: Session Room Foyers, Level 300

7:00 am – 8:00 am

Targeted Topics

◆**Behind the Curtain: Developing Clinical Knowledgebase Systems**
Location: Rooms 309-310, Level 300
CE Credit: 1
Path: Informatics

Behind the Curtain: Developing Clinical Knowledgebase Systems

Malachi Griffith, PhD, Washington University School of Medicine, St. Louis, MO, USA

Session Description: Clinical interpretation of variants remains a major bottleneck for translation of genomic observations. Recognizing this need, a number of variant knowledgebases have emerged to organize efforts to synthesize complex evidence about variants and their clinical relevance. These resources differ widely in their curation approach, data sharing model, adoption of standards, overall scope and target applications. Many of these efforts remain siloed from each other. Consensus on the correct interpretation of individual variants remains elusive. To the extent that any "final" assertions emerge, their stability and reliability is largely unknown, leaving the burden of extensive vetting on the end user. In this session, the current state of the art for clinical variant knowledgebase systems and ongoing efforts to improve curation interfaces, practices, and interoperability will be discussed. Existing options such as CIViC (civicdb.org) will be used to stimulate discussion on the current state of the field, major outstanding challenges, and future directions.

Session Objectives:

- Upon completion, participants will be able to define the concept of a knowledgebase.
- Upon completion, participants will be able to understand the informatics aspects of developing a knowledgebase.
- Upon completion, participants will understand the strengths and limitations of the CIViC knowledgebase and its approach to curating cancer variant interpretations from the literature.

◆**Blood Bank & HLA**
Location: Rooms 318-323, Level 300
CE Credit: 1
Path: Inherited Conditions

Blood Group Genotyping from High Density Arrays to Whole Genomes

Bill Lane, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA

Session Description: Genotyping has expanded the number of blood group antigens that can be readily typed, but it often represents a large additional testing cost. In addition, most currently available genotyping assays only target a limited number of antigens and therefore full typing of the >300 blood group is not possible. Genotyping from next generation sequencing data can in theory be used to genotype for all antigens with a known genetic basis, but early attempts required lengthy subject matter expert analysis. In addition, this manual analysis is likely error prone and not scalable for full evaluation of all 46 blood group associated genes which contain more than 2000 known antigenic allelic variants, including many structural variations. We recently developed automated software (bloodTyper) which can fully determine all genetically understood blood group antigens from whole genomes, whole exomes, and targeted next generation sequencing. Furthermore, bloodTyper was recently expanded to evaluate a cost-effective high density DNA array that targets all known blood group antigens, allowing for full blood group antigen genotyping in over 8,000 blood donors.

FRIDAY PROGRAM

Session Objectives:
- Describe the major genetic changes underlying the most commonly tested blood group antigens.
- Describe the pros and cons between available genotyping methodologies.
- Describe how genotyping can be used to effectively determine blood groups antigens in both donors and recipients.

◆Case Studies in Hematopathology

Location: Rooms 324-326, Level 300
CE Credit: 1
Path: Cancer/Oncology

B-lymphoblastic Leukemia with ZNF384 Gene Rearrangement
Shweta Bhavsar, MBBs, MD, University of Pittsburgh Medical Center, Pittsburgh, PA, USA

Molecular Diagnosis of MDS in a Non-Diagnostic Bone Marrow Specimen
Jeffrey SoRelle, MD, University of Texas Southwestern Medical Center, Dallas, TX, USA

The Role of Lymphoma Sequencing Panel in the Diagnosis of Pediatric-Type Follicular Lymphoma
Guang Yang, MD, PhD, University of Pennsylvania, Philadelphia, PA, USA

5q- in a Patient with Chronic Myelogenous Leukemia in Accelerated Phase
James Corines, DO, SUNY Upstate Medical University, Syracuse, NY, USA

Session Description: Challenging Case Studies are presented by trainees or technologists. They will discuss the case's clinical history, molecular analysis, interesting features, and the proposed diagnosis. Other molecular testing methods, if applicable, will be included in the presentation, including biopsies, gross/microscopic pathology, immunohistochemistry/flow cytometry, and cytogenetic findings.

Session Objectives:
- Describe the context of a challenging clinical case.
- Discuss the molecular pathology techniques used in the diagnosis of the case.
- Propose a final diagnosis based upon findings and diagnostic evidence.

◆How to Validate Rare Findings

Location: Rooms 314-317, Level 300
CE Credit: 1
Path: Cancer/Oncology

How to Validate Rare Findings - Focus on Novel Fusions
John Iafrate, MD PhD, Massachusetts General Hospital, Boston, MA, USA

Did I Find the Right Needle in the Haystack? Sensitivity and Specificity Challenges Revealed by Ultra-accurate NGS
Rosana Risques, PhD, UW Pathology, Seattle, WA, USA

Session Description: The rapid expansion of molecular oncology testing has presented new challenges for clinical laboratories focused on developing and validating novel molecular oncology tests. Two clinical scenarios where these challenges have been notable are the RNA assays for gene fusion detection and liquid biopsy assays. The expanding role of targetable cancer gene fusions has made RNA assays that target one partner particularly appealing, but it is increasingly difficult to identify appropriate positive controls for these multiplexed assays. The advent of cell-free DNA testing in plasma has also introduced extremely rare variant detection through ultra-deep sequencing with innovative technologies and bioinformatic processing. This session will highlight the promises and pitfalls of detecting new variants in oncology and discuss strategies for how to clinically validate findings.

Session Objectives:
- Understand the challenges associated with validating rare cancer mutations.
- Describe validation strategies for multiplexed RNA assays.
- Recognize the potential for ultra-low cancer-related variants in normal tissue to interfere with cell-free tumor DNA assays.

FRIDAY PROGRAM

◆**Novel Mechanisms of Acquired Resistance to Targeted Therapies in Cancer**
Location: Rooms 327-329, Level 300
CE Credit: 1
Path: Cancer/Oncology

Novel Mechanisms of Acquired Resistance to Targeted Therapies in Cancer
Fei Dong, MD, Brigham and Women's Hospital, Boston, MA, USA

Session Description: As new targeted therapies for cancer become available, new genetic mechanisms of acquired resistance have emerged. This session discusses mechanisms of resistance to kinase inhibitors, anti-hormone therapy, PARP inhibitors, and other treatment modalities, the evolution of new strategies to overcoming resistance, and the current and anticipated value of molecular testing to aid therapy selection for patients with cancer.

Session Objectives:
- Describe genetic mechanisms of resistance to targeted therapies, including tyrosine kinase inhibitors, anti-hormone therapies, and PARP inhibitors.
- Interpret resistance mutations to guide patient care in the selection of second-line cancer therapies.
- Anticipate evolving challenges and needs in molecular testing with the emergence of resistance to current and future targeted therapies.

8:00 am – 8:15 am

Break

8:15 am – 9:45 am

Symposia Sessions

◆**Carrier Screening: The Good, The Bad, and The Ugly**
Location: Rooms 314-317, Level 300
CE Credit: 1.5
Path: Inherited Conditions

The Limitations and Consequences of Ethnicity-specific Guidelines for Carrier Screening
Dale Muzzey, PhD, Myriad Women's Health, Inc., South San Francisco, CA, USA

Current Complexities and Future Directions of Expanded Carrier Screening
Nicole Faulkner, PhD, FACMGG, Invitae Corporation, San Francisco, CA, USA

Technological Advances and Detections Rates: Demystifying the Influence of Ethnicity on Carrier Detection and Residual Risk
Lisa Edelmann, PhD, Sema4, New York, NY, USA

Session Description: Carrier screening tests have been available for clinicians to order for many years. Current guidelines rely on a patient's self-reported ethnicity, which conflates genetic and cultural factors. Common questions being asked about the future of carrier screening are: How many genes and what genes should be on Expanded Carrier Screening panels? Should we only be testing for severe/prevalent autosomal recessive disorders? Should carrier screening evolve to a healthy patient screen including pre-symptomatic gene results? How do we make complex, clinically relevant testing more accessible and digestible to the average patient? Guidelines/recommendations for expanded carrier screening relevant to residual risk estimates will be reviewed. The ambiguity, misalignment, incompleteness, deficiency, inequity, and inconsistency of current guidelines will be explored by combining a novel genetic-ancestry analysis method and several retrospective analyses on hundreds of thousands of patients tested with expanded carrier screening. Analytical detection rates of different sequencing technologies will be compared and contrasted. Calculation of residual risk estimates will be explained, and the current shortcomings will be reviewed. A path forward for guidelines that avoid current shortcomings will be elucidated.

FRIDAY PROGRAM

Session Objectives:

- Upon completion participants will be able to describe the original intent of carrier screening and current challenges for the laboratory.
- Upon completion of this session, participants will understand how to calculate residual risk after a negative carrier screening result.
- Upon completion of this session, participants will be able to explain how self-reported ethnicity is an imperfect proxy for carrier risk that measurably impairs discovery of carriers if screening is based on current guidelines.

◆**Emerging Technology for Circulating Tumor Cells, Beyond Counting/ctDNA Alternative Fluids**
Location: Ballroom, Level 400
CE Credit: 1.5
Path: Cancer/Oncology; Molecular Methodologies & Technologies

Advances in Liquid Biopsy: Isolation, Analysis and Expansion of CTCs
Sunitha Nagrath, PhD, University of Michigan, Ann Arbor, MI, USA

Microfluidic Platforms for the Efficient Isolation of Circulating Leukemia Cells and Circulating Plasma Cells
Steven A. Soper, PhD, The University of Kansas, Lawrence, KS, USA

Session Description: New technology based on microfluidic devices are being developed for the isolation and preservation of circulating tumor cells for downstream applications, and to be able to use them to advance precision cancer medicine.

Session Objectives:

- Understand new technology for separation and preservation of CTCs for downstream applications.
- Introduce a description of the new microfluidic devices being developed and describe the operational parameters of these devices for the selection of liquid biopsy markers.
- Describe the downstream molecular information that can be garnered from the isolated markers in diseases such acute myeloid leukemia (circulating leukemia cells) and multiple myeloma (circulating plasma cells). Using liquid biopsy markers for these two diseases circumvents the need for a painful bone marrow biopsy. Information will be provided on using these liquid biopsy markers to monitor relapse from minimum residual disease, and staging patients for directing therapy (i.e., precision medicine).

◆**Structural Variation Detection in Human Disease**
Location: Rooms 309-310, Level 300
CE Credit: 1.5
Path: Informatics

Patterns of Complex Structural Variation across Thousands of Cancer Whole Genomes
Marcin Imielinski, MD, PhD, Weill Cornell Medical College, Brooklyn, NY, USA

Identification and Characterization of Cryptic Structural Variation in Human Genomes
Ryan Mills, PhD, University of Michigan, Ann Arbor, MI, USA

Session Description: Structural variations in the form of DNA rearrangements and aneuploidies are well-known genomic alterations underlying human disease. Despite the ubiquitous nature of genome sequencing in basic research and clinical diagnostics, the mutational processes driving structural variation are yet to be well characterized. In this session, the speakers will describe the strengths of different sequencing technologies and informatics algorithms in identifying different types of genomic structural variation in both cancer and individual genomes.

Session Objectives:

- Upon completion, participants will be able to describe the landscape of structural variation in human genomes and cancers.
- Upon completion, participants will be able to describe features of several complex structural variant patterns commonly observed in human cancer.
- Upon completion, participants will be able to describe the strengths and weaknesses of different sequencing techniques and algorithms in SV detection.

FRIDAY PROGRAM

9:45 am – 10:45 am

Coffee Break - Visit Expo Hall and View Posters

Location: Exhibit Hall A-G, Level 100

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

10:45 am – 12:15 pm

Breakout Sessions

◆**Hands-on Workshop: Variant Interpretation & Classification**
Location: Rooms 318-323, Level 300
CE Credit: 1.5
Path: Informatics; Inherited Conditions

Hands-on Workshop: Variant Interpretation & Classification

Mark Routbort, MD, PhD, University of Texas MD Anderson Cancer Center, Houston, TX, USA

Session Description: Variant interpretation and classification and the generation of a test report in clinical genomics are the critical last steps of a workflow that involves major upstream bioinformatics processes. While standardized criteria for variant interpretation and classification have been developed, such criteria do not include the recognition of different technical and informatics artifacts introduced either during the wet-lab processes or by the bioinformatics algorithms. In addition, despite the broad adoption of genomic sequencing in clinical laboratories, the methods and file formats widely used in bioinformatics pipelines are not formally standardized. In this hands-on workshop session, the 'informatics' aspects of variant annotation, classification and interpretation will be discussed with the aid of example case files that will be available to the participants both for preview and for live review during the session as the speaker goes over the various principles of the bioinformatics pipeline.

Session Objectives:

- Upon completion, participants will be able to understand important features that distinguish technical artifacts from valid calls.
- Upon completion, participants will be able to understand the key concepts of variant classification and interpretation.
- Upon completion, participants will have knowledge of different informatic approaches underlying variant annotation and classification.

◆**Metagenomics in Prime Time**
Location: Rooms 314-317, Level 300
CE Credit: 1.5
Path: Infectious Diseases

Panel Discussion

Robert Schlaberg, MD, MPH, IDbyDNA, Salt Lake City, UT, USA; Charles Chiu, MD, PhD, University of California, San Francisco, San Francisco, CA, USA; Erin Graf, PhD, Mayo Clinic Hospital, Arizona, Phoenix, AZ, USA; Patricia Simner, MSc, PhD, Johns Hopkins University School of Medicine, Baltimore, MD, USA

Session Description: Metagenomic Next Generation Sequencing is a promising approach to indiscriminately detect all pathogens present in a single sample including parasites, bacteria, viruses and fungus. But is it ready for prime-time use? In this session, a group of experts will provide insight on the current state of metagenomics in infectious disease diagnosis. The panel may cover on the different metagenomic assays, barriers to validation and implementation, and regulatory issues. This is an interactive session with the audience so come ready to ask questions and share your opinion!

Session Objectives:

- Describe the benefits and limitations of metagenomics next generation sequence.
- Discuss challenges to implementing the test in the clinical laboratory.

◆**Picking a LIMS System**
Location: Rooms 327-329, Level 300
CE Credit: 1.5
Path: Advocacy/Lab Management; Informatics

Do-It-Yourself Molecular LIMS

Long P. Le, MD, PhD, Massachusetts General Hospital, Charlestown, MA, USA

Picking a LIMS System

Kristina Cusmano-Ozog, MD, Children's National, Palo Alto, CA, USA

FRIDAY PROGRAM

Development of a Laboratory Information System to Support Clinical NGS Testing

Michael Kluk, MD, PhD, Weill Cornell Medicine, New York, NY, USA

Session Description: Many of the laboratory information management systems (LIMS) in use today were originally developed with clinical pathology or anatomic pathology workflows in mind and have since been adapted to include minimal functionality for the molecular lab. With the continually increasing complexity of molecular testing along with the need for rapid delivery of results, having a LIMS in today's molecular laboratory designed for the unique and highly-complex workflows is crucial. This session will discuss LIMS currently used by 3 U.S. medical centers offering highly-complex molecular testing and how they have overcome challenges from receiving orders, tracking samples, and managing complicated workflows, to integrated reporting of complex NGS results.

Session Objectives:

- Discuss the role of the LIMS and the unique needs of the molecular lab.
- Identify basic functionality necessary for an effective molecular LIMS.
- Describe some options currently in use to manage complex, end-to-end molecular workflows and reports.

◆**Process Validation and Quality Assurance Around the World**

Location: Rooms 339-342, Level 300
CE Credit: 1.5
Path: Advocacy/Lab Management

ESP Molecular Pathology WG: Diagnosis and Clinical Research Reproducibility

Giorgio Stanta, MD, PhD, University of Trieste, Duino-Aurisina, Friuli-Venezia Giulia, Italy

Quality Assessment Experience in Brazil

Roberta Sitnik, MSc, PhD, Departamento de Patologia Clínica e Anatomia Patológica, São Paulo, Brazil

Session Description: The European Society of Pathology has a working group devoted to Molecular Pathology. This WG collaborates with several European Organizations and projects. The WG's main goal is to increase reproducibility not only for diagnosis but also for clinical research performed directly in today patients. The issues developed are pre-analytics of clinical material, standardization of methods, evaluation of intra-tumor heterogeneity and training.

Session Objectives:

- The Participants will be able to know which are the major objectives of the ESP Molecular WG.
- The objectives of the ESP-WG are especially oriented for molecular diagnostics and clinical research. This is performed with the collaboration of several European organizations and projects.
- The ESP proposal for pre-analytics, method standardization and intra-tumor heterogeneity will be presented.

◆**Updates on Emerging Technologies**

Location: Rooms 309-310, Level 300
CE Credit: 1.5
Path: Molecular Methodologies & Technologies

Nanopore Sequencing Comes of Age

Miten Jain, PhD, University of California Santa Cruz, Santa Cruz, CA, USA

Extreme Molecular Diagnostics

Carl Wittwer, MD, PhD, University of Utah, Salt Lake City, UT, USA

Session Description: This session is provide attendees with updates on the development and progress of Extreme PCR and Nanopore sequencing and explore their potential utility in molecular diagnostics and research.

Session Objectives:

- Discuss how advances in sample prep, PCR and melt analysis are enabling significant reduction in total test time and the impact of Extreme PCR on molecular diagnostics.
- Discuss the technology behind Nanopore Sequencing and understand the capabilities for direct, real-time DNA & RNA sequencing.
- Understand the applications of these technologies for molecular diagnostics and research.

FRIDAY PROGRAM

12:15 pm – 1:30 pm

General Lunch - Visit Expo Hall and View Posters

Location: Exhibit Hall A-G, Level 100

Networking Lunches: Please see lunch descriptions in the "Highlights & General Information" section of the Program Book, Pages 19-20.

AMP Central Activities: Education Showcase

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

Speed Networking: Please visit the Networking Corner in the Expo Hall from 12:30pm – 1:00pm. Open to all registered attendees.

1:30 pm – 2:45 pm

Breakout Sessions

- **Cell-free DNA testing for Autosomal Dominant disorders**
  Location: Rooms 309-310, Level 300
  CE Credit: 1.25
  Path: Inherited Conditions

Non-invasive Prenatal Sequencing for Multiple Mendelian Monogenic Disorders using Circulating Cell-free Fetal DNA
Shashikant Kulkarni, PhD, FACMG, Baylor College of Medicine, Houston, TX, USA

Prenatal Diagnosis: The Next Generation
Mark I. Evans, MD, Comprehensive Genetics & Icahn School of Medicine Mt. Sinai, New York, NY, USA

Session Description: Incredible technological advances in molecular diagnostics have enabled high resolution prenatal diagnosis. However, there has been widespread confusion as to the benefits and limitations of non-invasive prenatal screening (NIPS) as compared to diagnostic testing. NIPS has been expanded beyond detection of chromosomal abnormalities in a fetus and is increasingly used for sex chromosomal aneuploidies and microdeletions,. but current methods often fail to identify multi-system developmental disorders. Our experience focusing on sequencing a panel of 30 genes for relatively common dominant disorders will be reviewed. When validated, such can herald a new beginning where detection of a comprehensive spectrum of aneuploidies, copy number variations and single gene disorders is within reach. However, the gap between the cutting edge of technology and provider understanding continues to widen - not narrow, and patients' understanding of the difference between screening and diagnosis are similarly sub-optimal. Current reliance upon NIPS has led to an epidemic of abnormalities missed that could have been diagnosed using more expanded testing.

Session Objectives:

- Understand the process of development and validation of non-invasive prenatal diagnosis (NIPD) and understand the value of NIPD in identifying fetal dominant monogenic disorders through clinical case vignettes.
- Understand the multimodal improvements in capabilities for screening and diagnosis of genetic and congenital abnormalities.
- Understand the trade-offs of accepting a non-invasive screening test versus actual diagnostic testing, including missing thousands of abnormalities each year by foregoing diagnostic testing.

- **New Players in Reimbursement: Laboratory Benefit Managers *(Sponsored by the AMP Economic Affairs Committee)***
  Location: Rooms 339-342, Level 300
  CE Credit: 1.25
  Path: Advocacy/Lab Management

Panel Discussion
Geoffrey Baird, MD, PhD, University of Washington, Seattle, WA, USA; Trish Brown, MS, LCGC, Illumina, Inc., San Diego, CA, USA; Heather Agostinelli, Xifin, Inc., San Diego, CA, USA

Session Description: The Economic Affairs Committee invites you to attend a workshop focused on an increasingly significant player for laboratories and their relationship with health insurers: laboratory benefit managers (LBM). In recent years, health plans have created, or contracted with, companies to deploy new systems to manage laboratory services; these services include medical policy, claims editing, and network services. A

FRIDAY PROGRAM

major aspect of LBMs are prior authorization programs, which require that laboratories obtain approval from the health plan before it will cover the cost of a laboratory procedure. LBMs vary in operating style and focus and include companies such as BeaconLBS, Avalon Healthcare Solutions, and eviCore Healthcare. This session will include an introduction to LBMs and explore the different aspects of these companies. All attendees will leave with an understanding of why it is important to have LBMs on their radar screen.

Session Objectives:

- Explain the scope of services provided by and the financial incentives to LBMs.
- Understand how LBMs implement and operate prior authorization programs for laboratories.
- Learn how laboratories can best position themselves with LBMs.

◆**Point Counterpoint: Who Owns Molecular Infectious Disease Testing?**
Location: Rooms 324-326, Level 300
CE Credit: 1.25
Path: Advocacy/Lab Management; Infectious Diseases

Point Counterpoint: Who Owns Molecular Infectious Disease Testing?
Nathan Ledeboer, PhD, Medical College of Wisconsin, Milwaukee, WI, USA; Frederick S. Nolte, PhD, Medical Univ of South Carolina, Charleston, SC, USA

Session Description: Technological advancements in molecular diagnostics for infectious diseases offer greater accuracy, portability, simplicity and cost-effectiveness. These technological advancements creative new challenges for how to best delivery these services and integrate them into laboratory medicine. Other than microbiology laboratories, should other points of service be considered. This point-counter point session will debate whether molecular testing for infectious diseases should be performed in the microbiology laboratory or can be performed throughout the clinical laboratory. Dr. Ledeboer will argue that while molecular techniques are shared among many areas of pathology, the expertise for interpretation of infectious disease testing is within microbiology. Dr. Nolte will provide the rationale and supporting arguments for decentralization of molecular infectious disease testing.

Session Objectives:

- Describe the challenges and opportunities that advancements in molecular technology have created for delivery and integration of molecular microbiology testing into laboratory medicine.
- Describe advantages and disadvantages of performing molecular microbiology testing in different laboratory sections.
- Discuss how microbiologists can remain engaged with molecular microbiology testing regardless of the point of service.

◆**Practical Approaches to Centralizing (or Decentralizing) Molecular Testing**
Location: Rooms 307-308, Level 300
CE Credit: 1.25
Path: Advocacy/Lab Management

Centralized Testing in Molecular Pathology via Lean Laboratory Design
John W. Longshore, PhD, Carolinas Pathology Group, Charlotte, NC, USA

Molecular Laboratory Organization: the University of Washington Experience
Daniel E. Sabath, MD, PhD, University of Washington School of Medicine, Seattle, WA, USA

Session Description: With the changing landscape of healthcare, clinical laboratories are under immense pressure to deliver high quality, complex results despite poor payment and reimbursement rates that often do not cover the cost of performing the tests. As a cost-savings measure, some institutions are using LEAN approaches and consolidation efforts to maximize efficiency and enable sharing of resources across molecular specialties. The advantages and disadvantages of centralized versus decentralized molecular laboratories will be explored in this session.

Session Objectives:

- Describe differing needs of various types of molecular testing.

FRIDAY PROGRAM

- Define key areas where streamlining molecular testing is beneficial to patient care and how the LEAN approach can be applied to improve the molecular lab.
- Discuss the implications for future molecular diagnostic laboratory needs.

◆**Updates in Myeloma Genomics**
Location: Rooms 318-323, Level 300
CE Credit: 1.25
Path: Cancer/Oncology

Advances in Multiple Myeloma Genomics
Brian A. Walker, BSc, PhD, University of Arkansas for Medical Sciences, Little Rock, AR, USA

Molecular Monitoring of Myeloma
Nikhil Munshi, MD, Dana-Farber Cancer Institute, Boston, MA, USA

Session Description: The use of new genome sequencing technologies has revolutionized the field of myeloma genomics, enabling the analysis of large datasets of patient material and the identification of new genomic markers associated with disease progression and prognosis. The main new findings relating to these datasets will be presented, including the mutational landscape of myeloma, mechanisms of gene dysregulation, and the genomic abnormalities associated with poor prognosis. In addition, monitoring of patients with myeloma for therapeutic resistance and minimal residual disease will also be discussed.

Session Objectives:
- Describe findings of genomic landscape studies in myeloma and the genetic markers which relate to prognosis.
- Understand the main deregulated pathways involved in myeloma pathogenesis and association with therapy resistance.
- Discuss methods of minimal residual disease monitoring in myeloma.

2:45 pm – 4:00 pm

Coffee Break - Visit Expo Hall and View Posters

Location: Exhibit Hall A-G, Level 100

Posters: Even-numbered posters attended from 2:45pm - 3:45pm.

AMP Central Activities: Get Involved with AMP! AMP Committee "Meet & Greet" Event

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

4:00 pm – 5:00 pm

Plenary Session

◆**Climate Change and Global Surveillance of Emerging Pathogens**
Location: Ballroom, Level 400
CE Credit: 1
Path: Infectious Diseases

Climate Change and Global Surveillance of Emerging Pathogens
Arturo Casadevall, MD, PhD, Johns Hopkins, Baltimore, MD, USA

Session Description: The World Health Organization (WHO) estimates that climate change will have a significant impact on human health, particularly in developing countries. In addition to the increase in the number of emerging pathogens, climate change may result in the introduction of both established and emerging pathogens in new geographic areas. A genomic based approach to global surveillance of pathogens has the potential to prevent or allow for better response to potential outbreaks and epidemics.

Session objectives:
- Describe the impact of climate change on emerging pathogens
- Discuss genomic approaches to global surveillance of emerging pathogens

FRIDAY PROGRAM

5:00 pm – 5:15 pm

Break

5:15 pm – 6:30 pm

Business Session

- **Business Meeting and Awards Session**
  (Open to All Registered Attendees)
  Location: Rooms 314-317, Level 300
  CE Credit: Not CME/CMLE
  Path: Special Session

Business Meeting and Awards Session

Session Description: This session, open to all meeting attendees, provides both AMP members and those interested in molecular pathology an overview of the projects and accomplishments of the many AMP committees and working groups. The work of AMP committees have a significant impact on molecular pathology, including practice guidelines, molecular curricula for residents and technologists, and policy advocacy. The session opens with a very brief business meeting and closes with the presentation of awards, including the Technologist, Young Investigator, and Jeffrey A. Kant Leadership Awards.

Session Objectives:

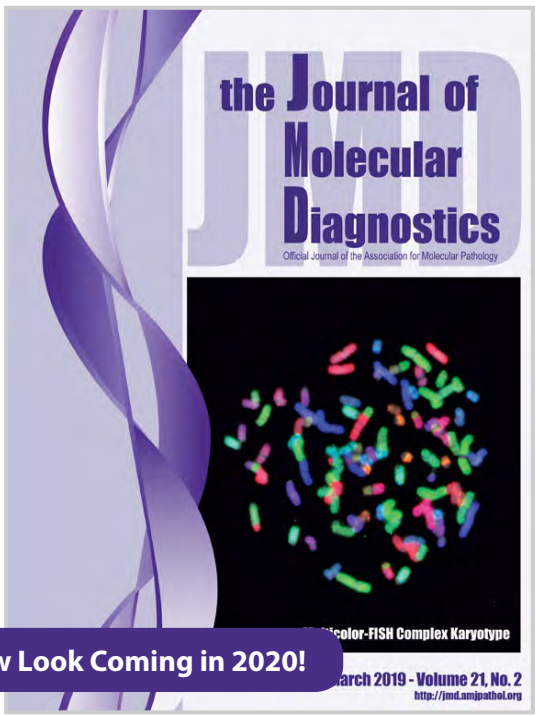
- Identify the relationship between selected projects of the Clinical Practice Committee and their own clinical practice.
- List the regulatory and reimbursement policies in the midst of discussion or implementation that impact molecular pathology.
- Summarize the contributions of the Leadership Award recipient to advance the field of molecular pathology.

7:00 pm – 10:30 pm

Social Event

Location: Hilton, Key Ballroom 1-6

Amazing Molecular Party
(25th Anniversary Celebration)
(Separate Registration)
The AMP Social Event is intended to facilitate networking opportunities between trainees, new, and long-standing AMP attendees. There will be mingling, dancing, amateur acts and great food! Attendees who purchased tickets when registering for the meeting will receive their ticket when they check-in at the registration desk for their name badge. If any tickets are still available for sale, they may be purchased at the Registration Desk.



CELEBRATING 20 YEARS OF *JMD* WITH NEW AND EXCITING CHANGES

As we celebrate the 20th Anniversary of *The Journal of Molecular Diagnostics* (*JMD*) we are pleased to announce exciting changes are coming for AMP's Official Journal!

What You Can Expect in 2020:

- **Monthly Publication** - *JMD* will now be published 12 times a year! This will shorten your wait time to see your article in print.
- **New Author and Reviewer Interface:** Editorial Manager
- **Discounted Page Charges for AMP Members** - Corresponding authors who are regular members of AMP will now receive a 25% discount on page charges
- **Discounted Open Access Fees for AMP Members** - Corresponding authors who are regular members of AMP will now receive 20% off Open Access fees

Now is a great time to submit your original research to *JMD*!

JMD IS CO-OWNED BY:

AMP Association for Molecular Pathology

ASIP American Society for Investigative Pathology

AMP.ORG/JMD

"As ***JMD*** celebrates 20 years of publication, we look proudly at our accomplishments and excitedly towards the future. We thank our authors and readers for the support you have given us in our journey to bring ***JMD*** to the very forefront of the field of molecular diagnostics. We can't wait to share with you what we have in store for the next 20 years!"

- Barbara A. Zehnbauer, PhD, Editor-in-Chief
Emory University School of Medicine, Atlanta, GA

SATURDAY PROGRAM

Tumor Mutational Burden:

CHALLENGES AND OPPORTUNITIES FOR IMPROVING CANCER PATIENT CARE

- AND-

DIAGNOSTIC INNOVATIONS AND CLINICAL IMPLICATIONS

Join us for this free online learning experience that explores the challenges and opportunities for tumor mutational burden (TMB) testing to improve cancer patient care. Our TMB Series now includes five segments with the first three exploring current best practices in TMB testing, interpretation, and reporting and the second two examining implications for TMB in the clinic.

INCLUDED IN THE SERIES

PART I

Tumor Mutational Burden: Clinical and Diagnostic Utilization in Oncology

Tumor Mutational Burden: Best Practices to Address Clinical and Technical Challenges

Tumor Mutational Burden: Result Reporting and Application to Improve Patient Care

PART II

Updates on Tumor Mutational Burden and the Immunotherapy Biomarker Landscape

Making TMB Relevant in the Clinic: Best Practices for TMB Calculation, Reporting, and Interpretation

www.amp.org/TMB

This program has been supported through an educational grant from Bristol-Myers Squibb

SATURDAY PROGRAM

November 9, 2019

6:45 am – 8:00 am

Continental Breakfast

Location: Session Room Foyers, Level 300

7:00 am – 8:00 am

Targeted Topics

◆**A Review of FGFR Related Inherited Disorders**

Location: Rooms 318-323, Level 300
CE Credit: 1
Path: Inherited Conditions

The Skeletal Dysplasias; the Long and Short of It

Deborah Krakow, FACMG, UCLA School of Medicine, Los Angeles, CA, USA

Session Description: This session will review the identification of disease genes and biologic mechanisms that lead to the inherited osteochondrodysplasia, a group of more than 350 distinct genetic disorders. This session will specifically review the diagnosis and natural history from prenatal detection to adulthood, of patients with FGFR related disorders including, but not limited to, achondroplasia, hypochondroplasia and thanatophoric dysplasias types I and II.

Session Objectives:

- Recognize the radiologic differences between thanatophoric dysplasias types I and II.
- Recognize the phenotypic impact of single base changes in the FGFR3 gene.

◆**Case Studies in Solid Tumors**

Location: Rooms 324-326, Level 300
CE Credit: 1
Path: Cancer/Oncology

An Interesting Case Involving a CIC-NUTM1 Rearranged Epitheliod Tumor

Latrice Landry, PhD, MMSc, MS, Dana Farber Cancer Institute/ Brigham and Women's Hospital, Boston, MA, USA

Detection of Rare Fusion using Foundation One and Oncomine Tests: A Male in his 20's with an Aggressive Orbital Tumor

Terri Jones, MD, University of Pittsburgh Medical Center, Pittsburgh, PA, USA

A Case of Cutaneous Lymphoma with PCM1-JAK2 Rearrangement

Talent Theparee, MD, Stanford Healthcare, Stanford, CA, USA

Microsatellites: Instability in an Apparently Stable World

Patrick Leach, BS, TriCore Reference Laboratories, Albuquerque, NM, USA

Session Description: Challenging Case Studies are presented by trainees or technologists. They will discuss the case's clinical history, molecular analysis, interesting features, and the proposed diagnosis. Other molecular testing methods, if applicable, will be included in the presentation, including biopsies, gross/microscopic pathology, immunohistochemistry/flow cytometry, and cytogenetic findings.

Session Objectives:

- Describe the context of a challenging clinical case.
- Discuss the molecular pathology techniques used in the diagnosis of the case.
- Propose a final diagnosis based upon findings and diagnostic evidence.

◆**Genetics & Immunity In Bone Marrow Failure Syndromes**

Location: Rooms 307-308, Level 300
CE Credit: 1
Path: Cancer/Oncology

Genetic Pathways of Myeloid Transformation in Bone Marrow Failure Syndromes

Coleman Lindsley, MD, PhD, Dana-Farber Cancer Institute, Boston, MA, USA

Session Description: Patients with inherited bone marrow failure syndromes have an elevated risk of developing myeloid neoplasms. Recognition of germline

SATURDAY PROGRAM

predispositions can be difficult due to the variability of clinical phenotypes, but can impact prognosis and clinical decision making. Routine screening in children and adults can identify patients with unsuspected germline syndromes. Among patients with known predisposition, development of rational surveillance strategies may be disease-specific, and depends on integration of morphologic and genetic evaluation.

Session Objectives:

- Describe findings of genomic landscape studies in Shwachman-Diamond Syndrome.
- Describe the TERT rare variants that are identified in patients with myelodysplastic syndromes.
- Describe the clinical impact of underlying germline predispositions on clinical outcomes in patients with myelodysplastic syndromes.

◆**Integrating Genomics into the EHR**
Location: Rooms 327-329, Level 300
CE Credit: 1
Path: Advocacy/Lab Management; Informatics

Barriers to Integrating Genomics More Fully into the EHR

Brian H. Shirts, MD, PhD, University of Washington, Seattle, WA, USA

Session Description: Although genome sequencing is near universally adopted in human disease diagnostics, the integration of genomic testing results into the electronic health record (EHR) has lagged behind. Despite technical advances and consensus on desiderata, biological and systemic barriers prevent rapid integration of genomic data into the EHR. In this session, the speaker will describe desiderata for integrating genomic information into the EHR in a way that facilitates clinical decision support. The speaker will also describe technical advances such as those included in SMART standards and FHIR API specifications that help overcome technical barriers for integrating genomics into the EHR.

Session Objectives:

- Upon completion, participants will be able to list four technical requirements for integrating genomic information into the electronic health record.
- Upon completion, participants will be able to describe two standards or specifications that can be used to integrate genomic information into the electronic health record.
- Upon completion, participants will be able to evaluate possible solutions to address biological and systemic barriers to integrating genomic information into the electronic health record.

◆**Liquid Biopsy in Infection and Cancer**
Location: Rooms 314-317, Level 300
CE Credit: 1
Path: Infectious Diseases; Molecular Methodologies & Technologies

Opportunities and Challenges of Fungal Cell-Free DNA Testing for Diagnosis of Invasive Fungal Infection

Niaz Banaei, MD, Stanford University, Stanford, CA, USA

Detecting HPV Circulating Tumor DNA by Liquid Biopsy

Daniel Higginson, MD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

Session Description: Liquid biopsy, the use of a liquid specimen such as blood, urine or cerebral spinal fluid to detect circulating cell-free tumor cells or DNA is increasingly being used as an alternative to invasive surgical biopsies. Oropharyngeal, cervical, and anal cancers are each associated with high risk HPV subtypes, which can either be integrated into tumor genomes or remain episomal. HPV DNA is an attractive substrate for liquid biopsy detection because one cancer cell may have many copies of HPV DNA. Emerging reports find a high sensitivity of detection and possible utility in minimal residual disease detection for these diseases. In infectious disease diagnosis, the utility of liquid biopsy for deep-seated infection is similarly being explored and reports are emerging on its applications in the detection of cell-free fungal DNA to diagnose invasive fungal infections.

SATURDAY PROGRAM

Session Objectives:
- Review the concept of liquid biopsy and cell free DNA detection for molecular diagnosis.
- Describe applications of liquid biopsy and cell-free DNA detection for the diagnosis of fungal infections.
- Discuss the role of HPV in oropharyngeal squamous cell cancer.

◆**Methylation Analysis Technologies**
Location: Rooms 309-310, Level 300
CE Credit: 1
Path: Molecular Methodologies & Technologies

DNA Methylation and Machine Learning in Molecular Pathology for Diagnosis and Clinical Management
Matija Snuderl, MD, NYU Langone Medical Center, New York, NY, USA

Oncogene Activation by Pan-Cancer DNA Hypermethylation
Wei Li, PhD, Baylor College of Medicine, Houston, TX, USA

Session Description: Methylation of CpG dinucleotides is a key epigenetic regulator of gene function during development and disease. DNA methylation-based biomarkers can be useful targets in the diagnosis and prognosis of tumors. This session will focus on methods used for methylation analysis, integration of DNA methylation results with histopathology and NGS methods and clinical applications for tumor subclassification.

Session Objectives:
- Discuss the importance of DNA methylation on gene expression and methods for analysis.
- Identify pre-analytical variables affecting DNA methylation based classifiers
- Integrate DNA methylation results with histopathology and next-generation sequencing methods

8:00 am – 8:15 am

Break

8:15 am – 9:45 am

Symposia Sessions

◆**Incidental Findings from Somatic Testing/ Cancer Predispositions**
Location: Ballroom, Level 400
CE Credit: 1.5
Path: Cancer/Oncology; Inherited Conditions

Approaches to Returning Germline Results in an Era of Agnostic Cancer Predisposition Testing
Michael F. Walsh, MD, Memorial Sloan Kettering Cancer Center, New York City, NY, USA

The Evolving Landscape of Clinical Genomic Testing: Elective Genome Sequencing
Birgit Funke, Dr, Veritas Genetics, Newton, MA, USA

What to Expect When You Find the Unexpected: Pregnancy and Incidental Findings in Noninvasive Prenatal Screening
Susan Hancock, MS, Myriad Women's Health, Salt Lake City, UT, USA

Session Description: The classic pregnancy handbook "What to Expect When You're Expecting" is widely read by patients as a means to prepare and better understand pregnancy. In a similar spirit, this session will focus on providing a resource to the laboratory professional to better understand unexpected findings that occur in noninvasive prenatal screening via cell-free DNA analysis. Attendees will gain an understanding of the nature, cause, and impact of these unexpected findings in the clinical setting. The session will also explore the most recent clinical opinions on appropriate follow-up for patients impacted by incidental findings.

Session Objectives:
- List several incidental findings encountered in noninvasive prenatal screening (NIPS) and identify their origin.
- Summarize the clinical conditions diagnosed subsequent to atypical NIPS results and understand the magnitude of risk based on the most recent literature.
- Recognize health care provider attitudes toward incidental findings in the clinical setting.

SATURDAY PROGRAM

◆**Precision Medicine in Infectious Disease**
Location: Rooms 314-317, Level 300
CE Credit: 1.5
Path: Infectious Diseases

Genotypic Antiretroviral Resistance Testing
Benjamin Pinsky, MD, PhD, Stanford University School of Medicine, Palo Alto, CA, USA

Bacteriome and Mycobiome Imbalance and Design of Precision Medicine and Nutrition
Mahmoud A. Ghannoum, PhD, EMBA, FIDSA, FAAM, Case Western Reserve University and

Session Description: In infectious diseases, the concept of precision medicine – the right medicine, at the right dose, for the right patient, at the right time – can be applied in various ways including the analysis of an individual patient microbiome to predict disease or health outcomes as well as in the more precise monitoring of antimicrobial resistance of pathogens. Preventing and managing the emergence of antiretroviral drug resistance is a key component of worldwide efforts to reduce antimicrobial resistance. Additionally, while many studies have focused on the characterization of the gut bacterial microbiome (bacteriome), a better understanding of the microbiome impact on patient health will need to include evaluation of other human ecosystems including the fungal microbiome (mycobiome).

Session Objectives:
- Discuss the history of genotypic antiviral resistance testing.
- Describe the application of various technologies to the identification of drug resistance mutations and the utility of such testing for individual patient management (HIV, CMV and TB).
- Describe the gut Mycobiome and understand the interactions between the bacteriome and mycobiome and its consequences on health outcomes.

◆**Standards and Applications of RNA-seq in Cancer**
Location: Rooms 309-310, Level 300
CE Credit: 1.5
Path: Cancer/Oncology; Informatics

RNA-seq for the Detection of Gene Fusions and Other Alterations in Cancer
Kevin C. Halling, MD, PhD, Mayo Clinic, Rochester, MN, USA

Applications of RNA-Seq in Cancer
Olena Vaske, PhD, FCCMG, University of California Santa Cruz, Santa Cruz, CA, USA

Session Description: Transcriptome sequencing (RNA-seq) of cancer samples for expression profiling and variant and gene fusion detection is a well-established method in scientific research and a powerful and rapidly emerging tool in clinical diagnostics. Various whole-transcriptome and targeted RNA sequencing methods as well as associated informatics algorithms have been developed for RNA-seq; however, standards for RNA-seq are still evolving. In this session, the speakers will discuss the utility of RNA-seq for profiling tumor samples, including informatics approaches for splicing analysis, gene fusion detection, expressed variant detection, and gene expression analysis.

Session Objectives:
- Upon completion, participants will be able to describe the applications of RNA-seq in cancer.
- Upon completion, participants will be able to understand the technical challenges in standardizing RNA-seq.
- Upon completion, participants will be able to understand the strengths and limitations of the RNA-Seq technology.

9:45 am – 10:45 am

Coffee Break - Visit Expo Hall and View Posters
Location: Exhibit Hall A-G, Level 100

Posters: Odd-numbered posters attended from 9:45am - 10:45am.

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

SATURDAY PROGRAM

10:45 am – 12:15 pm

Breakout Sessions

◆**Featured Selections from the Journal of Molecular Diagnostics in 2019**
Location: Rooms 339-342, Level 300
CE Credit:
Path: Infectious Diseases

Featured Selections from the Journal of Molecular Diagnostics in 2019

James Versalovic, MD, PhD, Texas Children's Hospital, Houston, TX, USA; Kevin C. Halling, MD, PhD, Mayo Clinic, Rochester, MN, USA; Stephen Lincoln, Invitae, San Francisco, CA, USA

Session Description: The session will feature oral presentations from authors of articles featured by the Journal of Molecular Diagnostics in 2019 issues. The articles were selected based on their innovation, high importance, and impact. Diverse specialty areas of the practice of molecular diagnostics will be included.

Session Objectives:
- Bring recognition to the scientific scope of JMD.
- Highlight articles in the JMD which contribute significant advances to molecular pathology laboratory practice.
- Provide opportunity to hear directly from the authors.

◆**Future of Molecular Pathology**
Location: Rooms 327-329, Level 300
CE Credit: 1.5
Path: Special Session

Panel Discussion

Gabriel Bien-Willner, MD, PhD, Palmetto GBA, TX, USA; Samuel K. Caughron, MD, MAWD Pathology Group, Lenexa, KS, USA; Karen L. Kaul, MD, PhD, NorthShore University Health System, Evanston, IL, USA; Federico A. Monzon, MD, Castle Biosciences, Friendswood, TX, USA; Timothy Stenzel, MD PhD FACMG FCAP, FDA, Rockville, MD, USA

Session Description: Are the walls closing in? This panel discussion with expert molecular diagnosticians representing diverse perspectives of our specialty – academia, community, industry, regulatory, and insurance – will address how our specialty will evolve, not in terms of advances in technology and science, but rather in how our personal roles in the practice of medicine will change with the shifting landscape of health care.

Session Objectives:
- At the end of this discussion, learners will feel "pumped and jacked" that molecular diagnostics is a vibrant field with a bright future as the cornerstone of 21st century medicine.
- Attendees will understand diverse models of molecular care delivery, and the contexts in which molecular diagnostics can, and will, be practiced as health care evolves.

◆**Tumor Mutation Burden, Clinical Utility/ Efficacy and Harmonization Project**
Location: Rooms 314-317, Level 300
CE Credit: 1.25
Path: Cancer/Oncology

Tumor Mutational Burden (TMB): Harmonization and Future Application

Jeff Allen, PhD, Friends for Cancer Research, Washington, D.C., USA

TMB: The Case for Understanding and Harmonizing Complex Biomarkers

Albrecht Stenzinger, MD, University Hospital Heidelberg, Heidelberg, Germany

Session Description: Tumor mutational burden (TMB) by next-generation sequencing is emerging as a biomarker of response to immunotherapy agents in cancer patients. However, heterogeneity in experimental and analytical protocols, as well as bioinformatic pipelines, influence the variability for TMB estimation and reporting, demonstrating the need for standardization and harmonization of TMB assessment methodology across assays and clinical centers. Friends of Cancer Research (Friends) and the Quality Assurance Initiative Pathology (QuIP), have collaborated to coordinate efforts for international multi-stakeholder initiatives to address this need.

Session Objectives:
- Review TMB as a biomarker for immunotherapy response in cancer patients.
- Describe methodologies for TMB assessment and quantification.

SATURDAY PROGRAM

- Review the many factors that influence TMB assessment.

◆**Hands-on Workshop: Informatic Tools in Metagenomics**
Location: Rooms 337-338, Level 300
CE Credit: 1.5
Path: Informatics; Infectious Diseases

Hands-on Workshop: Informatic Tools in Metagenomics

Alexander L. Greninger, MD, PhD, MS, MPhil, University of Washington, Seattle, WA, USA; Samia Naccache, PhD, LabCorp, Seattle, Seattle, WA, USA

Session Description: Metagenomic sequencing is a powerful and emerging tool in infectious disease diagnostics. While substantial challenges remain in informatics approaches and the lack of standardized test systems, ongoing development of such methodologies hold promise in the area of clinical microbiology. In this session, the speakers will discuss freely available bioinformatic tools used to analyze metagenomic data today as well as the challenges and opportunities for future metagenomic analysis tools.

Session Objectives:
- Upon completion, participants will be able to demonstrate an understanding of the key concepts of metagenomics data analysis.
- Upon completion, participants will be able to describe examples of false positive taxonomical assignments.
- Upon completion, participants will be able to describe the bioinformatics steps involved from in the clinical application of metagenomics.

◆**Pipeline Showcase**
Location: Rooms 309-310, Level 300
CE Credit: 1.5
Path: Informatics

Pipeline Showcase

Jeremy Segal, MD, PhD, University of Chicago, Chicago, IL, USA and Ahmet Zehir, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

Session Description: Each individual laboratory validates its own combination of software and thresholds for their secondary bioinformatics processes. In this session, we will have participants discuss their approaches to analyze data files from cancer sequencing studies (SEQC2). The obtained results and the analytic methods used to generate the results will be presented by each participating institution, after which, the nuances and differences in the bioinformatics analytic approach and the results will be discussed. This session is expected to be both enjoyable and informative with active discussions.

Session Objectives:
- Upon completion, participants will be able to appreciate the complexity and difficulty in the bioinformatics analyses and interpretation of NGS data.
- Upon competition, participants will have knowledge about different methods for analyzing somatic variation, with the understanding that there is no "one size fits all" for NGS data analysis.
- Upon competition, participants will learn that different bioinformatics pipelines have unique advantages and complexities, and to take these into consideration when implementing them internally.

◆**Whole Genome Sequencing for Bacterial Strain Typing & Genomic Surveillance**
Location: Rooms 314-317, Level 300
CE Credit: 1.5
Path: Infectious Diseases; Molecular Methodologies & Technologies

Real-time Clinical Applications for Whole Genome Sequencing of Bacteria

Brad Cookson, MD, PhD, University of Washington, Seattle, WA, USA

Bacterial Strain Typing in the Age of Whole Genome Sequencing: Promises and Pitfalls

Richard Goering, PhD, Creighton University School of Medicine, OMAHA, NE, USA

Session Description: The history and evolution of molecular approaches to bacterial strain typing and its importance for infection control and epidemiological analysis will be presented in this session. The use of next-generation, whole genome sequencing for strain typing will be discussed including the associated

SATURDAY PROGRAM

benefits and challenges. Applications for NGS strain typing in epidemiological investigations, infection control, public health, and patient management will also be described.

Session Objectives:

- Learn the history and importance of molecular strain typing for epidemiological analysis and infection control.
- Discuss the utility of NGS for investigation of hospital acquired infections.
- Gain perspective on leveraging the power of whole genome sequencing while managing the complexities in a clinical setting.

12:15 pm – 1:30 pm

General Lunch - Visit Expo Hall, and View Posters

Location: Exhibit Hall A-G, Level 100

AMP Central Activities: "Meet & Greet" with the JMD Editor-in-Chief

Innovation Spotlight Schedule: See Schedule on Mobile App and by each stage located in the Expo Hall.

Speed Networking: Please visit the Networking Corner in the Expo Hall from 12:30pm – 1:00pm. Open to all registered attendees.

1:30 pm – 2:45 pm

Breakout Sessions

◆**Platform Presentations of Selected Genetics Abstracts**
Location: Rooms 339-342, Level 300
CE Credit: 1.25
Path: Cancer/Oncology; Informatics; Inherited Conditions

G008 - Germline RAD51B Loss-of-function Variants Confer Susceptibility to Hereditary Breast and Ovarian Cancers and Result in
Diana Mandelker, MD, PhD, Memorial Sloan Kettering Cancer Center, NEW YORK, NY, USA

G014 - A Framework of Critical Considerations in Interpretation of NGS Based Tests for Germline Disorders - On Behalf of CLSI Document Development Committee (DDC) on Nucleic Acid Sequencing (MM09)
Avni Santani, PhD, Children's Hospital of Philadelphia, Philadelphia, PA, USA

G023 - Integrated Germline and Somatic Analysis Identifies Actionable Cancer Predisposing Germline Mutations in 9,734 Patients with Advanced Cancers
Liying Zhang, MD, PhD, Memorial Slone Kettering Cancer Center, New York, NY, USA

G036 - Significance Associated with Phenotype (SAP) Score – A Method for Ranking Genes and Genomic Regions Based on Sample Phenotype
Jianling Ji, MD, MS, Children's Hospital of Los Angeles, South Pasadena, CA, USA

G010 - A Method to Missense Madness: Improving Clinical Variant Interpretation with a Pathway-Focused Functional Assay
Sarah E. Brnich, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

Session Description: Platform presentations of selected Genetics abstracts.

Session Objectives:

- Analyze platform presentations of abstracts highlighted by the Genetics Subdivision leadership as particularly significant.
- Evaluate the scientific merit and significance of these selected studies through further discussion with the authors.

◆**Platform Presentations of Selected Hematopathology Abstracts**
Location: Rooms 307-308, Level 300
CE Credit: 1.25
Path: Cancer/Oncology; Informatics; Molecular Methodologies & Technologies

H034 - Identification of Neoplastic Clonal T-cell Sequences in Unrelated Healthy Individuals: Limitations of High Throughput TRG Sequencing for Minimal Residual Disease (MRD) Analysis
Siddhartha Sen, MD, PhD, Duke University Medical Center, Durham, NC, USA

H039 - Measurable Residual Disease Monitoring for Patients with Acute Myeloid Leukemia Following Hematopoietic Cell Transplantation Using Error Corrected Hybrid Capture Next Generation Sequencing
Vidya Balagopal, PhD, University of Chicago, Chicago, IL, USA

SATURDAY PROGRAM

H021 - IGH Locus Assessment using Hybrid-capture, a Proof-of-concept Study
Etienne Mahe, MD, MSc, FRCPC, FCAP, University of Calgary, Calgary, Alberta, Canada

H027 - Convergence on Genomic Abrogation of the DNA Damage Response Pathway in CLL is Observed in Patients with Loss of18p
Waihay Wong, Brigham and Women's Hospital and Harvard Medical School, Boston, MA, USA

H020 - IDH1 p.S280F Mutation is Potentially a Novel Mechanism of Resistance to Ivosidenib Therapy in an IDH1 Positive Acute Myeloid Leukemia
Zoltan N. Oltvai, MD, University of Pittsburgh, Pittsburgh, PA, USA

Session Description: Platform presentations of selected Hematopathology abstracts.

Session Objectives:
- Analyze platform presentations of abstracts highlighted by the Hematopathology Subdivision leadership as particularly significant.
- Evaluate the scientific merit and significance of these selected studies through further discussion with the authors.

◆**Platform Presentations of Selected Infectious Diseases Abstracts**
Location: Rooms 318-323, Level 300
CE Credit: 1.25
Path: Infectious Diseases; Molecular Methodologies & Technologies

ID019 - Mycoplasma Genitalium Assay Results from High and Low Risk Populations: Implications for Sexually Transmitted Infection Panel Menu
Kimberle Chapin, MD, Brown Biology and Medicine, Providence, RI, USA

ID018 - Cell-free RNA is More Sensitive than DNA for the Detection of Pediatric Bacterial Sepsis via Shotgun Metagenomic Sequencing
Caitlin Dougherty, The Children's Hospital of Philadelphia, Philadelphia, PA, USA

ID020 - Clinical and Histologic Features of Patients Tested Using the BioFire FilmArray Gastrointestinal Panel
Jonathan Mowers, MD, PhD, Michigan Medicine, Ann Arbor, MI, USA

ID043 - Investigation of Amplicon Sequencing Technology in Diagnosis of Drug Resistant Tuberculosis by Testing FFPE Specimens
Nanying Che, PhD, Department of Pathology, Beijing Chest Hospital, Medical Capital University, Beijing, Beijing, China

ID003 - Microbial Cell-free DNA Sequencing for Multiplexed Detection and Quantitation of Cytomegalovirus, Epstein-Barr Virus, and BK Virus
Timothy Blauwkamp, PhD, Karius, Inc., Redwood City, CA, USA

Session Description: Platform presentations of selected Infectious Diseases abstracts.

Session Objectives:
- Analyze platform presentations of abstracts highlighted by the Infectious Diseases Subdivision leadership as particularly significant.
- Evaluate the scientific merit and significance of these selected studies through further discussion with the authors.

◆**Platform Presentations of Selected Informatics Abstracts**
Location: Rooms 324-326, Level 300
CE Credit: 1.25
Path: Cancer/Oncology; Informatics

I031 - Platform-agnostic Deployment of Bioinformatics Pipelines for Clinical NGS Assays using Containers, Infrastructure Orchestration, and Workflow Manager
Sabah Kadri, PhD, Lurie Children's Hospital of Chicago, Chicago, IL, USA

I013 - Benchmarks for Difficult-to-Sequence Genes and Structural Variants
Justin M. Zook, PhD, National Inst of Standards & Tech, Gaithersburg, MD, USA

I040 - Machine Learning Applications for Patient Testing: Computational Assessment of MSI by NGS in the Clinical Laboratory
Gregory Omerza, PhD, The Jackson Laboratory, Farmington, CT, USA

I020 - Mixed Reality for a Precision Medicine Laboratory: the Future is Now!
Andrea Sboner, PhD, Weill Cornell Medicine, New York, NY, USA

SATURDAY PROGRAM

I004 - Impact of Next Generation Sequencing Panel Composition on Tumor Mutation Burden Calculation – In Silico Comparison of Frequently Utilized Panels
Nicholas Bevins, MD PhD, University of California at San Diego, San Diego, CA, USA

Session Description: Platform presentations of selected Informatics abstracts.

Session Objectives:
- Analyze platform presentations of abstracts highlighted by the Informatics Subdivision leadership as particularly significant.
- Evaluate the scientific merit and significance of these selected studies through further discussion with the authors.

◆**Platform Presentations of Selected Solid Tumors Abstracts**
Location: Rooms 309-310, Level 300
CE Credit: 1.25
Path: Cancer/Oncology; Molecular Methodologies & Technologies

ST132 - The Impact of Clinical Molecular Testing and Precision Medicine in Thyroid Cancer
Dora Dias-Santagata, PhD, FACMG, Massachusetts General Hospital - Harvard Medical School, Boston, MA, USA

ST009 - Improved Detection of MET Exon 14 Skipping Mutations in Lung Adenocarcinoma with Combined DNA/RNA Testing and Refined Analysis Methods
David Manthei, MD, PhD, University of Michigan, Department of Pathology, Ann Arbor, MI, USA

ST010 - Detection of Point Mutations in Paediatric Low Grade Glioma (PLGG) and Diffuse Intrinsic Pontine Glioma (DIPG) Patients: Validation of a Novel Liquid Biopsy Assay
Monique Johnson, Masters of Science, The Hospital for Sick Children, Toronto, Ontario, Canada

ST015 - Clonal Hematopoiesis Mutations in Plasma cfDNA RAS/BRAF Genotyping of Metastatic Colorectal Cancer
Fei Huang, Zhongshan Hospital, Fudan University, Shanghai, Shanghai, China

ST094 - STK11 Loss of Function Variants Mediate Immune Evasion in NSCLC via Dysregulation of the FAK/Hippo Signaling Axis and Subsequent Alterations in Tumor-Intrinsic Cytokine Expression
Liam Donnelly, MD, University of Vermont Medical Center, Burlington, VT, USA

Session Description: Platform presentations of selected Solid Tumors abstracts.

Session Objectives:
- Analyze presentations of abstracts highlighted by the Solid Tumors Subdivision leadership as particularly significant.
- Evaluate the scientific merit and significance of these selected studies through further discussion with the authors.

◆**Platform Presentations of Selected Technical Topics Abstracts**
Location: Rooms 327-329, Level 300
CE Credit: 1.25
Path: Cancer/Oncology; Informatics; Molecular Methodologies & Technologies

TT011 - A Comprehensive Assessment of Onco-panel Sequencing across Multiple Laboratories and Technologies
Joshua Xu, FDA's National Center for Toxicological Research (NCTR), Jefferson, AR, USA

TT066 - Variants Reported by Tumor-Only Clinical Oncology NGS Testing Are Frequently Found in the Germline of Pediatric Patients
Azhar Saeed, MD, MSc, University of Kansas Medical Center, Kansas City, KS, USA

TT071 - EXaCT-2: Augmented Whole Exome Sequencing Optimized for Clinical Testing in Oncology
Duane C. Hassane, PhD, Weill Cornell Medicine, New York, NY, USA

TT072 - Dissimilarity Score (DisScore): Identifying Potential Discordance between Anatomic Pathology and Mutation Landscape in the Evaluation of Clinical Sequencing as Part of a Molecular Tumor Board
Grzegorz T. Gurda, MD, PhD, Gundersen Health System, La Crosse, WI, USA

SATURDAY PROGRAM

TT055 - Digital Methylation Specific Multiplex Ligation-Dependent Probe Amplification: A Novel MLPA Based Technique for Assessing Promoter Methylation Status in Cancer
Jan Smout, MSc, MRC Holland, Amsterdam, Netherlands

Session Description: Platform presentations of selected Technical Topics abstracts.

Session Objectives:
- Analyze platform presentations of abstracts highlighted by the Technical Topics leadership as particularly significant.
- Evaluate the scientific merit and significance of these selected studies through further discussion with the authors.

◆**The Future of the AMP v. Myriad Decision: Exploring potential impacts on multigene panel testing and patient care *(Sponsored by the AMP Professional Relations Committee)***
Location: Rooms 339-342, Level 300
CE Credit: 1.25
Path: Advocacy/Lab Management

Panel Discussion
Charles Duan, JD, The R Street Institute, Washington, DC, USA; Robert Nussbaum, MD, Invitae, San Francisco, CA, USA; Sandra Park, JD, American Civil Liberties Union, New York, NY, USA; Hans Sauer, JD, Biotechnology Innovation Organization, Washington, DC, USA

Session Description: The Professional Relations Committee (PRC) invites you to participate in a conversation about the past, present and future landscapes of patent law as it relates to genes and gene-disease associations. In 2013, the U.S. Supreme Court ruled unanimously in AMP v. Myriad Genetics that isolated genomic DNA was not patent eligible under Section 101 of the Patent Act. In the aftermath of this decision and others, genetic testing and genetic medicine has flourished with the introduction and evolution of a wide array of testing methodologies, including next generation sequencing. The field has also witnessed the emergence of new knowledge about the relationship between variants and clinical information. However, proposed legislation to rewrite Section 101 of the Patent Act threatens the future of gene patent ineligibility. Please join us for an in-depth discussion amongst AMP and other stakeholders to learn more about this issue.

Session Objectives:
- Explain the legal rationale and reasoning behind the 2013 AMP v. Myriad decision.
- Become aware about current legislative efforts to redefine what is and what is not patentable, and the effect that these efforts would have on patents for genes and gene-disease associations.
- Understand how changes to current legislation could impact innovation and patient care.
- Discuss current advocacy efforts in this space and how you can get involved.

2:45 pm – 3:00 pm

Break

3:00 pm – 3:45 pm

Open Forums

◆**Genetics Subdivision Open Forum**
Location: Rooms 339-342, Level 300
CE Credit: 0.75
Path: Inherited Conditions

Genetics Subdivision Open Forum
Elaine Spector, PhD, University of Colorado School of Medicine, Aurora, CO, USA

Session Description: In the past 25 years, the AMP Genetics Subdivision and multiple AMP volunteers have spearheaded substantial contributions to the field of molecular diagnostics. As we look to the future, AMP leadership would like to invite genetics subdivision members and meeting attendees with an interest in genetics to attend an open format town hall session. Please bring your ideas, energy, and enthusiasm to the conversation as we discuss the future of genetics molecular diagnostics within AMP.

SATURDAY PROGRAM

◆**Hematopathology Subdivision Open Forum**
Location: Rooms 307-308, Level 300
CE Credit: 0.75
Path: Cancer/Oncology

Hematopathology Subdivision Open Forum
Annette Kim, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA

Session Description: In the past 25 years, the AMP Genetics Subdivision and multiple AMP volunteers have spearheaded substantial contributions to the field of molecular diagnostics. As we look to the future, AMP leadership would like to invite genetics subdivision members and meeting attendees with an interest in genetics to attend an open format town hall session. Please bring your ideas, energy, and enthusiasm to the conversation as we discuss the future of genetics molecular diagnostics within AMP.

◆**Infectious Diseases Subdivision Open Forum**
Location: Rooms 318-323, Level 300
CE Credit: 0.75
Path: Infectious Diseases

Infectious Diseases Subdivision Open Forum
Frederick S. Nolte, PhD, Medical Univ of South Carolina, Charleston, SC, USA

Session Description: In the past 25 years, the AMP Genetics Subdivision and multiple AMP volunteers have spearheaded substantial contributions to the field of molecular diagnostics. As we look to the future, AMP leadership would like to invite genetics subdivision members and meeting attendees with an interest in genetics to attend an open format town hall session. Please bring your ideas, energy, and enthusiasm to the conversation as we discuss the future of genetics molecular diagnostics within AMP.

◆**Informatics Subdivision Open Forum**
Location: Rooms 324-326, Level 300
CE Credit: 0.75
Path: Informatics

Informatics Subdivision Open Forum
Somak Roy, MD, University of Pittsburgh Medical Center, Pittsburgh, PA, USA

Session Description: In the past 25 years, the AMP Genetics Subdivision and multiple AMP volunteers have spearheaded substantial contributions to the field of molecular diagnostics. As we look to the future, AMP leadership would like to invite genetics subdivision members and meeting attendees with an interest in genetics to attend an open format town hall session. Please bring your ideas, energy, and enthusiasm to the conversation as we discuss the future of genetics molecular diagnostics within AMP.

◆**Solid Tumors Subdivision Open Forum**
Location: Rooms 309-310, Level 300
CE Credit: 0.75
Path: Cancer/Oncology

Solid Tumors Subdivision Open Forum
Roger Klein, MD, JD, Roger D. Klein, MD JD, Beachwood, OH, USA

Session Description: In the past 25 years, the AMP Genetics Subdivision and multiple AMP volunteers have spearheaded substantial contributions to the field of molecular diagnostics. As we look to the future, AMP leadership would like to invite genetics subdivision members and meeting attendees with an interest in genetics to attend an open format town hall session. Please bring your ideas, energy, and enthusiasm to the conversation as we discuss the future of genetics molecular diagnostics within AMP.

3:45 pm – 4:00 pm

Break

SATURDAY PROGRAM

4:00 pm – 5:00 pm

Plenary Session

◆**Liquid Biopsies for MRD/Opportunities & Pitfalls in Monitoring AML Patients**
Location: Rooms 314-317, Level 300
CE Credit: 1
Path: Cancer/Oncology

MRD in AML - Promises, Problems and Perspectives
Christian Thiede, MD, University of Technics, Dresden, Germany

Session Description: Numerous studies have demonstrated the value of measurable residual disease (MRD) as a prognostic marker in patients with acute leukemia. While many markers have been well-validated for this approach such as NPM1 and specific recurrent fusions, some markers such as those associated with clonal hematopoiesis remain challenging. This session will discuss advances in the methods of MRD detection in acute myeloid leukemia (AML) and highlight some of the pitfalls.

Session Objectives:
- Describe different methods used to monitor acute myeloid leukemia following therapy.
- Discuss potential pitfalls associated with these methods.
- Synthesize an integrated approach to monitor therapy response in acute myeloid leukemia.

5:00 pm – 5:15 pm

Closing Remarks

Location: Rooms 314-317, Level 300
CE Credit: Not CME/CMLE
Path: Closing Remarks

Closing Remarks
Neal Lindeman, MD, Brigham & Women's Hospital, Cambridge, MA, USA (2019 Program Chair) and Jane Gibson, PhD, University of Central Florida College of Medicine, Orlando, FL, USA (2020 Program Chair)

CSI Laboratories

SPEAKER INFORMATION

Visit us at booth **#3049**
to learn more about our
comprehensive test services.

ABOUT CSI LABORATORIES

For over 20 years, CSI Laboratories has provided personalized cancer diagnostics to help pathologists and oncologists accurately diagnose and treat patients.

Flow Cytometry | Molecular | FISH | Tech-Only | Histology | Consultation | Cytogenetics

800-459-1185 | www.csilaboratories.com | contact@csilaboratories.com

SPEAKER INFORMATION

AMPED Educates

CONVENIENT ONLINE MOLECULAR EDUCATION FOR HEALTHCARE PROFESSIONALS

Have you explored AMP's online learning management platform, AMP*ED*™?

AMP*ED*™ aims to bring the world-renowned, cutting edge content you have come to expect from AMP's live events, but with the convenience of learning from your home, office, or lab. AMP*ED*™ can help you to get up to speed on current trends and techniques or provide a refresher on foundational concepts. New content is being added regularly so check back often at ***educate.amp.org***!

Many of our educational offerings include the opportunity to earn CME/CMLE and/or SAM credit.

The ever-expanding selection of content includes:

- **Online MGP Review Course**
- **Molecular Genetic Pathology Question Bank and Fellowship In-service Exam (FISE)**
- **NEW: PARP Inhibitor Online Learning Series**
- **NEW: Circulating Tumor DNA Testing Certificate Program**
- **NEW: Hot Topics in Infectious Diseases Certificate Program**
- **Tumor Mutational Burden Online Learning Series**
- **Horizons in Molecular Pathology Online Learning Series**
- ***And more…***

EDUCATE.AMP.ORG

"**AMP** is the best organization for anyone who wants to stay on the ***cutting edge*** of the future of molecular pathology."

— **Matthew Hiemenz, MD**
Molecular Pathologist
Assistant Director of Clinical Genomics, Center for Personalized Medicine, Children's Hospital Los Angeles

INVITED SPEAKER
Biographies

Note: The following bios listed below are for invited speakers. For a complete listing of all speakers, including Platform Presentation and Case Study speakers, please refer to the online Program & Mobile App.

A

Jeff Allen, PhD, serves as the President and CEO of Friends of Cancer Research (Friends). During the past 20 years, Friends has been instrumental in the creation and implementation of policies ensuring patients receive the best treatments in the fastest and safest way possible. As a thought leader on many issues related to Food and Drug Administration, regulatory strategy and healthcare policy, he is regularly published in prestigious medical journals and policy publications, and has contributed his expertise to the legislative process on multiple occasions. Recent Friends initiatives include the establishment of the Breakthrough Therapies designation and the development of the Lung Cancer Master Protocol, a unique partnership that will accelerate and optimize clinical trial conduct for new drugs. Dr. Allen received his Ph.D. in cell and molecular biology from Georgetown University, and holds a Bachelors of Science in Biology from Bowling Green State University.

B

Niaz Banaei, MD, is currently a Professor of Pathology and Medicine at Stanford University and is the Medical Director of the Clinical Microbiology Laboratory at Stanford Medical Center. He is also the director of Stanford Medical Microbiology Fellowship and the associate program director of Stanford Clinical Pathology residency training.His research interests include development, assessment, and improvement of novel infectious diseases diagnostics. Over the past 15 years he has developed and implemented more than dozen nucleic acid amplification tests and conducted multiple research projects locally and internationally to advance the field of infectious diseases diagnostics.

Frederick Bieber, PhD, is a member of the Faculty of Medicine at Harvard University where he directs formal courses in genetics and forensics offered to Harvard undergraduate, graduate, medical students as well as to post-doctoral fellows. As a Medical Geneticist at Brigham and Women's Hospital, Dr. Bieber provides clinical diagnostic genetic laboratory testing to patients and their families in the Partners Healthcare System. His academic work focuses on the laboratory and statistical aspects of DNA-based human identification, with a focus on kinship analysis and its attendant legal, ethical, and policy implications. Dr. Bieber has served as an appointed member of the National DNA Databank of Canada Advisory Committee since its inception in 2000, as a member of the DNA Subcommittee of the New York State Forensic Commission, and as Chair of the Quality Assurance oversight committee of the United States Army DNA Identification Laboratory (AFDIL). He has served as a member of numerous state and federal forensic advisory boards, including the congressionally mandated FBI DNA Advisory Board, and the Scientific Advisory Board of the Virginia Department of Public

SPEAKER BIOS

Safety, the National Commission on Forensic Science and the U.S. Forensic Sciences Standards Board (FSSB). As a commissioned officer in the United States Army Reserve, Dr. Bieber served on active duty at the U.S. Army Criminal Investigation Laboratory (USACIL/ Ft. Gillem, GA) and the Armed Forces DNA Identification Laboratory (AFDIL/Rockville, MD and Dover, DL). Professor Bieber was a member of the World Trade Center Kinship and Data Analysis Panel (KADAP) for the DNA-based identification of victims of the September 11th attack on the twin towers, and a member of the Hurricane Victim DNA Identification Expert Group (HVDIEG), assisting the Louisiana State Police in the DNA-based identification of victims of Hurricanes Katrina and Rita. Dr. Bieber has served as an expert witness in dozens of admissibility hearings and trials in state, federal, and military courts in the U.S. and abroad.

Gabriel Bien-Willner, MD, PhD, is the Medical Director of the MolDX program at Palmetto GBA, a Medicare Administrative Contractor (MAC). MolDX seeks to understand the molecular testing landscape to implement payer controls, coverage, and to set policy for affiliated MACs, which currently cover 28 states. He is a leader in the Precision Medicine space and practices as a Board-certified Anatomic Pathologist and Molecular Genetic Pathologist. Throughout his career, he has been active in research, development, and advancement of molecular diagnostic services, specifically next generation sequencing. He has worked closely with clinicians to develop clear clinical diagnostic and treatment pathways directing Precision Medicine programs for community cancer centers. Dr. Bien-Willner received his MD and PhD degrees from Baylor College of Medicine, with a PhD in Human Molecular Genetics. He completed his residency, fellowship, and attained a faculty appointment at Washington University in St. Louis prior to leadership roles in laboratory and biotech companies before joining Palmetto GBA.

Aaron Bossler, MD, PhD, is a clinical professor in the Department of Pathology at the University of Iowa and member of the Holden Comprehensive Cancer Center. He serves as the Director of the Molecular Pathology Laboratory and the Molecular Genetic Pathology Fellowship Program. He is involved in coding, coverage, and reimbursement issues and is a member of the Association for Molecular Pathology (AMP) Economic Affairs Committee, the AMA Proprietary Laboratory Assay Technical Advisory Group, the Medicare Advisory Group for the Centers for Medicare and Medicaid services and has been a member of the AMA Molecular Pathology Advisory Group. He serves as the AMP representative to the CAP Pathology Coding Caucus and on the editorial board for The Journal of Molecular Diagnostics. His research interests center on the role of HPV infection in the development of cancer and the development of new molecular diagnostic assays.

C

Arturo Casadevall, MD, PhD, is Bloomberg Distinguished Professor and Chair of the W. Harry Feinstone Department of Molecular Microbiology and Immunology at the Johns Hopkins Bloomberg School of Public Health. Previously he served as Director of the Division of Infectious Diseases at Montefiore Medical Center, the University Hospital and Academic Medical Center for Einstein, from 2000-2006 and as Chair of the Department of Microbiology and Immunology from 2006-2014. Dr. Casadevall received

both his M.D. and Ph.D. (biochemistry) degrees from New York University. Subsequently, he completed his internship and residency in internal medicine at Bellevue Hospital in New York. He then completed subspecialty training in infectious diseases at Montefiore and Einstein. The author of over 700 scientific papers, numerous books and book chapters, Dr. Casadevall's major research interests are in fungal pathogenesis and the mechanisms of antibody action. In the area of biodefense, he has an active research program to understand the mechanisms of antibody-mediated neutralization of Bacillus anthracis toxins. In recent years Dr. Casadevall has become interested in problems with the scientific enterprise and with his collaborators shown that misconduct accounts for the majority of retracted publications. He has suggested a variety of reforms to the way science is done. Dr. Casadevall is the editor-in-chief of mBio, the first open access general journal of the American Society of Microbiology, and is on the editorial board of several journals including the Journal of Infectious Diseases and the Journal of Experimental Medicine. He has also served in numerous NIH committees including those that drafted the NIAID Strategic Plan and the Blue Ribbon Panel on Biodefense Research. He served on the National Academy of Sciences panel that reviewed the science on the FBI investigation of the anthrax terror attacks of 2001. He has also served as a member of the National Science Advisory Board for Biosecurity from 2005-2014 and currently co-chairs the NIAID Board of Scientific Counselors. In 2008, he was recognized the American Society of Microbiology with the William Hinton Award for mentoring scientists from underrepresented groups. In 2015, Dr. Casadevall was appointed a Commissioner to the National Commission on Forensic Science, the United States Department of Justice. He has been elected to AAAS Fellowship, the American Society for Clinical Investigation, the American Academy of Microbiology, the American Association of Physicians and the National Academy of Medicine and the American Academy of Arts and Sciences.

Howard Cash, Before moving into computational biology, Howard Cash studied music at the University of Pennsylvania and, after a period as Assistant Conductor with the Pennsylvania Opera Theater, Psychoacoustics at Stanford. At the forefront of commercial bioinformatics since 1984, he was Senior Engineer and head of Expert Systems at IntelliGenetics where seminal bioinformatics tools were developed. In 1988, he founded Gene Codes Corp, where he designed and developed the "Sequencher" program used in thousands of academic and commercial DNA sequencing labs in 90+ countries. Specialized versions of Sequencher have been developed for applications including human identification, mtDNA typing, therapy review based on HIV strain dominance in AIDS patients, and rapid characterization of H1N1 flu variants from the 2009 worldwide outbreak. He has a strong interest in bioethics and issues of genetic privacy and surveilance. He was appointed to the Michigan Commission on Genetics, Privacy and Progress to recommended legislation on issues related to genetic information. He chaired the committee on Property Rights, Ownership, Collection, Use and Storage. He was a member of the HUGO Council of the Human Genome Organization After 9/11 he designed analysis software to identify remains of victims of the World Trade Center attacks, with a database and analysis tools integrating primary sequence, SNP and STR data. More than 60 licenses for M-FISys (the Mass-Fatality Identification System, pronounced "emphasis") have been deployed to domestic and international forensic investigations including the sexual assault and murder of hundreds of women in

SPEAKER BIOS

Juarez, post-conflict identifications in Central America and Africa, international child trafficking, industrial accidents, and general criminalistics. With this background, he has lectured on Genetic Genealogy and searching unregulated, public databases for criminal investigations, most recently at the International Society for Computational Biology LA meeting in Chile.

Sam Caughron, MD, lives in Kansas City with his wife and children where he is President & CEO of MAWD Pathology Group and Director of the MAWD Molecular Lab. In his practice, Dr. Caughron uses his training and expertise in Molecular Genetic Pathology to deliver state of the art genomic care in a community setting. He is recognized nationally for his insight and expertise in translating advanced technologies into viable, real-world clinical solutions. He has served on numerous national professional committees, boards and advisory panels for the Association for Molecular Pathology (AMP) as well as the College of American Pathologists (CAP). He currently serves on the Board of the AMP, as well as Chair of AMP's Economic Affairs Committee. He is also currently Vice President for the Missouri Society of Pathologists and a board member for the American Pathology Foundation (APF). Dr. Caughron received his medical degree and AP/CP training from Creighton University in Omaha, Nebraska and completed a fellowship in Molecular Genetic Pathology at Vanderbilt University in Nashville, Tennessee.

Charles Chiu, MD, PhD, is Professor of Laboratory Medicine and Medicine, Division of Infectious Diseases at University of California, San Francisco, Director of the UCSF-Abbott Viral Diagnostics and Discovery Center (VDDC), and Associate Director of the UCSF Clinical Microbiology Laboratory. Chiu currently heads a translational research laboratory focused on next-generation sequencing assay development for infectious disease diagnostics, discovery and investigation of emerging pathogens, including Borrelia burgdorferi (Lyme disease), Ebola virus, enterovirus D68, and Zika virus, and clinical / public health applications of new diagnostic technologies such as nanopore sequencing. He is also actively developing RNA sequencing approaches to detect and identify diagnostic profiles of the body's response to infection. His work is supported by funding from the National Institutes of Health (NIH), Abbott Laboratories, Department of Defense, NASA/Translational Research Institute, philanthropic grants (Charles and Helen Schwab and Steven and Alexandra Cohen Foundations), and the California Initiative to Advance Precision Medicine. Dr. Chiu has authored more than 80 peer-reviewed publications, holds over 15 patents and patent applications, and serves on the scientific advisory boards for Mammoth Biosciences, Inc.

Wendy Chung, MD, PhD, is a clinical and molecular geneticist and the Kennedy Family Professor of Pediatrics and Medicine. She received her B.A. in biochemistry and economics from Cornell University, her M.D. from Cornell University Medical College, and her Ph.D. from The Rockefeller University in genetics. Dr. Chung directs NIH funded research programs in human genetics of obesity, breast cancer, pulmonary hypertension, autism, and birth defects including congenital diaphragmatic hernia, esophageal atresias, and congenital heart disease. She is a national leader in the ethical, legal, and social implications of genomics. She leads the Precision Medicine Resource in the Irving Institute At Columbia University. She has authored over 350 peer reviewed papers and 50 reviews and chapters in medical texts. She was the recipient of the Westinghouse Science

Talent Search, American Academy of Pediatrics Young Investigator Award, the Medical Achievement Award from Bonei Olam, a career development award from Doris Duke, the NY Academy of Medicine Medal for Distinguished Contributions in Biomedical Science and the Rare Impact Award from the National Organization of Rare Disorders. Dr. Chung is renowned for her teaching and mentoring and received Columbia University's highest teaching award, the Presidential Award for Outstanding Teaching. She was the original plaintiff in the Supreme Court case that overturned the ability to patent genes and served on the Institute of Medicine Committee on Genetic Testing. Dr. Chung enjoys the challenges of genetics as a rapidly changing field of medicine and strives to facilitate the integration of genetic medicine into all areas of health care in a medically, scientifically, and ethically sound, accessible, and cost effective manner.

Brad Cookson, MD, PhD, is board certified in Clinical Pathology and a Fellow of the American Academy of Microbiology. As a Professor in the Departments of Laboratory Medicine and Microbiology at the University of Washington in Seattle, he has the privilege of teaching enthusiastic undergraduate and graduate students, resident physicians as well as clinical and post-doctoral fellows. His research and development work focuses on improving our ability to diagnose infectious diseases, unraveling genomic contributions to phenotypes and virulence attributes of bacterial pathogens, and understanding the cellular basis of inflammation. As Head of the Clinical Microbiology Division and Director of the Molecular and Next Gen Microbiology Laboratory, he and his talented staff and faculty collaborators develop detection systems, including Clinical Next Generation Sequencing, for diagnosing bacterial, fungal and parasitic infections. The goal is to improve the diagnosis and medical management of patients suffering from infectious diseases.

Emily Crawford, PhD, leads a basic research lab in the Infectious Disease Initiative at the Chan Zuckerberg Biohub in San Francisco, California, and holds an adjunct faculty appointment in the Department of Microbiology and Immunology at the University of California San Francisco (UCSF). Her group focuses on developing novel technologies for pathogen detection and helping to deploy them in a variety of research, clinical and public health settings. Dr. Crawford began her career developing expression profiling methods at the Broad Institute, and then went on to receive her PhD in 2012 from UCSF, where she used mass spec proteomics to investigate the evolution of programmed cell death in Jim Wells' lab. She completed postdoctoral work in Joe DeRisi's lab at UCSF, where she developed a plasmid-free CRISPR genome engineering system in the malaria parasite Plasmodium falciparum. In 2017 Dr. Crawford was hired as a Team Leader at the CZ Biohub, where she has developed the CRISPR-aided metagenomic NGS methods DASH and FLASH and deployed them to study diseases including malaria and tuberculosis. The primary goal of her work is to make these and other NGS-based infectious disease diagnostic methods more accessible to labs throughout the world doing surveillance, diagnostics, and outbreak response.

Kristy Crooks, PhD, is an Assistant Professor in the Department of Pathology, Director of the Colorado Center for Personalized Medicine Biobank Laboratory, and Director of the Heritable Disease section of the Colorado Molecular Correlates Laboratory at the University of Colorado. After earning her PhD at Duke University, she completed

SPEAKER BIOS

clinical laboratory fellowships at the University of North Carolina at Chapel Hill. She is board certified in Clinical Molecular Genetics and Clinical Cytogenetics by the American Board of Genetics and Genomics. Dr. Crooks' research interests focus primarily on the application of emerging technologies for genetic diagnosis and on leveraging population screening to improve health outcomes.

Karissa Culbreath, PhD, received her PhD from Vanderbilt University and completed a medical and public health microbiology fellowship at the University of North Carolina, Chapel Hill. She is a diplomate of the American Board of Medical Microbiology. Dr. Culbreath is Director of Infectious Disease Diagnostics at TriCore Reference Laboratories and Associate Professor in the Department of Pathology at the University of New Mexico. Her research focus in test utilization and emerging methods in clinical microbiology. She is a tireless advocate for women and underrepresented minorities in science and medicine supports these efforts as an Associate Vice Chancelor for Diversity, Equity and Inclusion at University of New Mexico Health Sciences Center.

Kristina Cusmano-Ozog, MD, is the Director of the Molecular Diagnostics and Biochemical Genetics Laboratories at Children's National Health Systems, where she also practices as a Medical Geneticist. She is an Assistant Professor of Pathology and Pediatrics at George Washington University. Her research and clinical work focus on diagnosing and treating individuals with inherited metabolic disorders. She holds a BS in Biochemistry from the University of Miami (Florida) and earned her MD at the University of South Florida, where she also completed training in pediatrics. She trained in Medical Genetics and Clinical Biochemical Genetics at Stanford University and obtained additional training in Clinical Molecular Genetics through the National Institutes of Health.

D

Fei Dong, MD, is a surgical pathologist and molecular pathologist at Brigham and Women's Hospital. He received his medical degree at Case Western Reserve University and completed anatomic pathology and molecular pathology training at Massachusetts General Hospital and Harvard Medical School. His clinical responsibilities include surgical pathology and molecular diagnostics with specialization in the interpretation of next generation sequencing results in solid tumors. Research interests include developing new methods to understand molecular data, including tools to infer microsatellite instability and allogeneic contamination from NGS data, and the clinical application of molecular technology in patient care. Dr. Dong serves as associate director for the pathology residency program at Brigham and Women's Hospital.

Eric Duncavage, MD, is the director of hematopathology at Washington University in St. Louis. He is board-certified in anatomic pathology, clinical pathology, molecular pathology, hematopathology, and clinical informatics and is active in both clinical care and translational research. Dr. Duncavage along with others in the department of Pathology and Immunology was instrumental in establishing the first next generation sequencing-based oncology diagnostics laboratory at an academic medical center in 2011. He has authored numerous manuscripts detailing clinical sequencing methods and is a world-recognized leader in field of sequencing-based diagnostics. Dr. Duncavage's grant-funded research is focused on understanding the clonal evolution and progression of myelodysplastic syndromes and

acute myeloid leukemia including the application of molecular-based measurable residual disease (MRD) monitoring to determine treatment response and whole genome sequencing as a replacement for conventional cytogenetic evaluation.

E

Lisa Edelmann, PhD, is the Chief Diagnostics Officer at Sema4 and holds the academic title of Associate Professor in the Department of Genetics and Genomic Sciences at the Icahn School of Medicine at Mount Sinai. Dr. Edelmann received her Ph.D. in Molecular Genetics from The Albert Einstein College of Medicine, and is certified in Clinical Molecular Genetics and Clinical Cytogenetics by the American Board of Medical Genetics and Genomics. Her scientific accomplishments include, elucidating the mechanism of chromosome 22q11 rearrangements and involvement in the first molecular sequencing of an entire human chromosome. She has also published extensively on Ashkenazi Jewish genetic disorders and has developed several novel tests, including a test for detection of silent carriers for spinal muscular atrophy, which is being licensed nationwide and abroad. Dr. Edelmann is a nationally recognized expert in population-based carrier screening, high-throughput clinical diagnostic sequencing as well as genomic disorders and clinical interpretation of copy number variation. She is well versed with the regulatory guidelines that govern clinical laboratories and has extensive experience with the process of validating LDTs and bringing them to market.

Philip Empey, PharmD, PhD, is the Associate Director of the Institute of Precision Medicine at the University of Pittsburgh and UPMC. He directs the Pharmacogenomics Center of Excellence and leads the PreCISE-Rx and Test2Learn teams to implement pharmacogenomics clinical, research, and educational initiatives. As a clinician-scientist in the Department of Pharmacy and Therapeutics of the School of Pharmacy, Dr. Empey conducts NIH-funded clinical and translational research aimed at understanding the mechanisms of the variability in drug response to improve medication-related outcomes in critically-ill patients. His research interests include large scale population preemptive testing, pharmacogenomics clinical implementation, collection of medication-related phenotype information, genotype-phenotype discovery, and understanding the role/impact of xenobiotic transporters following neurological injury.

Mark Evans, MD, is President of the Fetal Medicine Foundation of America, Professor of Obstetrics & Gynecology at Mt. Sinai School of Medicine, President of the International Fetal Medicine and Surgery Society Foundation, and President of Comprehensive Genetics, PLLC. He has helped developed multiple procedures for prenatal diagnosis, screening and fetal therapy including CVS, fetal muscle biopsy, fetal reduction, percutaneous and open fetal surgery, pharmacologic and stem cell fetal therapies. He is considered one of the major key opinion leaders in the fields of prenatal diagnosis, screening, and fetal therapy world-wide. He routinely lectures every year all over the world and is regularly invited as visiting professor to national and international obstetrics and genetics meetings. Dr. Evans has over 1200 scientific publications including 30 text books. He has had multiple NIH grants including being a principal investigator for the search for fetal cells in maternal blood. He has received numerous national and international honors including receiving the President's Award for Achievement from the Society for Gynecologic Investigation and was elected President of the International Fetal Medicine and Surgery Society twice.

SPEAKER BIOS

F

Helen Fernandes, PhD, is an Associate Professor of Pathology in the Department of Pathology and Cell Biology and the Co-director of Genomic Oncology in the Personalized Genomic Medicine Laboratory, at Columbia University Medical Center. Prior to her current position, Helen was at Weill Cornell Medicine in New York and Rutgers University in New Jersey. She has over 20 years of experience in molecular pathology that ranges from infectious diseases, to oncology and genomics. Much of her focus is on validation and implementation of diagnostic assays along with training and education of molecular diagnosticians. Dr. Fernandes is passionate about Quality Control in molecular diagnostics and has been invited to present at meetings and webinars globally. She has inspected clinical laboratories nationally and internationally and is an active member of several organizations including, Association for Molecular Pathology (AMP) and the American Association for Clinical Chemistry (AACC).

Birgit Funke, PhD, FACMG, received her Ph.D. in molecular genetics from the University of Würzburg, Germany and trained as a postdoctoral fellow at the Albert Einstein College of Medicine in New York where she identified the gene for 22q11 deletion syndrome. She subsequently completed a fellowship in Clinical Molecular Genetics at Harvard Medical School and has dedicated her career to personalized genetic medicine since then. She served as the director of Clinical Research and Development at the Laboratory for Molecular Medicine (LMM) and was among the first worldwide to implement clinical next generation sequencing (NGS). She also has a extensive experience in clinical diagnostic testing for inherited cardiovascular disorders and is co-chairing the cardiovascular domain working group of the Clinical Genome Resource (ClinGen) whose mission is to harmonize and centralize knowledge resources for genomic medicine. Today, Dr. Funke is Vice President of Clinical Affairs at Veritas Genetics and part time Associate Professor of Pathology at Harvard Medical School. Her long term goal is to use genomic testing for disease prevention.

G

Mahmoud Ghannoum, PhD, EMBA, FIDSA, FAAM, is the Director of the Medical Mycology Center of Excellence at Case, past President of the Medical Mycological Society of the Americas. Dr Ghannoum received the Rohda Benham Award for his meritorious contributions to medical mycology from the MMSA. He is an entrepreneur-scientist who launched a number of companies focusing on the treatment of biofilm infections and microbial dysbiosis as it relates to gut health. He coined the term 'Mycobiome". Author of Total Gut Health, Countryman Press, December 2019.

Richard Goering, PhD, is Professor and Chair of the Department of Medical Microbiology and Immunology at Creighton University School of Medicine in Omaha, Nebraska. With over 150 abstract presentations, a similar number of publications, and a Scopus h-index of 43 (Google Scholar h-index 54), he is internationally recognized for his research on mechanisms of antibiotic resistance and the epidemiology of problem pathogens, especially including the staphylococci. He was first in the United States to champion the use of pulsed field gel electrophoresis (PFGE) for microbial epidemiological surveillance and he is a co-author of the internationally recognized

guidelines for the interpretation of PFGE data. His current research centers on the use of DNA sequence-based approaches (especially including whole genome sequencing) for the identification and tracking of problem pathogens. With colleagues in the UK, he is senior author of the "Mims Medical Microbiology and Immunology" textbook (6th edition just released) which has been translated into multiple languages and used in the education of students in the health professions throughout the world.

Erin Graf, PhD, is a Senior Associate Consultant at the Mayo Clinic Hospital, Arizona. She was formerly the Director of the Infectious Disease Diagnostics Laboratory at the Children's Hospital of Philadelphia. Dr. Graf completed her Ph.D. in Cell and Molecular Biology in the Perelman School of Medicine at The University of Pennsylvania studying HIV latency. She then went on to complete an ASM accredited postdoctoral training program in medical and public health microbiology at ARUP Laboratories and the University of Utah. Dr. Graf is board certified in medical microbiology. Her research interests include sequence-based diagnostics in clinical microbiology, including the applications of next generation sequencing and metagenomics, as well as emerging technologies for rapid diagnostics.

Alex Greninger, MD, PhD, MPhil, MS, is an Assistant Professor in the Department of Laboratory Medicine at the University of Washington and Associate Director of the clinical virology laboratories. He did his dual medical and graduate training at the University of California-San Francisco and has master's degrees in epidemiology from Cambridge University and immunology/biological sciences from Stanford University. He has a 13 year history in metagenomics, starting out in the discovery of new human viruses and transitioning to the broad detection of infectious organisms in clinical material.

Malachi Griffith, PhD, completed a Bachelor of Science with Honors in Biochemistry and Biology in 2002 at the University of Winnipeg, followed by additional formal training in computer science. He worked as a molecular biologist and then as a computational biologist during 2003-2004 before beginning a PhD in Medical Genetics and Bioinformatics at the University of British Columbia under the mentorship of Dr. Marco Marra. He defended his PhD thesis in December, 2009, and joined Washington University School of Medicine in 2011. Dr. Griffith now has more than 14 years of experience in the fields of genomics, bioinformatics, data mining, and cancer research. He has published over 80 studies, received numerous research awards and honors and held several large grants including an NIH K99/R00 Career Development Award and V Scholar Award. He has mentored more than 30 bioinformatics trainees and taught more than 500 as an instructor for Cold Spring Harbor Laboratories and the Canadian Bioinformatics Workshops. Dr. Griffith's research is focused on improving our understanding of cancer biology and the development of personalized medicine strategies for cancer using genomics and informatics technologies. Dr. Griffith's lab has made substantial contributions to open source and open access resources for cancer research. Recently, the development of bioinformatics for immunogenomics has become a major focus of his lab.

SPEAKER BIOS

H

Kevin Halling, MD, PhD, is a molecular pathologist and a Professor in the Division of Laboratory Genetics at the Mayo Clinic in Rochester, Minnesota. He is a co-director of the Genomics Laboratory which performs molecular oncology and hereditary disorder testing. He received his M.D. and Ph.D. from the University of Kansas and completed an Anatomic and Clinical pathology residency and Clinical Molecular Genetics fellowship at the Mayo Clinic. His primary area of interest is in the development of genetic tests that can be used for the diagnosis and treatment of sporadic and hereditary cancer. He and his team have developed a clinical RNA Seq assay that can be used to detect gene fusions in patients with various types of malignancies and are also working on other clinical applications of RNA-seq and other RNA testing methodologies such as Nanostring. Dr. Halling has published over 100 papers that mostly relate to genetic testing of cancer.

Susan Hancock, MS, is a licensed, board-certified genetic counselor with nearly two decades of experience in clinical and industry settings. She has a wealth of experience providing direct patient care as a prenatal genetic counselor in a large prenatal diagnosis center, where she established a deep respect for the needs of proper education for patients and providers related to available genetic testing technology. In her current role as Clinical Product Specialst for Noninvasive Prenatal Screen at Myriad Women's Health, she utilizes her clnical knowledge to further research, education, and product development related to cell-free DNA technology.

Daniel Higginson, MD, is a physician scientist in the Department of Radiation Oncology at Memorial Sloan Kettering Cancer Center. His clinical interests include radiosurgery and stereotactic body radiotherapy for the treatment of diverse solid tumor malignancies. In his laboratory, he studies novel biomarkers of response to radiation therapy, including cell free DNA approaches, as well as basic mechanisms of DNA double strand break repair in response to therapeutic radiation.

Russell Higuchi, PhD, is a molecular biologist with > 30 years' experience in the molecular diagnostics industry, going back to its beginnings in PCR. He is currently a Distinguished Fellow in Cepheid's Innovation group. Prior to working in industry, he obtained his Ph.D. in molecular biology from UCLA. His thesis work was in the then nascent field of recombinant DNA technology. During his postdoctoral training with Allan Wilson at UC Berkeley, he published the first paper in the field of Ancient DNA. This paper applied recombinant DNA technology to the recovery of DNA sequences of an extinct zebra known as the quagga. The DNA sequences allowed the correct placement of this species in the family tree of zebras and horses. He then went on to work at Cetus Corp. with Henry Erlich, winner of the 2000 AMP award for Excellence in Molecular Diagnostics, and with Kary Mullis, co-winner of the 1993 Nobel Prize in Chemistry for his invention of PCR. While at Cetus, he worked on diverse applications of PCR including to forensic identification, DNA sequencing and genetic engineering. His most significant work was the invention of real-time PCR, which made the PCR process completely self-contained and quantitative. After Cetus he worked for Roche where he continued to help establish real-time PCR as the standard molecular diagnostics technology as well as working in disease-associated gene discovery. He began working at Cepheid ten

years ago, where he has been helping apply and improve Cepheid's fully automated, near-patient molecular diagnostic technology. Cepheid technology has allowed the widespread distribution of molecular diagnostics including into the developing world.

Sarah Hill, MD, PhD, is an Instructor at Dana-Farber Cancer Institute and Associate Pathologist at Brigham and Women's Hospital specializing in gynecologic pathology. Her independent research program at Dana-Farber focuses on using patient-derived epithelial ovarian cancer organoid models to understand the role of the DNA damage response in ovarian carcinogenesis and therapeutic sensitivity. She has developed media and growth conditions for patient-derived organoid models along with functional assays to profile the DNA damage repair capacity of these tumors and understand how specific repair defects lead to specific types of therapeutic sensitivity.

I

John Iafrate, MD, PhD, is a Professor of Pathology at Harvard Medical School and is the Vice Chair of Academic Affairs at the Massachusetts General Hospital (MGH) Pathology Department. Dr. Iafrate received his MD/PhD dual degree from the State University of New York at Stony Brook in 2000 and was trained in anatomic and molecular genetic pathology at Brigham and Women's Hospital. Dr. Iafrate is a board-certified Pathologist, and has been on staff at MGH since 2005. His research is focused on lung and brain tumors, where he has been closely involved in the clinical development of crizotinib and companion diagnostics in ALK- and ROS1 positive lung cancers. His lab has developed several technologies for sequencing tumors, including SNaPshot and the next-generation sequencing-based Anchored Multiplex PCR, both techniques have been widely used in the molecular diagnostics community. His lab has focused recently on the development of sequencing assays to detect circulating tumor DNA.

Marcin Imielinski, MD, PhD, is an Assistant Professor of Computational Genomics at Weill Cornell Medicine, Assistant Attending Pathologist at New York Presbyterian, and Core Member at NYGC. He is a board-certified certified Clinical and Molecular Genetic Pathologist. His laboratory studies the causes and consequences of complex structural variation in cancer using whole genome sequencing and chromatin profiling. Prior to starting his lab in 2015, he completed his residency and fellowship in Pathology and postdoctoral training in cancer genomics at Massachusetts General Hospital, Harvard Medical School, and the Broad Institute. He received his PhD in Genomics and Computational Biology and MD from University of Pennsylvania and a BS in Computer Science from Rutgers College.

J

Miten Jain, PhD, is an Assistant Research Scientist at University of California Santa Cruz, and works with the UCSC Nanopore Group. His research interests include optimizing nanopore technology and sequencing devices; analyzing bacterial and human epigenomes; and developing novel methods to detect regions of interest and base modifications in genomic DNA and native RNA. The overarching goals of this research are to contribute towards better clinical methods for diagnoses and treatment.

SPEAKER BIOS

K

Karen Kaul MD, PhD, is Chair of the Department of Pathology and Laboratory Medicine at NorthShore and is a Clinical Professor of Pathology at the University of Chicago's Pritzker School of Medicine. Dr. Kaul is board-certified in Anatomic Pathology, and Molecular Genetic Pathology. Following a postdoctoral fellowship at the NCI and pathology residency training at Northwestern, Dr. Kaul established one of the earliest Molecular Diagnostics laboratories in the US; she and her lab have been deeply involved in the development of laboratory tests for cancer, heritable conditions, microbial diseases, and antimicrobial susceptibility. She has been significantly involved in education, regulation, and standardization of the practice of molecular pathology, and has served on FDA, CLIAC, MEDCAC, and other panels, and testified before the Senate HELP committee on LDPs in 2016. She is a past president of the Association for Molecular Pathology, and served as Editor in Chief of the Journal of Molecular Diagnostics until 2010. She is the recipient of the 2008 Association for Molecular Pathology Leadership Award. She was an ELAM (Executive Leadership in Academic Medicine) fellow in 2011-2012. In 2011, she was appointed a Trustee of the American Board of Pathology where she is involved in professional examination and certification efforts, and is the past President of the ABP. She also served on the ACGME Residency Review Committee for Pathology, and Milestones committees, and currently leads the Association for Pathology Chairs GME committee. Dr. Kaul served as residency program director for 18 years, and served on PRODS council before becoming departmental chair in 2012. As Chair, she has led departmental efforts to improve laboratory efficiency and utilization, and maximize the impact of the laboratory on clinical care. She continues to practice and advocate for Molecular Pathology.

Michael Kluk, MD, PhD, is a Co-Director of Molecular Pathology at Weill-Cornell Medicine/New York Presbyterian Hospital. His also the Program Director of the Molecular Genetic Pathology Fellowship. He has ABP certifications in Molecular Genetic Pathology, Hematopathology, Anatomic Pathology and Clinical Pathology. The Molecular Pathology Laboratories at Weill-Cornell Medicine/New York Presbyterian Hospital provide a wide variety of traditional molecular assays and also provide several next generation sequencing panels.

Peter Kraft, PhD, is Professor of Epidemiology and Biostatistics and Director of the Program in Genetic Epidemiology and Statistical Genetics at the Harvard T.H. Chan School of Public Health. His research concentrates on the design and analysis of genetic association studies, with particular emphasis on the genetic epidemiology of cancer. He has participated in many international consortia studying genetics and environmental exposures in relation to cancer risk over the last fifteen years, including the *NCI's* PanScan and Cancer Genetic Markers of Susceptibility (CGEMS) projects; the Breast Cancer Association Consortium (BCAC); and the Cancer Risk Estimates Related to Susceptibility Genes (CARRIERS) consortium, which is sequencing cancer predisposition genes in a large population-based breast cancer case-control sample. His methodological work has focused on efficient and interpretable x environment *interaction analyses*; building and evaluating risk prediction models incorporating high dimensional genetic data; and integrative analyses combining genetic and environmental risk factors with

intermediate biomarkers (gene expression, metabolomics). He has taught courses in genetic epidemiology and statistical learning at the Harvard Chan School since 2004 and co-chaired the American Association for Cancer *Research's* Integrative Molecular Epidemiology workshop since it started in 2013. Dr. Kraft is currently President-Elect of the International Genetic Epidemiology Society.

Deborah Krakow, MD, FACMG, is a Professor and Chair of the Department of Obstetrics and Gynecology at UCLA. Dr. Krakow is also Professor of Orthopaedic Surgery and Professor of Human Genetics at UCLA. Dr. Krakow received her bachelor's degree from Arizona State University in Tempe and her medical degree from Chicago Medical School. After an internship and residency in obstetrics and gynecology at Cedars-Sinai Medical Center, she completed fellowships in maternal-fetal medicine at Harbor-UCLA Medical Center and in research and clinical genetics at the UCLA Intercampus Medical Genetics Training Program and is certified by the American Board of Medical Genetics and Genomics in Clinical Genetics and Genomics.

Shashikant Kulkarni, PhD, FACMG, is a tenured Professor and Vice Chairman for Research in the department of Molecular and Human Genetics at Baylor College of Medicine, Houston, Texas. He also serves as the Chief Scientific Officer (CSO) and Senior Vice President in Baylor Genetics. Dr Kulkarni brings in unique mix of research expertise, clinical genomics experience, and practical business acumen – including a focus on democratizing access of Precision Medicine at a National (working in partnership with the largest non-profit healthcare system in US) and International (Japan, other countries) scale. He trained at Harvard Medical School, Imperial College at London, UK and at AIIMS, India. He is an ABMGG Board-certified medical geneticist.

L

Bill Lane, MD, PhD, is an Assistant Professor of Pathology at Harvard Medical School and Director of Clinical Laboratory Informatics and Assistant Director of the Tissue Typing Laboratory at the Brigham and Women's Hospital (BWH), Boston, MA. He is board certified in Clinical Pathology, Blood Banking/Transfusion Medicine, and Clinical Informatics. He is co-founder and co-editor of Transfusion Medicine Question of the Day. His research interests include red blood cell and platelet antigen typing using next generation sequencing.

Sarah Leary, MD, MS, is the Medical Director of the Pediatric Brain Tumor Program at Seattle Children's Hospital, Associate Professor of Pediatrics at the University of Washington School of Medicine, and affiliate of the Fred Hutchinson Cancer Research Center. Her professional goal is to improve the outcome for children with brain tumors by developing novel diagnostics, therapeutics and clinical trials. She is the principal investigator of the Seattle Children's Tumor Bank, and founding member of the Children's Brain Tumor Tissue Consortium (CBTTC), Pacific Pediatric Neuro-Oncology Consortium (PNOC), and Collaborative Network for Neuro-Oncology Clinical Trials Consortium (CONNECT). She is the clinical vice chair of the Central Nervous System Committee of the Children's Oncology Group (COG) and serves on the Brain Malignancies Steering Committee of the National Cancer Institute (NCI).

SPEAKER BIOS

Amy Leber, PhD, received her PhD from the Ohio State University and did a post-doctoral Fellowship in Clinical and Public Health Microbiology at UCLA Medical Center. She is a diplomate of the American Board of Microbiology and active in the American Society for Microbiology, ASCP, and AMP. She is currently the Senior Director of Clinical Laboratories and Director of Microbiology at Nationwide Children's Hospital in Columbus Ohio and an Associate Professor of Pathology and Pediatrics at The Ohio State University. She is the editor-in-Chief of the Clinical Microbiology Procedures Handbook. Her research interests include new molecular diagnostics and diagnosis of infectious diseases in pediatric populations.

Nathan Ledeboer, PhD, received his Ph.D. Degree in Microbiology from the University of Iowa in 2005. Following two years of fellowship training in clinical and public health microbiology at Washington University School of Medicine in Saint Louis, MO, he joined the faculty of the Department of Pathology at the Medical College of Wisconsin in Milwaukee, WI. He is currently a Professor and Vice Chair of Pathology and Medical Director of Microbiology, Molecular Diagnostics, reference services, and laboratory client services at Froedtert Hospital and Wisconsin Diagnostic Laboratories in Milwaukee, WI.

Long Le, MD, PhD, is a practicing molecular pathologist who is currently the Director of Computational Pathology at Massachusetts General Hospital and Director of Technology Development at the MGH Center for Integrated Diagnostics. His clinical and research interests include development of novel target enrichment, bioinformatics analysis, and medical informatics solutions for next-generation sequencing and their application for clinical molecular diagnostics. He has a strong interest in applying big data descriptive and predictive analytics in healthcare with the goal of efficiently delivering laboratory results and clinical decision support.

Anthony Letai, MD, PhD, received his MD and PhD at the University of Chicago. His PhD on point mutations in blistering diseases was done under the supervision of Elaine Fuchs. Dr. Letai then completed clinical training in Internal Medicine at Brigham and Women's Hospital, Boston, followed by a fellowship in Hematology and Oncology at Dana-Farber Cancer Institute. He was introduced to apoptosis and BCL-2 family proteins as a post-doctoral researcher in the laboratory of the late Stanley Korsmeyer. In 2004, Dr. Letai became independent investigator at Harvard Medical School and Dana-Farber Cancer Institute where he is now a Professor of Medicine. Since that time, his laboratory has studied how apoptosis can be evaded, particularly in cancer cells, and how this evasion may be detected and targeted. Key to these studies is a novel assay - BH3 profiling. He has led efforts to translate BCL-2, BCL-XL, and MCL-1 inhibitors into the clinic. These include venetoclax, a BCL-2 inhibitor made by AbbVie approved by the FDA for CLL and AML and now being tested across nearly all blood cancers. The laboratory is testing whether BH3 profiling can be used as a broad predictive biomarker to assign clinical cancer therapy.

Michael Lewinski, PhD, is currently the Sr. Director of Medical Affairs, Microbiology and Smarticles technology at Roche Molecular Systems, Inc. in Pleasanton, California. He completed his Doctor of Philosophy degree in Microbiology and Immunology and a clinical postdoctoral Fellowship in Medical and Public Health Laboratory Microbiology

at UCLA. He is a Diplomate of the American Board of Medical Microbiology, a licensed Laboratory Director and a certified Molecular Biologist. Prior to joining Roche, he was the Chief of Microbiology and Associate Clinical Professor of Pathology and Laboratory Medicine, David Geffen School of Medicine at UCLA. Prior to UCLA he was the Senior Scientific Director of Infectious Diseases at Quest Diagnostics Nichols Institute and Focus Diagnostics, Inc. He is a past President of the Southern California Branch of the American Society for Microbiology, has served on the Council of the Pan American Society of Clinical Virology and as Chair of the Infectious Disease Subdivision of the Association for Molecular Pathology. He currently serves on the Membership/Nominations Committee of the Pan American Society for Clinical Virology, the Editorial Board of the Journal of Clinical Virology and is the Chair of an Association of Molecular Pathology Clinical Practice Committee on Infectious Disease Multiplex Testing. His research interests have focused on the development and the automation of molecular tests for the detection, quantification, and characterization of microorganisms for the diagnosis of disease and for monitoring disease progression and response to therapy. He holds several patents and has published in various disciplines within infectious diseases and laboratory medicine.

Coleman Lindsley, MD, PhD, is an Assistant Professor of Medicine at Harvard Medical School and Dana-Farber Cancer Institute, where he is Director of Molecular Diagnostics in Hematologic Malignancies. He received his M.D. and Ph.D. in Immunology from Washington University School of Medicine, then completed a residency in internal medicine at Brigham and Women's Hospital and a fellowship in oncology at the Dana-Farber Cancer Institute. He is a member of the MDS Genetics Subcommittee for the NIH National MDS Study, the International Working Group for Prognosis in MDS (IWG-PM) molecular committee, and the Laboratory Assays Working Group for the Myeloid Malignancies Precision Medicine Initiative at National Cancer Institute. The primary focus of his laboratory is the biology and treatment of myeloid malignancies. His genetic studies have led to new genomic models of leukemia classification and MDS outcome after stem cell transplantation. His laboratory uses mouse and cell line models to dissect the mechanistic basis of genetic cooperation during myeloid disease progression, with a specific focus on mechanisms of leukemia initiation in patients with predisposition syndromes.

Wei Li, PhD, is a Duncan Endowed Professor of Bioinformatics in the Dan L. Duncan Cancer Center at Baylor College of Medicine. He received his PhD in Bioinformatics from the Chinese Academy of Sciences (2003) and was an Associate Director of Bioinformatics at Beijing Genomics Institute (BGI; 2002-2004). After his postdoctoral training in the Department of Biostatistics and Computational Biology at Harvard (2004-2007), he was recruited to Baylor as an Assistant Professor in 2007. After less than 9 years, Dr. Li was promoted to tenured Full Professor in 2016 (Duncan Endowed Chair in 2018). His research is focused on the design and application of bioinformatics algorithms to elucidate global epigenetic mechanisms in normal development and diseases, such as cancer. He has a solid track record in developing widely used open-source bioinformatics software, such as MACS (~6,000 citations) for ChIP-seq. Since establishing his own bioinformatics lab, he has (as of August 2019) (1) Published ~160 peer-reviewed papers through solid methodology development and extensive collaborative research, including 20 senior-author papers in Nature and Cell series. (2) Been well-funded with total active external funding >$1.0 million per year, including 4 PI grants from NIH. (3) Mentored the first 7 postdoc trainees

SPEAKER BIOS

to start their tenure-track faculty positions in the US. Dr. Li received many prestigious awards, including the New Investigator Award from Department of Defense (2010), and the Michael E. DeBakey Excellence in Research Award (2016).

John Longshore, PhD, is the Director of Molecular Pathology for Carolinas Pathology Group. His primary professional responsibility is leading the Molecular Pathology Laboratory for Atrium Health, which is a full-service laboratory providing testing services in genetics, microbiology, virology, hematologic/solid tumor oncology, molecular cytogenetics, and clinical trial operations for a 48 hospital integrated health network. Dr. Longshore completed his undergraduate work at Georgia Tech, doctoral research at the University of Alabama at Birmingham, and a fellowship in Clinical Molecular Genetics at the Greenwood Genetic Center. John is a diplomate of the American Board of Medical Genetics and is an active member of the ACMG, ASHG, ESHG, AMP, IASLC, and ASCO. Over the past decade, Dr. *Longshore's laboratory* has served as central pathology for multiple pivotal clinical trials that led to the FDA approval of oncology companion diagnostic assays. His focal area of research interest is companion diagnostics and the use of molecular markers in personalized medicine.

M

Ryan Mills, PhD, is an Associate Professor of Computational Medicine and Bioinformatics at the University of Michigan Medical School. He is also an Associate Professor of Human Genetics. Dr. Mills obtained an A.B. in Biology from Wabash College and then continued his studies at Georgia Tech where he received his doctorate. His postdoctoral work at Emory University produced the first published genome-wide map of insertion/deletion (INDEL) variation in human populations. He then continued his focus on genomic variation as a research associate at Brigham and Women's Hospital where he participated in both independent and collaborative research projects to analyze and discover structural variation from microarray and whole genome sequence data and helped in the development and implementation of array-CGH for clinical application through the Center for Advanced Molecular Diagnostics. His current research is focused on developing methods to identify previously overlooked variation including complex genomic rearrangements consisting of multiple breakpoints as well as occult mobile element insertions. He is also studying the impact of somatic structural genomic variation in neuropsychiatric diseases as part of the Brain Somatic Mosaicism Network where he is currently investigating low frequency mosaic variation in human brain tissue with state-of-the-art technologies.

Federico Monzon, MD, is a molecular pathologist with extensive experience translating novel genomic technologies into clinical molecular tests, including leading studies on prostate and renal cancer genomics and the validation of one of the first FDA cleared gene expression clinical assays for the diagnosis of tumors of unknown origin while at the University of Pittsburgh and Houston Methodist Hospital. Currently, he is Chief Medical Officer at Castle Biosciences, a laboratory focused on providing genomic prognostic tools to patients with melanoma and other cancers. Prior to joining Castle, he served as Medical Director of Oncology and Medical Director for Latin America at Invitae Corporation, a provider of genetic diagnostics for hereditary disorders. Previously, Dr.

SPEAKER BIOS

Monzon served as Director of Pathology at the Cancer Genetics Laboratory from Baylor College of Medicine, where he maintains an academic affiliation as Clinical Associate Professor. He earned his M.D. from the Universidad Nacional Autónoma de México, and is board-certified by the American Board of Pathology in anatomic, clinical and molecular genetic pathology. Dr. Monzon was the 2017 President of the Association for Molecular Pathology (AMP) and continues to be engaged in AMP and other professional societies to shape the future of clinical genomic medicine.

Sejal Morjaria, MD, received her MD from the University of Miami, Miller School of Medicine and completed a residency in Internal Medicine at the Virginia Commonwealth University in Richmond, Virginia. She also completed an Infectious Disease fellowship at Memorial Sloan Kettering Cancer Center (MSKCC) where she currently is an Assistant Attending. There she specializes in Infectious Diseases, both clinically and through her research in Dr. Eric Pamer's laboratory. She was involved in high-resolution daily stool sampling from hematopoietic stem cell transplantation patients, investigating the antibiotic-induced rapid shifts in fecal microbial density and composition. Dr. Morjaria is also involved in Quality Improvement projects such as improving length of stay for patients, a mobility initiative aimed at maintaining walking independence for older patients, etc. She is also spear heading the Penicillin Skin Testing initiative, aimed to test patients with a history of a Penicillin Allergy in order to confirm their allergy. She also started the Pulmonary-ID Case Conference as a forum for multidisciplinary discussions regarding diagnostic and treatment aspects of patient care

Nikhil Munshi, MD, is Professor of Medicine at the Harvard Medical School and the Director of Basic and Correlative Science, and Associate Director of the Jerome Lipper Multiple Myeloma Center at the Dana Farber Cancer Institute. Dr. Munshi's research focus spans both basic sciences to understand oncogenomic changes driving myeloma to translational approaches directed at improving prognosis as well as developing novel targeted therapeutics including novel antigen-directed immunotherapy and targeted small molecules for myeloma. He has served as a co-chair of the National Steering Committee on Myeloma (National Cancer Institute, NCI) and is the president-elect of the International Myeloma Society. He was awarded the prestigious award "Waldenstrom's Award" for Distinguished Lifetime Achievement in Myeloma Research in 2013, the Dr. B.C. Roy National Award by the president of India in 2016 and the COMy "Multiple Myeloma Excellence Award for Translational Research" in 2019.

Dale Muzzey, PhD, received both his bachelor of arts and Ph.D. from Harvard University in biochemistry and biophysics, respectively. As a Damon Runyon Cancer Research Foundation postdoctoral fellow at UCSF, he performed NGS research involving genome assembly, haplotype phasing, and gene-expression analysis. He was a Senior Director of Scientific Affairs and Staff Scientist in Computational Biology at Counsyl prior to its acquisition by Myriad Genetics, where he served as Senior Director of Clinical Development and is now Vice President of Bioinformatics. In addition to leading assay development for Counsyl's expanded carrier screen and noninvasive prenatal screen, in the last two years Dr. Muzzey has authored more than a dozen peer-reviewed publications about these genetic tests.

SPEAKER BIOS

N

Samia Naccache, PhD, is the Technical Microbiology Director of LabCorp's Seattle, serving the clinical microbiology needs of the Swedish Medical Center system as well as *LabCorp's Microbiology* reference lab activities. Her areas of expertise are in Microbiology, Molecular Microbiology and Virology. As a postdoc in the UCSF Clinical Microbiology, she spearheaded the development of the first diagnostic metagenomic NGS assay for meningitis/encephalitis. She has technical and clinical expertise in adult and pediatric microbiology and public health microbiology, with an extensive publication record on assay and bioinformatics pipeline development, syndromic and pan-pathogen assay utilization, and viral outbreak characterization.

Sunitha Nagrath, PhD, is an Associate Professor of Chemical Engineering at University of Michigan. Dr. Nagrath did her Bachelor's degree in Chemical Engineering from Sri Venkateswara University College of Engineering, Tirupathi, India. She received her Ph.D. in 2004 from Rensselaer Polytechnic Institute, Troy, NY in Mechanical Engineering. She did her postdoctoral work (2004-2008) at Harvard Medical/Massachusetts General Hospital, Boston, MA. She later worked as an instructor/junior faculty at Harvard Medical School. Dr. Nagrath is the leading scientist who designed the MEMS based technology, "CTC-Chip" for the sensitive isolation of circulating tumor cells (CTCs) from the blood of cancer patients. She joined University of Michigan in 2010, where she established her laboratory focused on engineering innovative microfluidic devices and nanomaterials for implementing personalized precision medicine via liquid biopsy. Dr. Nagrath's major focus of research is on understanding cell trafficking in cancer through isolation, characterization and study of circulating cells and exosomes in peripheral blood of cancer patients.

Frederick Nolte, PhD, is currently Professor and Vice Chair for Laboratory Medicine in the Department of Pathology and Laboratory Medicine, and Medical Director of Clinical Laboratories and Molecular Pathology at the Medical University of South Carolina. He is a Diplomate of the American Board of Medical Microbiology and a Fellow of the American Academy of Microbiology. Dr. Nolte completed his B.S. degree in biology at the University of Cincinnati and his Ph.D. in medical microbiology at the Ohio State University. Dr. Nolte completed a postdoctoral fellowship in public health and medical laboratory microbiology at the University of Rochester. is active in and held positions of responsibility in the American Society for Microbiology, Association for Molecular Pathology, Clinical and Laboratory Standards Institute, Infectious Diseases Society of America, American Society for Clinical Pathology, American Association for Clinical Chemistry, and College of American Pathologists. He has authored numerous book chapters, practice guidelines, and more than 100 peer-reviewed publications in the areas of clinical microbiology and molecular diagnostics. He has served on the scientific advisory boards and provided consulting services to many early stage and established diagnostic companies as well as commercial reference laboratories. In addition, he has experience with FDA clinical trial work and served as a member and consultant to the CDRH FDA Microbiology Devices Panel and has served on several NIH and CDC advisory panels.

P

Vikram Pattanayak, MD, PhD, is an Assistant in Pathology at Massachusetts General Hospital and an Instructor in Pathology at Harvard Medical School. He leads a subgroup of Keith Joung's laboratory focused on the development of genome editing tools, with a focus on detecting and minimzing off-target effects. During his M.D., Ph.D. thesis work with David Liu in the Harvard Chemistry department, he developed assays to define the specificities of designer endonucleases, including homing endonucleases, zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and Cas9. As a member of the Joung lab, he engineered a variant of Cas9 (SpCas9-HF1) with minimal off-target effects. In addition to his research activities, Vikram has also completed a residency in clinical pathology at Massachusetts General Hospital and fellowship in molecular genetic pathology at Harvard Medical School. He currently serves as the director of the MGH Histocompatibility (HLA) laboratory.

Ben Pinsky, MD, PhD, is an Associate Professor of Pathology and Medicine, in the Division of Infectious Diseases and Geographic Medicine at the Stanford University School of Medicine. He also has a courtesy appointment in the Stanford Department of Pediatrics, Division of Infectious Diseases. He serves as the Medical Director of the Clinical Virology Laboratory and the Medical Director of Esoteric (Send-out) Testing for Stanford Health Care and Stanford *Children's Health*, as well as the Co-Medical Director for Point of Care Testing for Stanford Health Care. Dr. Pinsky earned his M.D. and Ph.D. degrees in the Medical Scientist Training Program at the University of Washington School of Medicine in Seattle. He received residency training in Clinical Pathology and fellowship training in Molecular Genetic Pathology at the Stanford University School of Medicine. Dr. *Pinsky's research* interests include the design of novel diagnostics and investigation of the clinical impact of virologic testing. Dr. Pinsky serves as the U.S. editor-in-chief for the Journal of Clinical Virology and is the co-editor of the 5th edition of the Clinical Virology Manual.

Victoria Pratt, PhD, Professor, Director of Pharmacogenetics and Molecular Genetics Laboratories, Indiana University School of Medicine Dr. Pratt is a Medical and Clinical Molecular Geneticist board-certified by the American College of Medical Genetics. Prior to joining Indiana University, she was Chief Director, Molecular Genetics, for Quest Diagnostics Nichols Institute. Dr. Pratt is the President of the Association for Molecular Pathology. Dr. Pratt is also the Past Chair of the Genetics, Clinical Practice and the Program committees and is currently a member of the Economic Affairs, Professional Relations committees for AMP. She is a former advisor of EurogenTest for genetic test validation. Dr. Pratt serves on the American Medical Association's (AMA) Molecular Pathology Current Procedural Terminology (CPT) Advisory committee. In addition to her work, Dr. Pratt served on the Centers for Medicare and Medicaid Services Clinical Diagnostic Laboratory Tests Advisory Panel. Dr. Pratt continues to serve on the Centers for Disease Control and Prevention (CDC) GeT-RM program for reference materials for Molecular Genetics. She is currently serving on the National Academy of Medicine's (formerly Institute of Medicine) Roundtable on Genomics and Precision Health. Dr. Pratt has authored over 75 peer-reviewed manuscripts and book chapters. She is also an Associate Editor for the Journal of Molecular Diagnostics. Dr. Pratt graduated with a Ph.D. in Medical and Molecular Genetics from Indiana University School of Medicine, Indianapolis, IN in 1994. Her fellowship training was in Ph.D. Medical and Clinical Molecular Genetics at Henry Ford Hospital, Detroit MI.

SPEAKER BIOS

R

Rosana Risques, PhD, is Associate Professor in the Department of Pathology at the University of Washington. She received her undergraduate degree in Molecular and Cell Biology and her PhD in Cancer Genetics from the Autonomous University of Barcelona, Spain. Then she did postdoctorate training at the Sidney Kimmel Cancer Center in San Diego and at the Department of Pathology at the University of Washington. Dr. Risques' main research interest is the study of the early genetic alterations that lead to cancer with the goal to enable a better understanding of tumor progression and the development of biomarkers for early cancer detection and prediction. Her research bridges cancer with aging and methods development with clinical applications. She optimized telomere length measurement by quantitative PCR, leading to a core service and multiple collaborative projects. With the advance of next-generation sequencing, she changed focus to somatic mutations and contributed to the development of Duplex Sequencing, an ultra-sensitive method for low frequency mutation detection. She implemented Duplex Sequencing for the detection of ovarian cancer in peritoneal fluid and uterine lavage and discovered the ubiquitous presence of low frequency TP53 mutations in normal tissue. The Risques lab is currently dedicated to develop biomarkers for early cancer detection using ultra-accurate sequencing and to characterize age-related somatic mutations and their association with cancer risk.

S

Daniel Sabath, MD, PhD, is the head of the Hematology Division in the Department of Laboratory Medicine at the University of Washington, where he has served on the faculty since 1993. His main clinical responsibilities include directing the hematology laboratories at the University of Washington Medical Center and Harborview Medical Center, which includes basic hematology testing, coagulation and red cell disorders. Dr Sabath is also responsible for signing out hematopathology cases, both tissue- and bone marrow-based. Finally, Dr Sabath has been involved in molecular diagnostic testing in hematopathology since the Southern blot days. He currently has significant signout responsibility for hematopathology molecular diagnostic cases, including B and T cell clonality, quantitative RT-PCR for BCR-ABL1, single gene mutation assays for FLT3, CEPBA, JAK2, CALR and NPM1 as well as a laboratory- developed amplicon-based next-generation sequencing assay for mutations associated with myeloid stem cell neoplasms. In addition to his clinical work, Dr Sabath has been collaborating with a Seattle biotech startup company to develop a new assay for circulating tumor cells. This assay was clinically validated and became available for patient testing in July 2019.

Robert Schlaberg, MD, MPH, is an Assistant Professor of Pathology at the University of Utah, a medical director at ARUP Laboratories, and Co-founder and CMO at IDbyDNA, Inc. He completed his Clinical Pathology residency and Master of Public Health training at Columbia University, and a Medical Microbiology fellowship at ARUP Laboratories. His research and practice are focused on next-generation sequencing-based infectious disease diagnostics. He has co-developed technology for ultrafast, user-friendly, and diagnostic-grade metagenomics data analysis to accelerate development of precision diagnostics for infectious disease. He is board-certified in Clinical Pathology and Medical Microbiology by the American Board of Pathology.

SPEAKER BIOS

Brian Shirts, MD, PhD, is a molecular genetic pathologist in the Department of Laboratory Medicine at the University of Washington whose research focuses on understanding family-specific genetic variants that causes of adult-onset disease. Dr. Shirts' research covers statistical, informatics, and philosophical issues surrounding interpretation of family-specific variants and communication of this risk among family members as well as related issues of reporting complex genetic information in the electronic health record. He has been a member of AMP for many years and has served as the Informatics Subdivision representative on the AMP Nominating Committee.

Patricia Simner, MSc, PhD, is an Associate Professor of Pathology at the Johns Hopkins University School of Medicine and the Director of the Medical Bacteriology and Infectious Disease Seqeuncing Laboratories at the Johns Hopkins Medical Institutions. Her research has focused on understanding the epidemiology and molecular mechanisms of resistance of Gram-negative bacteria, in particular those harboring β-lactamase enzymes. She is also interested in novel diagnostic tools for infectious diseases and is actively involved in developing metagenomic next-generation sequencing as a diagnostic tool. Dr. Simner is a voting member on the Subcommittee on Antimicrobial Susceptibility Testing for the Clinical and Laboratory Standards Institute, she is the Early Career At-Large representative for the American Society for Microbiology Council on Microbial Sciences, a member of the Microbiology Committee for the College of American Pathologists and an Editorial Board Member for the Journal of Clinical Microbiology.

Anthony Sireci, MD, is a Senior Medical Director at Loxo Oncology, a wholly owned subsidiary of Eli Lilly, where he leads medical affairs. Prior to joining Loxo, Nino was as Assistant Professor of Pathology and Cell Biology at Columbia University Medical Center, where he was a medical director in the Personalized Genomic Medicine Laboratory. Dr Sireci is an active member of the Association for Molecular Pathology (AMP) where he serves as a vice chair of the pricing and new codes subcommittee in the Economic Affairs Committee. He is a technical advisor on the Pathology Coding Caucus in the College of American Pathologists and a member of the Molecular Pathology Advisory Group (MPAG) in the American Medical Association (AMA). Nino received his BA in Chemistry from New York University and an MD from the Johns Hopkins University School of Medicine. He completed his residency training in Clinical Pathology at the New York Presbyterian Hospital-Columbia University Medical Center where he also served as chief resident. During this residency he also received an MSc in biostatistics from the Mailman School of Public Health at Columbia.

Roberta Sitnik, MSc, PhD, Biologist, Received her MSc and PhD in Sciences and Genetics from the University of São Paulo. Currently works as a Molecular Pathology Specialist at the Clinical Laboratory at Hospital Israelita Albert Einstein, in São Paulo, SP, Brazil. Has more than 20 years of experience in molecular pathology, focusing on Human and Medical Genetics, Infectious diseases, project management, tests validation and quality control.

Matija Snuderl, MD, is Associate Professor of Pathology. He obtained his MD degree from Charles University, Prague and completed his residency in Anatomic Pathology and Neuropathology at Massachusetts General Hospital. He then completed fellowship in Molecular Genetic Pathology at Harvard Medical School and post-doctoral fellowship

SPEAKER BIOS

at the Edwin L. Steele Laboratory for Tumor Biology at Massachusetts General Hospital. Dr. Snuderl joined the faculty at NYU School of Medicine in January 2013 and has been actively involved in designing new molecular tests and platforms particularly in molecular neuropathology and epigenetics. Dr. Snuderl has strong interest in tumor genetics, epigenetics and tumor microenvironment. The American Association of Neuropathologists awarded his work at its annual meetings, with the Lucien J. Rubinstein Award for the Best Paper on Neuro-oncology in 2009 and 2015 and Honorable Mention in the same category in 2008 and 2010.

Steve A. Soper, PhD, joined the faculty at Louisiana State University (LSU) in 1991 within the Department of Chemistry, where he filled the William H. Pryor Distinguished Chair of Chemistry. While at LSU, he founded the Center of BioModular Multi-Scale Systems for Precision Medicine, which has as its primary charge to develop enabling and transformative tools for making health-related measurements from rare disease markers, such as liquid biopsy markers, with full process automation. This Center has recently been awarded funding from the National Institutes of Health as part of their Biotechnology Resource Center Program (funded through the National Institute of Biomedical Imaging and Bioengineering). In 2011, Prof. Soper accepted a position within the Department of Biomedical Engineering and Department of Chemistry at the University of North Carolina, Chapel Hill. Prof. Soper is currently a Foundation Distinguished Professor in Chemistry and Mechanical Engineering at the University of Kansas, Lawrence. Prof. Soper also holds an appointment at Ulsan National Institute of Science and Technology in Ulsan, South Korea, where he is a World Class University Professor. As a result of his efforts, Prof. Soper has has published over 245 peer-reviewed manuscripts (h index = 66; 15,289 citations); 31 book chapters and 71 peer-reviewed conference proceeding papers, and is the author of 12 patents. He is also the founder of a startup company, BioFluidica, which is marketing devices for the isolation and enumeration of circulating tumor cells. His list of awards includes Chemical Instrumentation by the American Chemical Society, the Benedetti-Pichler Award for Microchemistry, Fellow of the AAAS, Fellow of Applied Spectroscopy, Fellow of the Royal Society of Chemistry, R&D 100 Award, Distinguished Masters Award at LSU and Outstanding Scientist/Engineer in the state of Louisiana in 2001. Finally, Prof. Soper has granted 46 PhDs and 6 MS degrees to students under his mentorship.

Amanda Sozer, PhD, founder, and president of SNA International, has a Ph.D. from the University of Tennessee - Oak Ridge Graduate School of Biomedical Sciences and spent her early career managing forensic DNA laboratory operations at Cellmark Diagnostics and Fairfax Identity Laboratories. She then served as a Technical Contractor to the National Institute of Justice, supporting the DNA backlog reduction programs and facilitating the National Institute of Justice Kinship and Data Analysis Panel for the World Trade Center Victim Identification Pannel. Dr. Sozer managed the Hurricane Katrina victim DNA identification project, facilitating the Hurricane Victim DNA Identification Expert Group for Louisiana and Mississippi. She is an internationally recognized expert in human identification and has served on numerous committees and panels in an advisory capacity. Dr. Sozer facilitated the writing of the AABB Guidelines for Mass Fatality DNA Identification Operations and was an advisory member of the Federal Bureau of Investigation's Scientific Working Group on Disaster Victim Identification (SWGDVI) Data Management Committee. Dr. Sozer has also written strategic plans and mass fatality response plans for a number of

organizations in the U.S. and has led a Subject Matter expert group developing guidelines for scientists working on human rights projects for the American Academy for the Advancement of Science. She currently sits on the New York State Forensic Commission DNA subcommittee. Dr. Sozer is an expert on Rapid DNA, participating in field exercises to illustrate the versatility of Rapid DNA in the Department of Homeland Security operations and disaster victim identification operations. She has contributed to Rapid DNA research and development on local, national and international scales.

Giorgio Stanta, MD, PhD, of the University of Trieste is an expert in molecular pathology for oncology. He started to work in molecular pathology at the Department of Pathology of the Yale University (CT) in the second part of the 80s. He is involved in many European organizations: He is the coordinator of the European group Archive Tissues: Improving Molecular Medicine Research and Clinical Practice IMPACTS. He is the chairman of the Biobanking and Molecular Pathobiology Working Group? of the OECI (Organisation of European Cancer Institutes). He is involved in the chairmanship of the Molecular Pathology Working Group of the ESP (European Society of Pathology). He is a member of the managing board of BBMRI.IT (Italian Biobanking Infrastructure). He is a member of the Committee of CEN (European Committee for Standardization) for Molecular in-vitro diagnostic examinations. He is the liaison representative for the ESP to the European Committee for Standardization (CEN/TC 140) and member of the CEN Committee for Molecular in-vitro diagnostics. He is a member of the European Commission Initiative on Breast Cancer (ECIBC) - Quality Assurance Scheme Development Group (QASDG), in which he is the Chair of the Clinical Research Subgroup. He is the chair of the European Molecular Pathology Master (EMPM) Steering Committee for the development of the Master. He is consultant of the Comprehensive Cancer Centre CRO in Aviano, Italy. -He was from 2013-2016 member of the Genetic Pathology Faculty of the European Society for Medical Oncology (ESMO). He was in the audit committee for INSERM in France for the biobanking (2014-2016). He is involved in several active European projects such as HERCULES on high grade serous ovary carcinoma, SPIDIA4P project on pre-analytical conditions, and InstandNGS4P on the clinical validation of NGS products commercially available.

Timothy Stenzel, MD, PhD, directs the FDA's Office of In Vitro Diagnostics and Radiological Health. He joined the FDA in July 2018 after a long executive career in both academics as well as industry including oversight of test development for both CLIA labs and IVD manufacturers. He completed an M.D./Ph.D., pathology residency, and Clinical Molecular Genetics fellowship at Duke University prior to joining the Duke faculty and subsequently then moved to industry.

Albrecht Stenzinger, MD, is Professor of Molecular Tumor Pathology and the Head of the IPH Center for Molecular Pathology (CMP) as well as Section Head for Molecular Diagnostics and Biomarker Development at the Institute of Pathology (IPH), University Hospital Heidelberg, Germany. He is holding an MD degree from the University of Giessen (Germany), completed his residency and fellowship training in pathology at the Charité University Hospital in Berlin and the University Hospital Heidelberg (Germany) and is a board-certified surgical pathologist and senior attending. Albrecht received postdoctoral training at the University of Heidelberg, Germany and Massachusetts General Hospital/Harvard Medical School, USA. He has a broad expertise in molecular pathology and works in thefield of translational research and genetics of solid tumors with a focus on lung cancer.

SPEAKER BIOS

T

Christian Thiede, MD, is a scientist with 25 years of research experience in the field of molecular analysis of human tumors, especially in the field of leukemia and lymphoma. After finishing his medical education at the FU Berlin, he had three years of Post-Doctoral training in the Department for Hematology and Oncology at Humboldt University/ Charité, Berlin where he worked on the molecular characterization of gastric marginal zone B-cell lymphoma of MALT. He then went to Dresden to build up a research group and a diagnostic laboratory at the newly established Medical Faculty at the University of Technics in Dresden. Since 2006, he holds a position as Professor for Molecular Hematology at the Medical Faculty Carl Gustav Carus, University of Technics Dresden. He is head of the working group for molecular Diagnostics of the German Society for Hematology and Oncology and leads the WP12 (MRD) of the European Leukemia Network (ELN). His major research focus is the understanding of the molecular mechanisms involved in leukemogenesis, alterations involved in treatment resistance, as well as the use of this information to perform targeted treatment and molecular monitoring of treatment response.

Andrei Thomas-Tikhonenko, PhD, my laboratory has a long-standing interest in pathobiology of solid and hematopoietic malignancies, in particular lymphomas and leukemias and other cancers driven by MYC overexpression. I trained in the MYC field in the early '90s as post-doctoral Research Associate and then Leukemia Society Special Fellow at the renowned Fred Hutchinson Cancer Research Center in Seattle. In 1997, I was recruited to the University of Pennsylvania, where I rose through the ranks to become tenured Professor of Pathology & Laboratory Medicine. For over 18 years, I have been continuously funded by NCI, beginning with the NIH FIRST Award (R29) and ending with 2 recently completed R21s and currently active R01 and U01 grants. In addition, I have received grants from numerous private foundations including American Cancer Society, Swiss Cancer League, Leukemia & Lymphoma Society, Alex's Lemonade Stand Foundation, WW Smith Charitable Trust, The V Foundation, William Lawrence & Blanche Hughes Foundation, and St Baldrick's Foundation. This robust extramural support allowed me to maintain an active lab, currently composed of four postdoctoral fellows, one Hem-Onc fellow, two bioinformatics scientists, three thesis-level graduate students, and one technician. We publish our work in top-notch journals, including Nature Genetics, Nature Immunology, Journal of Clinical Investigation, Journal of the National Cancer Institute, Blood, Cancer Research, etc. Of the Top 10 most frequently cited 2005-2014 MYC papers, my laboratory co-authored 3, which were cited >2,000 times. Ten years ago, I moved my lab across campus to The Children's Hospital of Philadelphia, where it became an integral part of the Center for Childhood Cancer Research. This integration allowed me to foster new collaborations with key physician-scientists and pursue several translational projects.

V

Olena Vaske, PhD, FCCMG, is the Co-Founder of the Treehouse Childhood Cancer Initiative at the University of California Santa Cruz Genomics Institute, where she is Assistant Professor of Molecular, Cell and Developmental Biology. Dr. Vaske's research

focuses on developing novel RNA-Seq analysis approaches for pediatric cancer patients. Dr. Vaske holds a PhD in Bioinformatics from the University of British Columbia and a BSc (Hons) in Molecular Genetics and Biology from the University of Toronto. She is a Fellow of the Canadian College of Medical Geneticists.

James Versalovic, MD, PhD, currently serves as Pathologist-In-Chief at Texas Children's Hospital. He also serves as Vice Chair of Pathology & Immunology at Baylor College of Medicine (BCM), and Director of the Texas Children's Microbiome Center. He holds the Milton J. Finegold endowed chair as Professor of Pathology & Immunology, and is Professor of Pediatrics, Molecular and Human Genetics, and Molecular Virology & Microbiology at BCM. He is Co-Director of the NIDDK-funded Texas Medical Center Digestive Diseases Center. He also served as Co-Director of the NIH-funded Medical Scientist (MD-PhD) training program for 12 years. He was Editor-in-Chief of the Manual of Clinical Microbiology and Editor of Therapeutic Microbiology: Probiotics and Related Strategies. Dr. Versalovic is board-certified in Clinical Pathology and Molecular Genetic Pathology. His clinical interests include human genomics, metagenomics, medical microbiology and the human microbiology of chronic diseases in children. As a Principal Investigator, his primary research interests include the human microbiome, gastrointestinal microbiology, and digestive diseases. His research program has been supported by the U.S. National Institutes of Health, Department of Defense, and Crohn's & Colitis Foundation. Dr. Versalovic has authored 172 primary manuscripts, 37 book chapters, and 2 patents. He received the Lansky Award as a national leader in pathology under the age of 45 from the College of American Pathologists Foundation. He also received the BioGaia Ivan Casas Probiotics Research Award and the BCM Graduate School of Biomedical Sciences Distinguished Alumnus Award. In 2019, Dr. Versalovic was elected as a Fellow of the American Academy of Microbiology (AAM).

David Viswanatha, MD, is board-certified diplomate in Anatomic Pathology (ABP and RCPSC) and Hematopathology (ABP). He is a graduate of the University of Western Ontario in Canada (now Western University) and completed his fellowship in Hematopathology under the mentorship of Drs. Kathy Foucar and Cheryl Willman at the University of New Mexico. He has held previous academic staff positions and laboratory director responsibilities at the University of New Mexico and the British Columbia Cancer Agency. He is currently a consultant hematopathologist at Mayo Clinic in Rochester, MN, where he also co-directs the Molecular Hematopathology and Clinical Genome Sequencing Laboratories. Dr. Viswanatha has been a long-standing AMP member, having served in the capacity of CPC and Nominating Committee representative (Hematopathology Subdivision), and as a participant on the Professional Relations Committee. Dr. Viswanatha is avidly focused on the challenge of developing high quality, cost-effective and technologically current clinical molecular assays to serve patients and the practice of hematology. His areas of research, education and practice interest include both myeloid neoplasms and lymphoma, as well as minimal residual disease evaluation.

Karl Voelkerding, MD, received his Bachelor of Science from the Ohio State University in 1978 and his Medical Degree from the University of Cincinnati College of Medicine in 1983. He completed post-doctoral research and clinical training in molecular biology and clinical pathology. In 1990, he joined the faculty of the Department of Pathology

SPEAKER BIOS

and Laboratory Medicine at the University of Wisconsin in Madison, Wisconsin, where he developed and directed a molecular diagnostics laboratory while also practicing transfusion medicine. In 2002, he moved to Salt Lake City, Utah to join the ARUP Laboratories. Currently, he is a Professor of Pathology at the University of Utah and a Medical Director of Genomics and Bioinformatics at the ARUP Laboratories. Dr. Voelkerding is board certified in clinical and molecular genetic pathology. He has a longstanding involvement in the translation of new technologies into molecular diagnostics, and this interest has focused over the past few years on next generation sequencing. He is currently Chair of the College of American Pathologists' Genomic Medicine Committee.

W

Brian Walker, BSc, PhD, graduated from the University of Edinburgh, UK, with a BSc (Hons) in Medical Microbiology in 1996 before completing a PhD at Imperial College London, UK, focussed on the co-evolution of antigen processing genes with MHC molecules. He was a Staff Scientist at The Institute of Cancer Research in London where his work has focussed on the genetics of multiple myeloma. He is currently a Professor at the Myeloma Center at the University of Arkansas for Medical Sciences, AR. Most of this work has revolved around utilising primary patient material with a range of techniques including gene expression and mapping arrays to next generation sequencing technologies to identify the genetic determinants that can be used to sub-classify myeloma. These determinants include common copy number abnormalities, somatic mutations and gene expression profiles which can accurately classify patients according to biological criteria, which in turn can determine the prognosis of the patient. With the introduction of next generation sequencing (NGS) it has been possible to utilise these data to determine the sub-clonal structure and evolution of tumour cells within a patient, which can be validated using single cell analysis, to illustrate the level of heterogeneity within a tumour and how treatment can affect this important substructure

Michael Walsh, MD, is a pediatrician, geneticist, and hematologist-oncologist. He treats children with cancer and takes care of families with a predisposition to cancer. As a member of the Niehaus Center for Inherited Cancer Genomics, the Department of Pediatrics and the Clinical Genetics team, Dr. Walsh prescribes treatments, offers risk-reductive options, generates surveillance plans, and contextualizes information for patients.

Carl Wittwer, MD, PhD, is a Professor of Pathology at the University of Utah. Carl has published more than 200 articles focusing on technique and instrument development in molecular diagnostics. In the early 1990s he developed rapid-cycle PCR for DNA amplification in 10-15 min and was the primary inventor of the LightCycler® system, with over 10,000 units placed worldwide by Roche. Carl holds 40 US patents and their foreign equivalents. He introduced SYBR Green I, adjacent hybridization probes, melting analysis, and high-resolution melting (HRM) to real-time PCR, techniques that are widely used today. Current projects are extreme PCR (< 1 min) and high speed melting (HSM) in <5 s. In 1990, Carl co-founded BioFire Diagnostics, a company that has grown to over 1,600 people today. He served as Chairman of the Board from 2012 until its acquisition by BioMerieux in 2014.

Z

Yaolin Zhou, MD, is Director of Molecular Pathology and Assistant Professor of Pathology at the University of Oklahoma Health Sciences Center (OUHSC). She trained at Duke Sanford School of Public Policy, Mayo Clinic, University of Alabama at Birmingham (UAB), and Cleveland Clinic. She was Chief Quality Resident at UAB and member of the Cleveland Clinic Enterprise-Wide Test Utilization Committee, for which she developed a "one-button" ordering approach (doi: 10.5858/arpa.2017-0031-OA). Dr. Zhou's experience at various institutions and interest in quality led her to create a new model for quality improvement. EPIDEM represents the steps of quality improvement: exploration, promotion, implementation, documentation, evaluation, and modification (doi: 10.1093/ajcp/aqy089 and 10.1093/labmed/lmy066). As director of OUHSC Molecular Pathology, Dr. Zhou applies EPIDEM to create molecular testing pathways for more efficient, evidence-based patient care. She also chairs the OU Physicians Quality Committee, is secretary of the Pharmacy and Therapeutics Committee, and co-founded the Stephenson Cancer Center Molecular Tumor Board. Dr. Zhou regularly presents to diverse audiences about test utilization and quality improvement. She has received research awards from USCAP, ACLPS, ASCP, and American Academy of Neurology, and her community leadership has been recognized by Duke University, Arnold P. Gold Foundation, Mayo Clinic, and College of American Pathologists. Because of her dedication to helping healthcare professionals across medical disciplines, Dr. Zhou was honored as an ASCP Choosing Wisely Champion (2017) and 40 Under Forty (2019). Since Dr. Zhou first joined AMP in 2014 as a pathology resident, she has served on the AMP Membership Affairs Committee and moderated the AMP Companion Meetings at USCAP 2018-2019. Dr. Zhou is grateful for her mentors and friends in the AMP community and the EPIDEMic of improved patient care we are creating together.

Justin Zook, PhD, leads the Human Genomics Team at the National Institute of Standards and Technology and is co-leading the Genome in a Bottle Consortium's work developing authoritatively characterized human genomes to benchmark sequencing methods. He developed methods to compare and integrate whole genome DNA sequencing data from multiple platforms and sequencing runs to characterize the first whole human genome Reference Material. He is now leading the GIAB Analysis Team work combining short, linked, and long read sequencing technologies to characterize structural variation and challenging regions of the genome. He is an Informatics Representative to the Association for Molecular Pathology Clinical Practice Committee. In addition, he was Chair of the Global Alliance for Genomics and Health Benchmarking Team, which recently published best practices for benchmarking genome sequencing results.

NOTES

Corporate Partners

AMP thanks our 2019 Corporate Partners for their generous support!

Diamond Partners

AstraZeneca

Roche

Platinum Partners

Bristol-Myers Squibb

HOLOGIC® The Science of Sure

myriad® WHEN DECISIONS MATTER

Gold Partners

Abbott

INVITAE

LOXO ONCOLOGY

MERCK

Silver Partners

Adaptive biotechnologies®

Agena BIOSCIENCE

Asuragen®

BAYER

illumina®

nanoString TECHNOLOGIES®

NOVARTIS

QIAGEN

ThermoFisher SCIENTIFIC

POSTER INFORMATION

POSTER INFORMATION

ELITe InGenius®

A Comprehensive PCR Solution for Specialty Testing

Automatic Sample-to-Result

- Fast Turnaround: 2.5 hours
- Broad Portfolio of Reagents
- 5000+ tests daily worldwide
- In-Depth Technical Support

See Us in Booth 2753

ELITechGroup
EMPOWERING IVD

www.elitechgroup.com
425-482-5555

POSTER INFORMATION

General Poster, Award Applicant, and Author/Presenter

- All posters are on display in the Convention Center, Expo Hall A-G, Level 100.
- Poster set-up is Thursday, November 7, 6:30am - 8:00am. All posters must remain on display through 1:00pm, Saturday, November 9.

Posters are listed in sequence by category and number in the following format:

Poster Number Abstract Title
First Author's Name

Key to poster categories:

G = Genetics

I = Informatics

HP = Hematopathology

OTH = Other

ID = Infectious Diseases

ST = Solid Tumors

TT = Technical Topics

- All Award Applicant posters display in Poster Number order in the areas of their subject category. They are identified as Award Applicant posters by a card mounted on the poster board.
- All Award Applicants must attend their posters on Thursday, November 7, 2:30pm - 4:15pm for interviews with members of the poster reviewing committees. Award candidates are required to stand at their poster until 4:15pm.
- All First/Presenting Authors, including Award Applicants, must attend their posters either Friday afternoon (even-numbered posters) or Saturday morning (odd-numbered posters):
    - Even-numbered posters must be attended on Friday, November 8, 2:45pm - 3:45pm.
    - Odd-numbered posters will be attended on Saturday, November 9, 9:45am -10:45am.
    - Authors who have more than one even- or odd-numbered poster may either ask another author to attend their additional poster or attend it themselves during the other session. In the latter case, the author should place a note on the poster board alerting attendees that they will attend the poster in the alternate session.
- Poster removal is Saturday, November 9, 1:00pm-1:30pm. Posters must remain in place until at least 1:00pm. Posters remaining past 1:30pm will be removed and discarded.
- Please note that poster-viewing is not eligible for Continuing Education credit.

POSTER LISTING

By Category

Even numbered posters:
Will be attended by their authors on Friday, November 8, 2:45pm - 3:45pm

Odd numbered posters:
Will be attended by their authors on Saturday, November 9, 9:45am-10:45am

GENETICS

G001. Utilization of Rapid Whole Genomic Sequencing (rWGS) Demonstrates Significant Improvement in Clinical Utility and Cost Effectiveness in Neonatal and Pediatric Hospital Intensive Care Units
S. Nahas

G002. Relative Information Content of Comprehensive High-Throughput Single Nucleotide Analyses in *PTEN*
A. Moon

G003. Characterization of Reference Materials for Genetic Testing of Rare *CYP2D6* Alleles: A GeT-RM Collaborative Project
A. Gaedigk

G004. Correlational Study on Altered Epicardial Adipose Tissue as a Stratification Risk Factor for Valve Disease Progression through IL-13 Signaling
M.M. Corsi Romanelli

G005. Prenatal Testing for Hereditary Cancer Risk Variants: Where Are We Now?
L.S. Rosenblum

G006. An Unusual Cause for Coffin-Lowry Syndrome in Three Siblings with a Novel Microduplication in the *RPS6KA3* Gene Affecting mRNA Expression Levels: Implication for Diagnosis
F. Vetrini

G007. Building an Integrated Clinical Noninvasive Prenatal Screening Program in a Large Reference Laboratory Setting: Lessons Learned Using a Single Nucleotide Polymorphism-Based Method
Y. Ji

G008. Germline *RAD51B* Loss-of-Function Variants Confer Susceptibility to Hereditary Breast and Ovarian Cancers and Result in Homologous Recombination Deficient Tumors
D. Mandelker

G009. Use of Synthetic Internal Standards to Measure Very Low Frequency *TP53*, *PIK3CA*, and *BRAF* Somatic Mutations in Normal Airway Epithelial Field of Injury Associated with Lung Cancer Risk
J. Willey

G010. A Method to Missense Madness: Improving Clinical Variant Interpretation with a Pathway-Focused Functional Assay
S.E. Brnich

G011. Clinical and Molecular Profile of *IDH1*-Mutant Cutaneous Melanoma
J.S. Ross

G012. Performance of AmplideX SMN1/2 Assay from Asuragen
L. Mazur

POSTER LISTING

G013. Mitochondrial Genome Sequencing Uncovers a Novel Alteration in MT-TL2 in a Patient with MELAS-Like Phenotype
J.L. Lopes

G014. A Framework of Critical Considerations in Interpretation of NGS-Based Tests for Germline Disorders: On Behalf of CLSI Document Development Committee (DDC) on Nucleic Acid Sequencing (MM09)
J. Buchan

G015. Accurate and Efficient Chimerism Determination Using a SNP-Based Chimeric ID Panel
K.E. Jackson

G016. North Carolina Newborn Exome Sequencing for Universal Screening (NC NEXUS) Detects Molecular Etiologies Underlying Inborn Errors of Metabolism and Hearing Loss
T.S. Roman

G017. Clinical Significance of Reinterpreting Previously Reported Immunologic Disease Genomic Tests
J.A. SoRelle

G018. Alpha-1 Antitrypsin Deficiency Genotype-Phenotype Correlations: Clinical Experience Testing S, Z, F, and I Alleles
K.S. Dhillon

G019. The VeriDose *CYP2D6* CNV Panel: A One-Well Solution for Copy Number and Hybrid Allele Detection of *CYP2D6*
R.E. Everts

G020. The VeriDose Core Panel: Strong Performance When Analyzing Challenging Pharmacogenetic Samples
A. Lois

G021. Target Selector DNA EGFR Kit for Tissue Demonstrates High Sensitivity without the Need for Macro-dissection
V. Alexiadis

G022. A Multiplex PCR/CE CFTR Assay Resolves Zygosity of the 23 ACMG/ACOG-Recommended CFTR Variants and Sizes Poly-T and TG Repeats in a Single Tube
P. Rao

G023. Integrated Germline and Somatic Analysis Identifies Actionable Cancer Predisposing Germline Mutations in 9,734 Patients with Advanced Cancers
G. Jayakumaran

G024. Assessment of Long IVT mRNA Fragments with the Fragment Analyzer System
C. Pocernich

G025. Validation and Diagnostic Utility of Targeted Next-Generation Sequencing Panel in Korean Patients with Retinitis Pigmentosa
C. Seol

G026. CHLA Ocular Disease Focused Exome: Precision Molecular Diagnosis Enabling Precision Therapies for Retinal Dystrophies
R.J. Schmidt

G027. Genetic Characterization of Spinocerebellar Ataxia 12 Patients in an Indian Cohort: KDAH Experience
J.C. Vyas

G028. Clinical Exome Sequencing, an Effective Tool for Detecting Causative Mutations for Rare Diseases: Retrospective Study of the Past Seven Years
C.C. Eno

POSTER LISTING

G029. Therapy-Related Clonal Hematopoiesis and the Risk of Secondary Hematological Malignancies in Patients with Prior Radiation Therapy
H. Jin

G030. Findings from the Global External Quality Assessment of Lung Cancer Liquid Biopsy Testing
J. Fairley

G031. Implementing Physician-Mediated Consumer-Driven Clinical Elective Genome Sequencing: One Laboratory's Experience
M. Leduc

G032. Chromosomal Microarray Complements Traditional Cytogenetics in Acute Myeloid Leukemia
J. Giffin

G033. Expansion of Clinical Carrier Screening in Spinal Muscular Atrophy through DNA Fragment Analysis by Capillary Electrophoresis
S. Turner

G034. HLA Diversity Score as a Predictor of Checkpoint Blockage Immunotherapy Survival
B. Zhang

G035. Development and Validation of an NGS Assay to Detect UGT1A1 and ABCG2 Polymorphisms Associated with Drug Metabolism
M. Fitarelli-Kiehl

G036. Significance Associated with Phenotype (SAP) Score: A Method for Ranking Genes and Genomic Regions Based on Sample Phenotype
J. Ji

G037. ddPCR-Based Differentiation between Constitutional and Acquired inv(11)(q21q23) Rearrangements in Acute Leukemia
C.J. Zepeda Mendoza

G038. Identity Testing of Paired Neoplastic and Non-neoplastic Samples Using a Custom Single-Nucleotide-Polymorphism-Based Next-Generation Sequencing Assay
K.J. Jensen

G039. Analytical Validation of a Circulating Tumor DNA (ctDNA) Genomic Profiling Assay for the Detection of Somatic Sequencing and Structural Variants
R. Snyder

G040. Clinical Relevance of Liquid Biopsies in Metastatic Adenocarcinoma of Non-small Cell Lung Cancer (NSCLC)
A. Chougule

G041. Analysis of Next-Generation Sequencing Data for Disorders of Somatic Mosaicism Reveals the Importance of Reanalysis in the Clinical Setting
M.J. Evenson

G042. Characterization of Complex *Mixed Lineage Leukemia 1 (MLL1)* Gene Rearrangements in Leukemia
G. Velagaleti

G043. Likely Pathogenic or Likely Benign: Analysis of Deletions of the *MBD5* Gene
J. Schleede

G044. A Rapid Diagnostic and Screening System for Spinal Muscular Atrophy That Reports Copy Number Changes, Single Nucleotide Variants, and Small Indels
H. Zhu

G045. Genomic Characterization of Pediatric Acute Megakaryoblastic Leukemia and the Clinical Impact
E. Lalonde

G046. Expanded Tumor Spectrum in Individuals with Large Germline Deletions Including CDKN2A and Additional Genes Including the Interferon Gene Cluster
P.R. Blackburn

G047. Standardization, Optimization, and Quality Management of FFPE Solid Tumor Diagnostic Samples in Next-Generation Sequencing: An Experience in Our Tata Memorial Centre India
A. Chougule

G048. RapiDxFire Thermostable Reverse Transcriptase: A Novel Reverse Transcriptase for Improved High-Temperature RNA Synthesis and Extended Stability
J. Kramer

G049. Using Isotachophoresis as a Novel Method to Improve the Yield and Quality of Nucleic Acid Purification from FFPE Samples
L.A. Marshall

G050. Challenges of Interpreting *DMD* Gene Duplication Variants
M.L. Fulmer

G051. A Multi-Platform Approach to Friedreich Ataxia Molecular Diagnostics
R. Majumdar

G052. Feasibility of a Synthetic Dried Blood Spot Mimic for Use as an External Control for Newborn Screening of Genetic Disorders
A. Parsons

G053. A Multiplexed SNP Panel Using Oligonucleotide Ligation Assays Run on the N-PLEX Platform for the Allelic Assignment of Genetic Risk Factors of Lung Cancer Development
S.B. Harkins

G054. Incidental Cases of NIPT-Associated Maternal Constitutional Aberrations
K.K. Phillips

G055. Methylation-Based NIPT Test on MALDI -TOF for Down's Syndrome Screening
H.H. Tao

HEMATOPATHOLOGY

H001. Integrative Genomic Testing Improves Clinical Management of Hematological Neoplasms: A Focus on Structural Variations
L. Boiocchi

H002. Clinical Validation of an NGS-Based IGHV Somatic Hypermutation Assay
C.C. Ho

H003. Performance of NGS in Evaluating *TP53* Aberrations in Lymphoid Neoplasm
A. Alsuwaidan

H004. The Result of 122 Consecutive NGS-Based Analysis of T-Lymphoblastic Leukemia/Lymphoma and Early T-cell Precursor Leukemia (ETP)
W. Xie

H005. Frequency of *JAK2* Mutations in Patients with Suspected Myeloproliferative Neoplasms
A. Judd

H006. WT1 Mutation Is an Independent Poor Prognostic Factor in Intermediate Risk Acute Myeloid Leukemia (AML): A Case of Relapsed AML with Leukostasis
N. Hakim

POSTER LISTING

H007. Rapid Next-Generation Karyotyping for Clinical Evaluation of Hematologic Malignancies
E. J. Duncavage

H008. Multidisciplinary Quality Improvement Involving the Molecular Pathology Laboratory Expedites Diagnosis of Acute Promyelocytic Leukemia
S.N. Asadbeigi

H009. Feasability of an RNAseq Assay for Detection of Translocations and Immunoglobulin Clonality in Aggressive B-Cell Lymphomas
X. Wang

H010. Evaluation of Intraclonal Heterogeneity in Diffuse Large B-Cell Lymphoma by Next-Generation Sequencing of Immunoglobulin Heavy Chain (IGH) Gene
M. Zhu

H011. Utility of Next-Generation Sequencing in the Workup and Diagnosis of Patients with Myelodysplastic Syndromes and Unexplained Cytopenias: A Single Institution Experience
D. Carr

H012. Cytogenetic Analysis of Adult T-Cell Leukemia/Lymphoma in a Caribbean Cohort: Correlation with Next-Generation Sequencing (NGS) Data, Clinical Features and Survival
X. Zhang

H013. Validation and Implementation of a Comprehensive Genomics Profiling (CGP) Assay for Hematologic Malignancies
S. Turner

H014. Clinically Significant *CUX1* Mutations Detected by a Targeted Next-Generation Sequencing Panel Are Common in Myeloid Disorders with a High Number of Co-mutated Genes and Dysplastic Features
J.K. Dermawan

H015. Mutant-p53 Antibody Stains Cytokeratin-Negative CTCs Enriched and Detected with a "Pan-CTC" Antibody Cocktail
S.H. Hsiao

H016. Non-coding *NOTCH1* Mutations in Chronic Lymphocytic Leukemia
F. Jelloul

H017. Development of Full-Process Quality-Control Material *BCR-ABL1* Panel Traceable to WHO International Standard
L. Liu

H018. Evaluation of Efficiency-Driven Adjustments to the Abbott RealTime *IDH1* and *IDH2* Assays
A.M. Carlin

H019. *GATA2* Variants Detected by Next-Generation Sequencing with Myeloid Comprehensive Panel: Pathogenic or Benign Polymorphism?
D. Morlote

H020. *IDH1* p.S280F Mutation Is Potentially a Novel Mechanism of Resistance to Ivosidenib Therapy in an IDH1-Positive Acute Myeloid Leukemia
Z.N. Oltvai

H021. *IGH* Locus Assessment Using Hybrid-Capture: A Proof-of-Concept Study
E. Mahe

H022. Benchmarking High-Resolution Optical Mapping to FISH, Karyotyping and Chromosomal Microarray
T. Mantere

POSTER LISTING

H023. A Rapid, Capture-Based Enrichment NGS Panel for Assessing Myeloid Malignancies
A. Barry

H024. *JAK2* Exons 12, 13, 14, and 15 Mutation Analysis
L. Cai

H025. When Do FISH and Next-Generation Sequencing Add Diagnostic or Prognostic Value in the Initial Marrow Evaluation of MDS?
P.C. Tsang

H026. Single-Step, Multiplex and Automated Droplet Digital PCR of p190 *BCR-ABL1* Fusion Transcript for Minimal Residual Disease Quantification in B Lymphoblastic Leukemia
R.J. Martinez

H027. Convergence on Genomic Abrogation of the DNA Damage Response Pathway in CLL Is Observed in Patients with Loss of 18p
W. Wong

H028. *CEBPA* Mutation Phasing Using Pacific Biosciences Circular Consensus Sequencing
L. Cai

H029. Nanopore "Flongle" Sequencing for Fusion Detection as a Rapid, Single Specimen Clinical Test
W. Jeck

H030. A Comparative Study of *FLT3-ITD* Allelic Ratio Evaluation Using Peak Height versus Peak Area Measurements
M. Mai

H031. Newly Discovered 74-Base Pair Insertion in *CALR* Exon 9 in a Myeloproliferative Neoplasm Patient
P.L. Ollila

H032. Exploring Driver Mutations and Tumor Mutational Burden Load in Enteropathy-Associated T-Cell Lymphoma by Next-Generation Exome Sequencing
J. Kim

H033. Long-Term Monitoring of Hematopathology, Cytogenetic, and Genetic Abnormalities in a Patient with MIRAGE Syndrome
S. Rentas

H034. Identification of Neoplastic Clonal T-Cell Sequences in Unrelated Healthy Individuals: Limitations of High-Throughput TRG Sequencing for Minimal Residual Disease (MRD) Analysis
S. Sen

H035. New Subtype of AML with a Very Poor Prognosis
C.A. Schandl

H036. Comprehensive Genomic Characterization of *ASXL1* and *SRSF2* Co-mutated Acute Myeloid Leukemia
L. Ramkissoon

H037. Development of a Modular and Comprehensive Myeloid Amplicon Panel
K.B. Gunning

H038. Performance Characteristics of the First FDA-Cleared Droplet Digital PCR (ddPCR) IVD Assay, the QXD BCR-ABL %IS Kit on the QXD ddPCR System for Monitoring Chronic Myelogenous Leukemia (CML)
N. Sepulveda

H039. Measurable Residual Disease Monitoring for Patients with Acute Myeloid Leukemia Following Hematopoietic Cell Transplantation Using Error-Corrected Hybrid-Capture Next-Generation Sequencing
V. Balagopal

POSTER LISTING

H040. Characterization of a Cryptic *PML/RARA* Fusion by Next-Generation Sequencing in a Newly Diagnosed Case of Acute Promyelocytic Leukemia with Normal FISH and Chromosome Studies
M.J. Schultz

H041. Development and Characterization an NGS Myeloid Panel: A Single-Tube, Multiplex-PCR-Based NGS Assay with 739 Tiled Amplicons
N.J. Lodato

H042. Antigen Receptor Stereotypy in Chronic Lymphocytic Leukemia
F. Jelloul

H043. Utility and Validation of a Comprehensive DNA Panel (523 Genes-TruSight Oncology 500) for Determination of SNVs, Indels, CNVs, TMB, and MSI on an NGS for Hematological Malignancies
R. Kolhe

H044. Copy Number Variant Detection by Targeted Gene Next-Generation Sequencing
C.E. Myers

H045. Clinical Utility of Chromosome Genomic Array Testing in Assessing TP53 Abnormalities in CLL
M. Fang

H046. Rapid Detection of TP53 Mutations in Hematopoietic Neoplasms
X. Xu

H047. Exploring Whole Exome Sequencing Data for Predisposing Germline Variants in Pediatric Myeloid Neoplasia
C. Soderquist

H048. Monitoring Haematopoietic Stem Cell Transplant Using Whole Blood and Lineage-Specific Chimerism
O. Shetty

INFECTIOUS DISEASES

ID001. Evaluation of the ELITechGroup MGB Alert CRE RUO Kit on the ELITe InGenius at the Indiana State Department of Health
C. Campion

ID002. Validation and Utility of HIV Drug Resistance Mutation (DRM) Analysis by NGS Platform
R. Kolhe

ID003. Microbial Cell-Free DNA Sequencing for Multiplexed Detection and Quantitation of Cytomegalovirus, Epstein-Barr Virus, and BK Virus
T.A. Blauwkamp

ID004. Next-Generation Sequencing-Based Approach to Detect Integration of HPV16 Following Exposure to Chronic Oxidative Stress
Y. Chen Wongworawat

ID005. Can Real-Time PCR Help in Diagnosis of Neglected Tropical Diseases?
V. Gupta

ID006. Development and Evaluation of a Novel, Sample-to-Answer Molecular Assay for the Detection of *Pneumocystis jirovecii* from Bronchoalveolar Lavage Fluid
B. Liu

ID007. Performance of Aptima HIV Quant Assay on Hologic Panther
B.G. Baltagjieva

POSTER LISTING

ID008. Developing a Clinical 16s rRNA Multi-amplicon-Based Metagenomic Sequencing Test for Bacterial Pathogen Detection in Body Fluid and Tissue Specimens
S. Realegeno

ID009. Performance Verification of the COBAS HEV Nucleic Acid Test on the COBAS 6800 Platform for Hepatitis E Virus Screening
C. Chai

ID010. Diagnostic Stewardship: Framework for Development of Best Practices Algorithm for Hepatitis C Testing
M. Andrade

ID011. Performance of Aptima *M. genitalium IVD* Assay on Hologic Panther
L.J. Mazur

ID012. Institutional Positivity Rates and Implications for the Treatment of Group A *Streptococcus* Pharyngitis with Conventional versus Molecular Alere i Strep A2 Nucleic Acid Amplification Testing
E.C. Calvaresi

ID013. Analytical Performance and Estimated Clinical Outcomes of a Molecular Multiplexed Bacterial Identification Blood Culture Panel
S.L. Mitchell

ID014. Evaluation of GeneXpert MTB/RIF Assay for Rapid Diagnosis of Extrapulmonary Tuberculosis in a Low-Prevalence Setting
P.M. Thwe

ID015. Quantification of Viral Load in AcroMetrix HPV 16, 18, and 68 Genotype Controls Using Bio-Rad Droplet Digital PCR System
H. Wang

ID016. Validation of Altona Real-Star Analyte-Specific Reagents for the Quantitative Detection of Epstein-Barr Virus and Human Herpesvirus 6 in Cerebrospinal Fluid
G. Patricia

ID017. Clinical Evaluation of a Robust Custom-Designed Multiplexed qPCR Microarray-Based Assay for Urinary Tract Infection
M. Shanmugam

ID018. Cell-Free RNA Is More Sensitive Than DNA for the Detection of Pediatric Bacterial Sepsis via Shotgun Metagenomic Sequencing
C.E. Dougherty

ID019. *Mycoplasma genitalium* Assay Results from High- and Low-Risk Populations: Implications for Sexually Transmitted Infection Panel Menu
M. Andrade

ID020. Clinical and Histologic Features of Patients Tested Using the BioFire FilmArray Gastrointestinal Panel
J.C. Mowers

ID021. High-Throughput, Cost-Effective Screening for Multi-drug Resistance Markers and Toxigenic *C. difficile* with ChromaCode's HDPCR Multi-drug Resistance Panel RUO
S. Powell

ID022. Performance Validation of PCR/Sequencing Assays for Upper Respiratory Pathogens
A. Pham

ID023. Performance Characterization of a Respiratory Pathogen Panel with an Automated High-Throughput System
C. Knoth

POSTER LISTING

ID024. Clinical Assessment of the Applied BioCode Respiratory Pathogen Panel
X. Zhang

ID025. Arbovirus Surveillance in a Private Brazilian Hospital: A Four-Year Retrospective Study
R. Petroni

ID026. Validation of the QuanDx MeltPro High Risk and Low Risk HPV Genotyping Assays in FFPE Tissue
L.M. Petersen

ID027. Increased Prevalence of Vabomere and Plazomicin Resistance among Carbapenem-Resistant Enterobacteriaceae from a Cancer Center
X. Zhang

ID028. Development of a Multiplex Qualitative Real-Time PCR Panel for Identification of Tick-Borne Pathogens from Whole Blood
L.M. Petersen

ID029. Profiling of Microbe Co-existence in Respiratory Tract Infections
J. Li

ID030. Detection and Monitoring of Adenovirus Infection in Post-HSCT Recipients by PCR with Patient Outcomes
R. Walia

ID031. Performance Evaluation of the Comprehensive Respiratory Tract Microbiota (RTM) Panel Using Clinical Repository Specimen and QCMD Controls
K. Li

ID032. Performance of a Rapid Multiplex Strep Assay on the Fully Automated NeuMoDx Molecular Systems
B. Keusch

ID033. A Novel Highly Sensitive Assay for Quantitative Detection of Human Immunodeficiency Virus-1 in Human Plasma
H. Lee

ID034. Performance Characteristics of a Fully Automated High-Throughput MDx Assay for the Detection of *Bordetella pertussis* and *Bordetella parapertussis*
B. Eaton

ID035. Development of Synthetic Multiplexed External Controls for Monitoring the Performance of Qualitative Laboratory Nucleic Acid Testing Panels Used for Identification of Lower Respiratory Pathogens
T. Spenlinhauer

ID036. Evaluation of an Automated Coronavirus Assay to Supplement Respiratory Pathogen Panel Testing on Board the Panther Fusion System using the Open Access Functionality
J.H. Moberly

ID037. Verification of the Roche COBAS HIV-1, HCV and HBV Tests on the COBAS 6800 System and Correlation to the COBAS Ampliprep/COBAS TaqMan System
M. Sabato

ID038. Comparative Yield of Culture and a Molecular Panel in the Diagnosis of Meningitis at a Tertiary Care Cancer Center
T. McMillen

ID039. Sensitive Hybridization Capture and Detection of Urine Cell-Free DNA for Tuberculosis Diagnosis
A. Oreskovic

ID040. Direct Detection of Bacterial and Fungal Pathogens Using Next-Generation Sequencing of Lower Respiratory Specimens
L.A. Cooper

ID041. Local Foodborne Disease and Outbreak Detection for *Salmonella javiana* and *Salmonella newport* Patient Samples in South Carolina Using Whole Genome Sequencing: Details of 192 *Salmonella* Cases
L.M. Lane

ID042. Withdrawn

ID043. Investigation of Amplicon Sequencing Technology in Diagnosis of Drug-Resistant Tuberculosis by Testing FFPE Specimens
N. Che

INFORMATICS

I001. Development and Validation of a Melanoma Genomic Index (MGI) Focused on CNVs and AOH from Whole-Genome SNP Aiding in Histological Assessments Complex Melanocytic Lesions
V. Agarwal

I002. Validation and Adoption of Somatic Gene-Level CNV Detection from Tumor-Only NGS Panels Identifies Clinically Significant Alterations in Childhood Tumors
R. Chandramohan

I003. Evaluation of Tertiary Analysis Software for Solid Tumor Next-Generation Sequencing
T.R. Sundin

I004. Impact of Next-Generation Sequencing Panel Composition on Tumor Mutation Burden Calculation: *In Silico* Comparison of Frequently Utilized Panels
N. Bevins

I005. Evaluation of the NAVIFY Mutation Profiler for Next-Generation Sequencing Variant Interpretation and Reporting
L. Bonomi

I006. Performance Analysis of Three Bioinformatic Variant Callers Using a Somatic Reference Standard
B. Porath

I007. Tracking of Index Hopping Percent as a Quality Control Metric for Illumina Sequencers with Patterned Flow Cell Technology
Y. Sakai

I008. Withdrawn

I009. Amplicon-Based Targeted Sequencing of Single Circulating Tumor Cells
N. Ericson

I010. Using RNA Expression Analysis to Find Non-fusion Translocations
J.R. Gagan

I011. Discovering SNVs and Indels from RNA-Seq: Comparison of Results of Whole Transcriptome Sequencing to Those of Whole Genome Sequencing
J. Lee

I012. Integrated Networks Dissect the Molecular Biology of Estrogen Receptor-Positive Breast Cancers
I. Katsyv

I013. Benchmarks for Difficult-to-Sequence Genes and Structural Variants
J.M. Zook

POSTER LISTING

I014. Variant Detection and Tumor Mutational Burden (TMB) Concordance in Blood and Tumor Tissue Using Next-Generation Sequencing (NGS) in Patients with Non-small Cell Lung Cancer (NSCLC)
J. Baden

I015. Curation of Pediatric Cancer Variants within the Clinical Genome Resource (ClinGen)
A. Roy

I016. Large-Scale Cytogenetic Profiling of Acute Myeloid Leukemia (AML) from the Mitelman Database Using CytoGenetic Pattern Sleuth (CytoGPS)
Z.B. Abrams

I017. Improve PPV without Sacrificing Sensitivity for Germline NGS Tests Using Lithium Software Package
L. Yang

I018. Oncogenic EGFR Kinase Domain Duplications Detected through Aberrant Splice Recognition in RNA-Seq
A. Garcia

I019. Assessment of SureSeq Interpret Software on Low-Frequency Variants Using Reference Standards
J. Reid

I020. Mixed Reality for a Precision Medicine Laboratory: The Future Is Now!
A. Sigaras

I021. Datanorm: A User Friendly Tool That Assists in the Validation of Next-Generation Sequencing Assays
V.S. Williamson

I022. Validation of a Novel Tumor Mutation Burden Assay Using a 130 Gene Tumor Only Targeted Sequencing Panel Covering Less Than 0.25 Megabases
R.P. Joshi

I023. Genomic Database for Assessing Specificity of Primers with Mismatches and Single-Base Bulges
Z.L. Dwight

I024. A Deep-Learning Method for High-Throughput *FMR1* Triplet Repeat Screening
L. Ringel

I025. Ultra-rapid and Accurate Data Analysis Solution for TSO500 ctDNA: Enabling Comprehensive Genomic Profiling with a Plasma-Based Assay
T. Jiang

I026. Targeted Informatics for Optimal FLT3-ITD Detection, Characterization, and Quantification across Multiple NGS Platforms
H. Tsai

I027. Identification of Low-Frequency Variants in AML Populations
S. Johnson

I028. Development of a Convolutional Neural Network Algorithm for Detection of Copy Number Loss in Exome Sequencing Data
S. Muthusamy

I029. InferCNV.org: Inferring Regional Copy Number Changes from Discrete Gene-Level Amplification Signals in Clinical Cancer Genomics Reports for Prioritization of Therapeutic Targets
P.A. Kenny

I030. Pratical Informatic Solutions for Molecular Diagnostics Quality Management
L.M. Scicchitano

I031. Platform-Agnostic Deployment of Bioinformatics Pipelines for Clinical NGS Assays Using Containers, Infrastructure Orchestration, and Workflow Manager
S. Kadri

I032. Evaluation of Nanopore Sequencing and Associated Bioinformatics Pipelines for Accurate Pathogen Identification and Antimicrobial Resistance Prediction
L.M. Petersen

I033. A Next-Generation Sequencing-Based Analysis of Clonality across 39 Subjects Treated for Lymphoproliferative Disorders Reveals Matching Clones in the Diverse IGH Locus
A.M. Zlotnicki

I034. Detection of Internal Tandem Duplications in the *FLT3* Gene Using PiVAT Software
S.M. Polvino

I035. Clinical Bioinformatics Pipelines in the Cloud: Considerations and Deployment
S. Kadri

I036. High-Throughput Genetic Variant Classification for Inherited Cancer Gene Panels through an Artificial Intelligence Inference Engine
S. Nohzadeh-Malakshah

I037. Clinical Validation and Informatic Implementation of Targeted NGS for Low-Input and Degraded Specimens
A. Chitturi

I038. Calculation of Tumor Mutational Burden (TMB) Using a Small, Targeted Next-Generation Sequencing (NGS) Panel for Solid Tumor Samples Absent Matched Normal Samples
P.D. Velu

I039. Downstream Third-Party NGS Pipelines in Comparison to In-House Semi-Automated Variant Processing May Demonstrate Limitations on Some Platforms
K. Ikemura

I040. Machine Learning Applications for Patient Testing: Computational Assessment of MSI by NGS in the Clinical Laboratory
G. Omerza

OTHER (E.G., EDUCATION)

OTH001. HLA Typing: Do We Need Secondary Typing Methods in the Era of NGS?
L. Kumer

OTH002. Alignment of Fellowship Training and Job Needs in Molecular Genetic Pathology
K.L. Kaul

OTH003. Development of Tumor-Specific NGS Gene Subpanels Based on a Medium-Sized NGS Panel (TST170) in a Small Hospital-Based Molecular Diagnostics Laboratory
K.C. Behling

OTH004. Single Cell Genomics and Spatial Transcriptomics Enable Novel Approaches to Dissect Tumor Heterogeneity
L.D. Gibbs

OTH005. Reporting Indeterminate Variants from Massively Parallel Sequencing Assays
J.J. Roth

OTH006. Standardized Process for Molecular Laboratory Engagement and Quality Improvement
K. Halverson

POSTER LISTING

OTH007. Laboratory Standards for Interpretation and Reporting of Acquired Copy Number Abnormalities and Copy-Neutral Loss of Heterozygosity in Neoplastic Disorders: A Consensus ACMG/CGC Document
G. Raca

OTH008. Real-Time Outbreak Investigation Informed by Whole Genome Sequencing and Data Mining: Expecting the Unexpected
M.M. Hernandez

OTH009. Whole Exome Sequencing in the Clinical Laboratory: Pre-analytical Challenges and Triumphs
J. Catalano

OTH010. Large Panel NGS Testing: Financial Barriers to Entry
J. Catalano

OTH011. Analysis of CAP Proficiency Testing Responses and Commonly Used Annotation Software Output Shows Substantial Discrepancy in Variant Nomenclature
R.J. Schmidt

SOLID TUMORS

ST001. Comparison of Next-Generation Sequencing Assays for Clinical Use in Solid Tumor Malignancies
T. Sundin

ST002. Development of a DNA/RNA Full Process Run Control for Next-Generation Sequencing Assays
A.E. Shean

ST003. Relevance of Next-Generation Sequencing in Lung Cancer: Data from a Tertiary Lab with Interesting Case Presentations
N. Sabnis

ST004. Quality Impact of Implementing Reflex Clinical Genomic Analysis in Non-Small Cell Lung Cancer
B.F. Smith

ST005. Correlation of MET Exon 14 Skipping and *TP53* Mutation with PD-L1 Expression in Chinese Patients with NSCLC
N. Che

ST006. Genomic Profiling of *KRAS*, *BRAF*, and *NRAS* Gene Mutations in Colorectal Cancer Patients: A Lebanese Major Center Cohort Study.
O.Z. Baba

ST007. Molecular Profiles of Lung Adenocarcinoma (LAC) from Rural Maine: Correlation of Next-Generation Sequencing (NGS) Data with Clinical Features and Outcome
L. Skacel

ST008. Diverse Landscape of Fibroblast Growth Factor Receptor 2 *(FGFR2)* Rearrangement Partners in Intrahepatic Cholangiocarcinoma (iCCA)
I.M. Silverman

ST009. Improved Detection of *MET* Exon 14 Skipping Mutations in Lung Adenocarcinoma with Combined DNA/RNA Testing and Refined Analysis Methods
D.M. Manthei

POSTER LISTING

ST010. Detection of Point Mutations in Paediatric Low Grade Glioma (PLGG) and Diffuse Intrinsic Pontine Glioma (DIPG) Patients: Validation of a Novel Liquid Biopsy Assay
M. Johnson

ST011. Microsatellite Instability Testing Using the Moffitt STAR Next-Generation Sequencing Panel
J.M. Rodriguez

ST012. Implementation and Analysis of Colorectal Cancer NGS Panel at a Brazilian Low Income Cancer Hospital
G.N. Berardinelli

ST013. Cell-Free Plasma miR-149 as a Biomarker for Screening Lung Cancer
W. Mahmud

ST014. CFL1 Promotes Proliferation and Invasiveness and Regulates NF-κB-Mediated Inflammatory Factors in Hepatocellular Carcinoma
C. Zhang

ST015. Clonal Hematopoiesis Mutations in Plasma cfDNA *RAS/BRAF* Genotyping of Metastatic Colorectal Cancer
B. Wang

ST016. Utility of NGS MSI Calling Software in a 0.35 Mb Targeted Panel Utilizing Amplicon-Based Target Enrichment on an Ion Torrent Platform
C.M. Sebastian

ST017. Correlative Analysis Genes Encoding Cholesterol Synthesis with Tumor Character and Clinical Parameters in Colorectal Carcinomas
K. Vaiphei

ST018. Accurate Classification of Salivary Gland Carcinomas Using a Custom AmpliSeq RNAseq Panel
D.M. Manthei

ST019. *IDH* Mutations, *MGMT* Methylation and 1p/19q Status Provides Better Diagnosis and Survival Prediction in an Indian Cohort of Diffuse Gliomas
A. Majumdar

ST020. Characterization and Prevalence of a 3-Gene Biomarker Signature (*PIK3CA*, *AKT1* and *PTEN*) for Selecting Breast Cancer (BC) Patients (Pts) for Treatment with the Oral AKT Inhibitor Ipatasertib (IPAT)
M. Wongchenko

ST021. Analytical Validation and Clinical Utility of a Custom 34-Gene Next-Generation Sequencing Fusion Panel for Bone and Soft Tissue Neoplasms
J.K. Dermawan

ST022. *TP53* Mutations Affecting Nuclear Localization Do Not Exhibit Classical Aberrant Patterns of p53 Immunoexpression: A Potential Diagnostic Pitfall for Gynecological High Grade Serous Carcinoma
W. P. Devine

ST023. Impact of Universal Screening and Immunotherapy Eligibility on Microsatellite Instability Testing
N. Singh

ST024. Evaluation of a Screening Tool to Detect Clinically Actionable DNA Variants in Lung Cancer Patients
F. Mularo

ST025. Systematic Re-examination of Pathological Diagnosis after Panel Sequencing for Clinically Suspected Non-Small Cell Lung Carcinoma
Y. Lo

POSTER LISTING

ST026. The Presence of an *FGFR2-INA* Fusion Could Represent a New Category of Low Grade Mixed Neuronal-Glial Tumors
C.M. Sande

ST027. An Automated Companion Diagnostic (CDx) IHC Assay for Detection of PTEN Loss in Metastatic Castration-Resistant Prostatic Cancer (mCRPC) Compares to DNA-Based Detection Methods
E. Harnish

ST028. Validation and Implementation of Ultra-rapid Mutation and MSI Assessment Using the Idylla Platform
K. Nafa

ST029. Impact of *Dicer1* Mutations on microRNA Expression Profiles in Ovarian Sertoli-Leydig Cell Tumors: Analysis of a Southeast Asian Cohort
Y. Mok

ST030. Pitfalls of RET Translocation Analysis In Non-Small Cell Lung Cancer Using *In Situ* Hybridization
W. Geurts-Giele

ST031. digitalMLPA for Detection of *BRCA1*- and *BRCA2*-Like Copy Number Profiles in Breast Cancer
A. Benard-Slagter

ST032. Prospective Multi-dimensional Genomic Testing in Newly Diagnosed Glioblastoma Facilitates Trial Analysis and Biomarker Discovery
A. Dubuc

ST033. Quality Assurance of Neoplastic Cellularity Estimation: Comparing Intradepartmental and Intraobserver Scores with the CAP Neoplastic Cellularity Proficiency Testing
T.E. Jones

ST034. RET M918T Mutations in Breast Cancer
M. Eldomery

ST035. RT-PCR and Sanger Sequencing as the Standardized Confirmatory Methods for Gene Fusion Detection in RNA-seq NGS Testing
W. Song

ST036. Clinical Utility of Oncomine Next-Generation Sequencing Test for Calculation of Tumor Mutation Burden
C. Kaya

ST037. Design and Clinical Validation of a 100-Gene DNA-Based Next-Generation Sequencing Panel for Solid Tumors
L. Mnayer

ST038. Clinical Utility of Oncomine Next-Generation Sequencing Test for Identification of Tier 1 and Tier 2 Alterations
A.I. Wald

ST039. Value of Comprehensive Clinical Molecular Testing in Pediatric Malignancies: Single Center Experience
N.S. Kataria

ST040. Design and Validation of an RNA-Based Fusion Panel for Solid Tumors
L. Mnaye

ST041. Patterns of Common Genomic Alterations in Colorectal Cancer: A Tertiary Cancer Centre Experience on Western Indian Patients
O. Shetty

ST042. Mutations in DNA Repair (DR) Genes: Another Indicator of High Tumor Mutation Burden (TMB)
R.K. Yang

POSTER LISTING

ST043. Grid Study: A Simulated Sampling Study to Assess the Equivalency of Tumor Resections and Biopsy Specimens of Gastric or GEJ Adenocarcinoma Tissues
Y. Lin

ST044. Concurrent Cross-Platform Comparison of an NGS LDT and an FDA-Approved Companion Diagnostic for Detecting *EGFR* Mutations in Lung Adenocarcinoma Reveals Unanticipated Discrepancies
J.B. Murry

ST045. Validation of the BioCartis Idylla Platform Using Extracted Nucleic Acid as Input
K.D. Davies

ST046. Clinical Implications of Improved Variant Detection Using In-House Developed Bioinformatic Workflow Compared to Vendor Provided Bioinformatic Solution
N. Kip

ST047. Optimized Conditions for Whole Blood Analysis in the AVENIO Analysis Kits Enable Filtering of Clonal Hematopoetic Variants in ctDNA Analysis
S. Saelee

ST048. Monitoring Breast Cancer Biomarkers from Circulating Tumor DNA Using Target Selector NGS Breast Panel
R.D. Schultz

ST049. Validation of Target Selector Next-Generation Sequencing Lung Panel for the Detection of Circulating Tumor DNA Alterations
R.D. Schultz

ST050. Withdrawn

ST051. Implementation of a Patient-Centric Protocol for the Comprehensive Genomic Profiling of Pediatric Tumors and Hematologic Disease
C.E. Cottrell

ST052. Highly Sensitive and Specific Detection of a Cytokeratin Positive and Negative Circulating Tumor Cells
J.A. Mayer

ST053. Detection of Potential Epithelial Mesenchymal Transition Cells in Localized Prostate Cancer
J.A. Mayer

ST054. Differential Network Analysis Identifies Differences in Tumor Immune Response between Colon and Rectal Adenocarcinomas
D. Chen

ST055. Validation of Extracted DNA for Detection of *KRAS* Mutations with Idylla PCR-Based Molecular Diagnostic Aassay: Can We Rescue Small Samples?
Q. Wei

ST056. Clinical Correlates of Circulating Tumor DNA Shed in *BRAF* V600+ Melanoma Patients: Defining a High-Yield Cohort for Cell-Free Validation Studies
J.M. Tsai

ST057. Development of Novel Copy Number Variation (CNV) Reference Materials for Solid and Liquid Biopsy Next-Generation Sequencing Assays
K. Banjara

ST058. Reflex Testing Using a Targeted Fusion Panel for Optimal Patient Management
H. Fernandes

POSTER LISTING

ST059. Evaluation of a Targeted Realtime Assay for Rapid Identification of IDH1 and IDH2 Disease-Associated Variants in Brain Tumors
S.E. Herlihy

ST060. Performance of a Targeted RNA Sequencing Panel in the Detection of Gene Fusions in Solid and Hematologic Tumors
L. Sun

ST061. Assessment of Tumor Mutational Burden Using a Rapid, Amplicon-Based NGS Target Enrichment Strategy for Accurate and Comprehensive Tumor Profiling
L. Lee

ST062. Development and Validation of a Pan-solid Tumor Next-Generation Sequencing Panel with a Customized Bioinformatics Pipeline
L. Yin

ST063. Analytical Performance of a Novel Microsatellite Instability Digital Droplet PCR Assay
Z. Iemier

ST064. Identification of Gene Fusions and Single Nucleotide Variants by a Custom-Designed Next-Generation Sequencing-Based Panel Improved Diagnostic Accuracy for Salivary Gland Tumors
C.M. Sande

ST065. Application of a Staged Testing Model for cfDNA Samples from a Series of 100 NSCLC Patients at Time of Diagnostic or Progressing on *EGFR* Tyrosine Kinase Inhibitor Therapy
A. Sartori

ST066. Mutational Landscape of Gastrointestinal Stromal Tumors: An Indian Perspective
O. Shetty

ST067. Association of Mutational Profile and Human Papillomavirus Status in Patients with Head and Neck Squamous Cell Carcinoma
S. Doerstling

ST068. Molecular Genetic Profiling Reveals Prognostic Markers of Survival and Recurrence in Glioma
K. Shee

ST069. Primary Central Nervous Lymphomas: A Study on Its Cell of Origin Subtypes
M.M. Gurav

ST070. RNA-seq Analysis Reveals Differences in Tumor Mutation Burden between Lynch Syndrome Associated Tumors and Tumors with Defective DNA Mismatch Repair Due to MLH1 Promoter Hypermethylation
M.J. DiGuardo

ST071. Analytical Validation of Tumor Mutation Burden Using a Targeted NGS Panel Compared to Whole Exome Sequencing
L. Keefer

ST072. From One Case to See the Role of Molecular Testing in Colorectal Cancer Screening
J. Shi

ST073. The Development of a Highly Multiplexed FFPE Reference Standard for Somatic Cancer Panels
P. Nagarajan

ST074. Accurate Detection of *MET* Exon 14 Skipping Mutations in Non-small Cell Lung Cancer with DNA-Based NGS Analysis
W.R. Geurts-Giele

POSTER LISTING

ST075. Utility of Salvaged CytoLyt-Fixed FNA Supernatant for Next-Generation Sequencing Using AmpliSeq Cancer Hotspot Panel and Oncomine Comprehensive Assay: An institutional Experience
A. Waluszko

ST076. Droplet Digital PCR as a Rapid Test for NRAS Q61R in FFPE Biopsies of Melanoma
E.G. Hughes

ST077. Impact of Immunohistochemistry Chromogen on Microdissection and Downstream Molecular Analysis of Archival Specimens
S. Laun

ST078. *MLH1* Promoter Methylation Analysis
L. Cai

ST079. Correlation of PD-L1 SP142 Immune Cell Positivity with Tumor Mutational Burden and Microsatellite Instability in Triple Negative Breast Cancer
C.A. Brown

ST080. Reduction of Unsatisfactory Molecular Test Results on Cytology Specimens: Process Improvement
F.K. Bruehl

ST081. Frequency of Biomarker Testing In Lung Cancer: A Study from an Academic Hospital
T. Zhang

ST082. Validation of the TruSight Oncology 500 Gene Assay for High-Throughput Deployment on the NovaSeq 6000 Sequencer
J.T. Welle

ST083. Clinical Validation of a Digital Droplet PCR Assay for Detecting Microsatellite Instability in Tumor and Plasma cfDNA Samples
M. Freed

ST084. Characterization of Tumor-Normal Cell Line Pairs for TMB Standardization
M. Butler

ST085. False Retained Mismatch Repair Protein Expression in Microsatellite Instability-High Cancers Is Associated with Missense Mutations in Mismatch Repair Genes
S. Rana

ST086. Comparative Analysis of Immunohistochemistry and Fluorescence In Situ Hybridization Assays to Establish Reporting Criteria for ALK and ROS1 Immunohistochemical Stains for Lung Adenocarcinomas
D. Sirohi

ST087. Detection of Genomic Structural Variation in Primary and Metastatic Ovarian Cancer Using a Novel Genome Wide High-Resolution Optical Mapping Approach
S. Bocklandt

ST088. Withdrawn

ST089. Fusion Gene Detection in Cell-Free Plasma by NanoString Low Input Fusion Assay
C. Huang

ST090. Assessment of the Oncomine Cell-Free DNA Lung Assay to Detect Low-Frequency Hotspot Mutations in Plasma from Cancer Patients
H. Rennert

POSTER LISTING

ST091. Development of a Comprehensive Next-Generation Sequencing Assay for Gene-Fusions Detection in Solid Tumors
V. Mittal

ST092. *MLH1* Promoter Hypermethylation in Circulating Cell-Free DNA from Patients with Colorectal Cancers Showing High Microsatellite Instability
P. Ward

ST093. Pick-Seq: A Novel Technology to Retrieve Image-Defined Micro-regions for RNA Sequencing
R. Podyminogin

ST094. STK11 Loss-of-Function Variants Mediate Immune Evasion in NSCLC via Dysregulation of the FAK/Hippo Signaling Axis and Subsequent Alterations in Tumor-Intrinsic Cytokine Expression
L.L. Donnelly

ST095. Tumor Mutation Burden Assessment Comparison between Whole Exome Sequencing and Target Panel Sequencing
W. Song

ST096. Differences in Clonality of Tumor Infiltrating Lymphocytes in Colorectal Cancers with High-Microsatellite Instability Due to Lynch Syndrome versus *MLH1* Promoter Methylation
P. Ward

ST097. Enzymatic DNA Repair Enables High-Quality Library Preparation and Accurate Sequencing from Highly Damaged FFPE DNA Inputs
M.R. Heider

ST098. Variance in Tumor Mutation Burden between Primary and Metastatic Lesions
C.A. Pagan

ST099. A Multi-laboratory Investigation of 18 Oncogenic RNA Fusions in FFPE and Purified RNA-Based Reference Materials
D.J. Ruminski Lowe

ST100. Evaluation of Anchored Multiplex-Based Next-Generation Sequencing for Detecting Clinically Significant Variants in Liquid Biopsy Samples from Pediatric Solid Tumor Patients
J.N. Reuther

ST101. Analytical Validation of Tumor Mutational Burden and Microsatellite Instability in a Plasma-Based Targeted Sequencing Panel
Y. Fu

ST102. Evaluation of the Performance of the Biocartis Idylla BRAF Cartridge with Low DNA Input
A. Judd

ST103. Correlation between Mutations Found in FFPE Tumor Tissue and Paired CfDNA Samples
L. Saunders

ST104. *TGFB1* Pathway Activation Predicts Early Relapse in *EGFR*-Sensitive NSCLC Patients Treated with EGFR TKIs
G. Khullar

ST105. Clinical Validation of ctDNA Liquid Biopsies in Resected Pancreatic Cancer
S.L. Riel

ST106. Oncogenic Fusion Detection Using RNA-seq in a Cohort of 158 Sarcomas
M.A. Atiq

ST107. Development of a Targeted NGS Oncology Assay for Detection and Reporting Comprehensive Genomic Profiling
V.K. Mittal

POSTER LISTING

ST108. Comparison of MSK-IMPACT Results Generated on 2 Sequencing Platforms: HiSeq2500 and NovaSeq6000
R. Bacares

ST109. Analytical Performance of TSO500 ctDNA on Small Nucleotide Variations, Gene Amplifications and Gene Rearrangements Using Circulating Tumor DNA Extracted from the Plasma of Cancer Patients
J.S. LoCoco

ST110. Identification of Chromothripsis in a Lipoblastoma with a Complex *PLAG1* Rearrangement
J. Lanceta

ST111. Development of an Expanded Microsatellite Instability Panel with Automated Data Analysis
C. Baudo

ST112. Clinical Utilization of a 50-Gene Next-Generation Sequencing Panel in Colorectal Cancer
J. Xu

ST113. Rapid, High-plex, Amplification-Free Direct RNA Expression Profiling from FFPE Tissue Using Hyb & Seq Counting Mode
P.M. Ross

ST114. Integration of Data from Orthogonal Testing for Continuous Quality Assessment of a Somatic Cancer Gene Panel
A.M. Eckel

ST115. Therapeutically Targetable Gene Fusions Are Enriched in a Subset of Microsatellite Unstable Colorectal Cancer
C.A. Brown

ST116. Utility of Biomarkers to Differentiate Adenocarcinoma of the Uterine Cervix from Its Mimics
G.J. Nuovo

ST117. Utility of Whole Genome Single Nucleotide Polymorphism Microarray (SNPM) and Targeted Somatic Mutations in Evaluation of Pancreatic and Bile Duct Brushings with Atypical Cytology
S. Heneidi

ST118. A Quality Management System for Clinical Next-Generation Sequencing
D.H. Barakat

ST119. The DNA Damage Repair Pathway Gene *EXO5* Is Hypermethylated in Glioblastomas: Correlation with MGMT Hypermethylation, Genomic Alterations and Patient Outcome
F. Khan

ST120. Using DNA Methylation Signatures to Predict the Anatomic Origins of Primary Head and Neck Squamous Cell Carcinomas
D. Xia

ST121. Whole Exome and Transcriptome Sequencing of Pediatric Ependymomas: A Single Institution Experience
M.L. Miller

ST122. Evaluation of the Suitability of Cytology Fluid Samples for Molecular Testing in Lung Cancer
A. Judd

ST123. Development of SureSelect Sequencing Panels and Algorithms to Detect Copy Number Variations, DNA Rearrangement and Tumor Mutational Burden in FFPE Specimens
A. Khare

ST124. Highly Efficient Capture of Small (Sub-nucleosomal) ctDNA Fragments
M.J. Lodes

POSTER LISTING

ST125. Segmental Involuting Congenital Hemangioma: An Unusual Case as Characterized by Pathogenic *GNA11* Mutation
T. Phung

ST126. Analytical Performance of an Immunoprofiling Assay Based on RNA Models
J.R. Armstrong

ST127. Genetic Alterations in Genes in Adult Gliomas
H. El Achi

ST128. Correlation among Single Gene, NGS Panel and Clinical Management in Metastatic Colon Cancer Patients
Y. Akkari

ST129. The Association of Genetic Alterations Identified Targeted Next-Generation Sequencing (NGS) and PD-L1 Expression in Triple-Negative Breast Cancer
W. Kim

ST130. Oropharyngeal Metastasis as the Initial Presentation of Lung Adenocarcinoma 12 Months Before the Primary Cancer
A. Plagov

ST131. A Partner Agnostic Approach for Gene Fusion Detection with Targeted Next-Generation Sequencing
A. Marcovitz

ST132. The Impact of Clinical Molecular Testing and Precision Medicine in Thyroid Cancer
D. Dias-Santagata

ST133. A Comparison of a 5-Gene Panel Using MALDI-TOF-Based Technology to Multiple Single-Gene Real-Time PCR Assays When Profiling FFPE Tissue Samples
B. Boyadzhyan

ST134. Genomic Characterization of Breast Cancer Heterogeneity Using Breast Cancer 360
H. Brauer

ST135. Comparison of NGS-Based RNA Sequencing Assays for the Detection of Gene Fusions
W. Song

ST136. Biomarker Selection of Cancer Patients for Treatment with *FGFR* TKI
S. Manjeshwar

ST137. A Pathology Group Experience with Targeted Next-Generation Sequencing (NGS) for Non-Small Cell Lung Cancer (NSCLC)
D. Xu

ST138. A 15-Gene Panel for *BRCA1*, *BRCA2* and *DDR* Genes for Reporting Variants on FFPE Samples
F.L. Hyland

ST139. Impact of Recent 2018 ASCO-CAP *HER2* Testing Guidelines on 2713 Breast Cancer Cases Treated According to 2013 ASCO-CAP *HER2* Guidelines: Western Indian Tertiary Cancer Centre Experience
T. Pai

TECHNICAL TOPICS

TT001. Development of SNP-Matched NIPT Reference Materials for Validation, Proficiency Testing and Quality Control
F.L. Tomson

TT002. Blood Collection Tube Selection and Storage Time Impact the Quantity and Quality of Cell-Free Total Nucleic Acids
H.E. Saunders

TT003. FISH Slides Preparation by BioDot Instruments: A Semi-automated System
W. Zhou

TT004. The Application of Droplet Digital PCR for *EGFR* Mutation Testing in Formalin-Fixed, Paraffin-Embedded Tissues with Poor DNA Quality
F. Wang

TT005. Elevated *BCR-ABL1* IS in Ph(+) ALL: Laboratory Error or Biological Phenomenon?
N. Willard

TT006. Analytical Validation of a Quantitative Intracellular Protein Signaling Panel for the Analysis of FFPE Breast Cancer Biopsies
J. Lee

TT007. Advanced Quality Control System for Clinical Metagenomic Sequencing Assays
S. Siddhanti

TT008. Comparative Study of Lower Limit of Detection of *EGFRvIII* Variant Detection Using Amplicon-Based NGS Testing and RT-PCR
G. Shen

TT009. Withdrawn

TT010. Comparison of QIAact Myeloid DNA UMI Panel versus Traditional Methods for the Detection and Quantification of Myeloid Mutations
R.A. Allen

TT011. A Comprehensive Assessment of Onco-panel Sequencing across Multiple Laboratories and Technologies
J. Xu

TT012. *FLT3* Variants Near Codon 835: An Institutional Experience Comparing Rapid Restriction Digest Testing with Massively Parallel Sequencing
S. Garces

TT013. *EGFR* Mutation Analysis: Performance Evaluation of Blood Collection Tubes for ccfDNA Stabilization
A. Ullius

TT014. Alternative Method of DNA Fragment Analysis for the Detection of *CALR* and *FLT3*-ITD Mutations
E.S. Walker

TT015. Concurrent Detection of Target Copy Number Variants and Gene Variants (SNV/Indels) in CLL Samples Using a Next-Generation Sequencing Panel
L. Georgieva

TT016. Utilization of Unique Molecular Barcodes in Next-Generation Sequencing Reveals Startling Differences in Library Chemistries in Read Depth and Allelic Frequencies
B. Anderson

TT017. Validation of a Novel Multiplex Assay for the Detection of 30 Fusion Genes in Leukemia Patients
L. Hamadeh

POSTER LISTING

TT018. Liquid Handling Methods Impact Insert Size and Overall Mate Pair Library Quality
E. Zimmerman Zuckerman

TT019. A Method for Absolute Quantification of Tumor Markers and Viral Genomes by Massive Parallel Sequencing of Cell-Free DNA
M.L. Gulley

TT020. Comparison of Traditional and Repeat-Primed PCR for Clinical Testing of Spinocerebellar Ataxia Types 1, 2, 3, 6, and 7
D. Kronemann

TT021. Comparison of Hemolysis in Circulating Cell-Free DNA Stabilization Tubes
T. Hailemariam

TT022. Low-Input Method for Cell-Free DNA Quality Assessment Improves Circulating Tumor DNA Next-Generation Sequencing Assay Performance
A. Lovejoy

TT023. Circulating Tumor DNA (ctDNA) Reference Materials for Commercial RT-PCR Assays
F. Tomson.

TT024. Experience at MSKCC with Several Clinical Assays for Multiplex and Single Variant Detection Using the Raindrop Picodroplet Digital PCR Technology on Clinical Samples
U. Patel

TT025. Evaluation and Comparison of Liquid Biopsy Reference Materials from Commercial Sources Using Oncomine Pan-Cancer Cell-Free Assay
K. Lea

TT026. Measuring Yield and Variation: Evaluation of Plasma Circulating Cell-Free DNA Extraction and Measurement Methods
J.E. Till

TT027. Amplified ccfDNA for Assay Development, Validation, and Proficiency Testing
Y. Konigshofer

TT028. Enhanced Performance of Targeted NGS Assays Using Single-Vial Amplification
S. Barua

TT029. Validation of the *EGFR* Uncommon Variants Multiplex ddPCR Assay for Blood-Based Testing in NSCLC
J. Reese

TT030. A Novel Approach for Identifying High Confidence Variants in Commercial Reference Materials
P. Hakimpour

TT031. Analytical Validation of BKN Panel with Integrated Molecular Barcoding to Identify Low-Frequency Variants
C. Weller

TT032. Improving the Reliability of Buccal Swab Germline Control Sampling with Rapid Cell Culture
E. Degelman

TT033. A Performance Evaluation of Microsatellite Instability and Mismatch Repair Testing in Endometrial Samples
S.R. Lewis

TT034. Pre-analytics Verification Studies for a Cell-Free DNA Collection Tube to Support Liquid Biopsy of NSCLC Patients Using Plasma-Based *EGFR* Molecular Testing
J. Shabbeer

POSTER LISTING

TT035. Validation and Implementation of a Modular Targeted Capture Assay for the Detection of Clinically Significant Molecular Oncology Alterations
A.J. Kuo

TT036. Concordance Testing of Software to Automate Determination of Microsatellite Instability Status
K. Oostdik

TT037. Validation of a Custom Pediatric Cancer Fusion Sequencing Assay in Keeping with AMP/CAP Guidelines
A.J. Church

TT038. Sandwich High-Resolution Melting Analysis: A Fast Sensitive ALK Fusion Variants Detection and Auto-genotyping Assay
M. Li

TT039. nRichDX Revolution Instrument and cfDNA Isolation Kit for Extraction of cfDNA from Large Plasma and Urine Sample Volumes Improves Yield of Rare Targets
R.S. Creager

TT040. Establishing the Sensitivity, Specificity, Interlaboratory Reproducibility, and Analytical Limit of Detection of the UltraSEEK Liquid Biopsy Application Using Well-Defined Seraseq Reference Materials
D.J. Demetrick

TT041. Evaluation of the Asuragen Amplidex PCR/CE HTT Kit: A User Laboratory Experience
C.C. Eno

TT042. A Versatile DNA Library Preparation Workflow for Multiple Applications
M. Hong

TT043. Precision and Robustness of the PAXgene Blood ccfDNA Workflow
T. Krenz

TT044. Assessment of the nRichDX Revolution Instrument and Isolation Kit for Cell-Free DNA Extraction from Liquid Biopsy
E.G., Hughes

TT045. Evaluation of a Cartridge-Based Assay to Assess Microsatellite Instability from FFPE Colorectal Cancer Tissues
A.E. Mindiola-Romero

TT046. Implementation of an Automated Illumina TruSight Tumor 170 Workflow with the Biomek NXP Span8 Liquid Handler
S.j. Deharvengt

TT047. Comparative Purification Methodologies and Synthetic Long-Read Sequencing for Fecal Microbiome Identification
D. Wieczorek

TT048. High-Throughput Semi-automated RNA Extraction from White Blood Cells Using the Hamilton STAR and Promega SimplyRNA
D. Devine

TT049. A Single-Platform Technology for Proteogenetic Biomarker Analysis in Oncology: Complementary Protein and RNA Quantification Relevant to Targeted and Immunotherapies in Non-small Cell Lung Cancer
G.J. Latham

TT050. Evaluation of Illumina TSO500 Performance in Clinically Significant Sample Types and Input Levels
A. Beams

TT051. Iso-Seq Resolves and Identifies Novel and Aberrant Gene Transcripts Resulting from Complex Genomic Alterations in a Patient-centric Cancer Protocol
V. Magrini

POSTER LISTING

TT052. Highly Multiplexed, Sequencing-Based Genotyping in Human Samples Can Discriminate Sample Identity
S. Bowman

TT053. A Comparison of Commercial Extraction Kits for the Isolation of Total RNA from FFPE for RNA-Seq NGS Testing
W. Song

TT054. Comparing DNA Extraction Methods for the LymphoTrack IVD TRG Assay
M. Kaminsky

TT055. Digital Methylation-Specific Multiplex Ligation-Dependent Probe Amplification: A Novel MLPA-Based Technique for Assessing Promoter Methylation Status in Cancer
J. Smout

TT056. Development and Validation of a Next-Generation Sequencing Assay to Evaluate T-Cell Diversity in a CAP-Accredited, CLIA-Certified laboratory
J.B. Williamson

TT057. Evaluation of an Alternative Fragmentation Method in High-Throughput NGS Sample Testing of Minimal Residual Disease in Hematological Malignancies
Y. Huang

TT058. A Novel Approach to Next-Generation Sequencing-Based Assessment of T-cell Clonality
D.A. Oldridge

TT059. Mutation Profiling by Next-Generation Sequencing in Low-Yield DNA *Intraocular Liquid Biopsies: A Case Series*
J. Hirschhorn

TT060. Development and Integration of Clarity LIMS in a Clinical Molecular Laboratory
C. Burnes

TT061. Withdrawn

TT062. Optimization of Library Preparation for NGS: Memorial Healthcare System Archer VariantPlex Solid Tumor Implementation.
B.E. Montoya

TT063. LabChip GX Touch microfluidics technology to assess RNA quality for the Illumina TruSight Tumor 170 Assay
S.J. Deharvengt

TT064. Proteomic Analysis from Whole Blood Collected in LBgard Blood Tubes
J.M. Vasquez

TT065. Withdrawn

TT066. Variants Reported by Tumor-Only Clinical Oncology NGS Testing Are Frequently Found in the Germline of Pediatric Patients
A. Saeed

TT067. Improving Quantification of DNA in the Presence of Both Double- and Single-Stranded Forms
F. Ye

TT068. Assessment of Pooled Plasma as Reference Material for Quality Assurance of ctDNA Assays
J. Doshi

TT069. Analytical Performance of TruSight Oncology 500: Detection of Small Nucleotide Variants, Gene Amplifications, Fusions and Splice Variants from Highly Multiplexed Libraries Sequenced on the NovaSeq
D.M. Chou

TT070. Polymerase Chain Reaction Directly from Whole Blood and Dry Blood Spots after NaOH Treatment
F. Ye

TT071. EXaCT-2: Augmented Whole Exome Sequencing Optimized for Clinical Testing in Oncology
D.C. Hassane

TT072. Dissimilarity Score (DisScore): Identifying Potential Discordance between Anatomic Pathology and Mutation Landscape in the Evaluation of Clinical Sequencing as Part of a Molecular Tumor Board
G.T. Gurda

AUTHOR LISTING

Index

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

AUTHOR LISTING

nanoString®

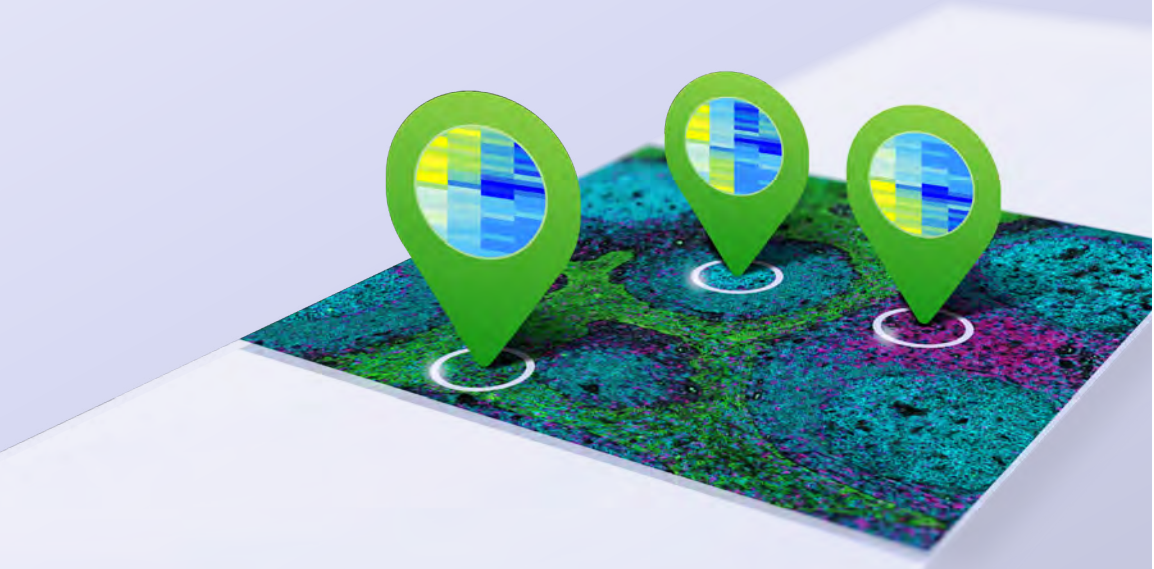
Map the tumor microenvironment

Introducing GeoMx™ Digital Spatial Profiler
Your GPS for immuno-oncology

Quantify and locate up to 1000 RNA or 96 protein targets on a single slide with no tissue loss.

Stop by NanoString booth #38

EXPO INFORMATION



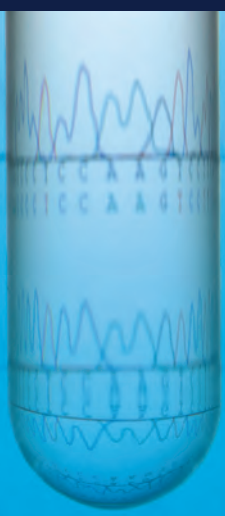
SEP 2019 MK1945

UCSF Center for Next-Gen Precision Diagnostics

UNIVERSITY OF CALIFORNIA, SAN FRANCISCO

EXPO INFORMATION

Novel genetic sequencing to diagnose neurological infections



VISIT US IN BOOTH 3050 to learn about the UCSF mNGS test to identify rare pathogens causing encephalitis and meningitis

- Eliminate unnecessary tests
- Accelerate time to treatment
- Guide therapy with appropriate antibiotics
- Reassure patients and their families with a clear diagnosis

415.502.2632 ▪ NGDx@ucsf.edu
nextgendiagnostics.ucsf.edu

Hear one of UCSF's leading scientists in metagenomic sequencing

Charles Chiu, MD, PhD
Metagenomics in Prime Time
Friday, Nov. 8 ▪ 10:45 am – 12:15 pm
Rooms 314–317

Win an Amazon Echo Show!

Scan your badge at Booth 3050 to be entered to win.

GENERAL INFORMATION

Explore the Expo Hall

The **AMP Expo Hall** is a cornerstone of the AMP Annual Meeting, presenting attendees with the opportunity to learn about the latest technology, innovation, and patient care improvements. When planning your time at the AMP 2019 Meeting & Expo, be sure to check out all that our expo hall has to offer! Our international exhibitors are marked with next to their name.

Meet the AMP 2019 Exhibitors

Explore the AMP Expo Hall and meet nearly 180 exhibiting companies! Take a few moments to peruse the list of exhibitors found on page 194. You can also read about this year's exhibitors in the meeting program on page 196 or the Mobile App.

AMP 2019 Welcome Reception in the Expo Hall

Supported by QIAGEN

Join us for the Welcome Reception in the AMP Expo Hall, supported by QIAGEN on Thursday 5:45pm – 7:00pm as we celebrate AMP's 25th Anniversary and *JMD's* 20th Anniversary. This event is open to all AMP registrants and exhibitors.

Preview the Abstracts & Plan your Poster Viewing

Check out the scientific posters which are sure to educate you on the latest and most innovative developments in the field! Refer to the Exhibit Hall Map on page 193 for poster locations.

Innovation Spotlight Stage

The Innovation Spotlight Stages 1 & 2, located centrally in the Expo Hall are a great opportunity to check out AMP exhibiting companies presenting leading edge products, services, or emerging innovation through "Ted-Talk like" presentations right on the show floor. In addition, attendees can catch AMP led presentations including "Meet the Authors". Innovation Spotlights are open to all meeting registrants and seating will be on a first come, first served basis.

AMP Central

AMP's booth in the Expo Hall is the perfect place for AMP members looking to network and attendees who are interested in learning more about all of what AMP does throughout the year.

General Lunches

Lunches will be served in the Expo Hall, giving you an opportunity to explore, learn about new products, and continue building on relationships you have made earlier in the meeting.

Networking Corner/Speed Networking

Sponsored by the Membership Affairs Committee

AMP is a great place to meet, share ideas, and explore new opportunities. Join the us at the Networking Corner to build new connections and network with the AMP community. You might find a new boss, collaborator, employee, troubleshooter, mentor, scientist, enthusiast, inspiration, advocate, motivator, travel guide in a new city, admirer, colleague, or just a new friend. During lunch on Friday (12:30 – 1:00 PM) and Saturday (12:30 – 1:00 PM), this space will feature speed networking sessions. Speed networking is simply a format to encourage greater interaction. The key is to come, start a conversation, then connect and follow up after. All you need to bring is your business cards and a willingness to meet someone new.

CONVENTION CENTER

Expo Hours & Dates

Thursday, November 7

11:30am – 12:45pm | General Lunch - Visit Expo Hall and View Posters (Award Judging & General Viewing)

- **Networking Lunches:** Please see lunch descriptions in the "Highlights & General Information" section of the Program Book, Pages 19-20.
- **Innovation Spotlight Schedule:** See Schedule on Mobile App and by each stage located in the Expo Hall.

2:00pm – 3:45pm | Coffee Break - Visit Expo Hall, AMP Central and View Posters

- **AMP Central Activities:** Technologist Mixer
- **Innovation Spotlight Schedule:** See Schedule on Mobile App and by each stage located in the Expo Hall.

5:45pm – 7:00pm | Welcome Reception in the Expo Hall *(Supported by QIAGEN)*

- **AMP Central Activities:** Celebrate AMP's New Vision

Friday, November 8

9:45am – 10:45am | Coffee Break

- **Innovation Spotlight Schedule:** See Schedule on Mobile App and by each stage located in the Expo Hall.

12:15am – 1:30pm | General Lunch - Visit Exhibit Hall and View Even-numbered Posters

- **Networking Lunches:** Please see lunch descriptions in the "Highlights & General Information" section of the Program Book, Pages 19-20.
- **AMP Central Activities:** Education Showcase
- **Innovation Spotlight Schedule:** See Schedule on Mobile App and by each stage located in the Expo Hall.
- **Speed Networking:** Please visit the Networking Corner in the Expo Hall from 12:30pm - 1:00pm. Open to all registered attendees.

2:45pm – 4:00pm | Coffee Break - Visit Exhibit Hall, AMP Central (Schedule) and View Posters

- **AMP Central Activities:** Get Involved with AMP! AMP Committee "Meet & Greet" Event
- **Innovation Spotlight Schedule:** See Schedule on Mobile App and by each stage located in the Expo Hall.

Saturday, November 9

9:45am – 10:45am | Coffee Break - Visit Exhibit Hall, AMP Central (Schedule) and View Odd-numbered Posters

12:15pm – 1:30pm | General Lunch

- **AMP Central Activities:** "Meet & Greet" with the JMD Editor-in-Chief
- **Innovation Spotlight Schedule:** See Schedule on Mobile App and by each stage located in the Expo Hall.
- **Speed Networking:** Please visit the Networking Corner in the Expo Hall from 12:30pm – 1:00pm. Open to all registered attendees.

INNOVATION SPOTLIGHT

Stage Schedule

This year's Innovation Spotlight Stages will continue to provide a unique opportunity for exhibiting companies to showcase products or services and cutting-edge AMP produced content. The TWO Innovation Spotlight Stages are located in the main cross aisles on the back and right corners of the Expo Hall. Innovation Spotlight presentations are open to all Meeting Registrants and seating will be on a first come, first served basis. Please see complete schedule and descriptions below.

◆**Thursday, November 7**

12:00pm - 12:30pm ***Stage 1*** ***Hosted by Training & Education Committee***

New AMP Educational Content

Speakers: Erin Graf, Susan Hsiao, Cinthya Zepeda Mendoza, and Preeti Pancholi

AMP Education and the AMP Training and Education Committee are committed to bringing the most relevant and useful content to our members and extended audience. This includes AMP certificate programs (self-paced thematically bundled webinars designed to help you develop knowledge and skills needed for success in molecular pathology and diagnostics), the AMP Horizons Series (forward-looking information about emerging science and technology that will likely soon impact the practice of molecular pathology) and other initiatives. Join us at the Innovation Stage where we'll showcase new AMP Education initiatives.

Attendees will receive coupon codes for some of the AMP Programs presented.

◆**Thursday, November 7**

12:00pm - 12:30pm ***Stage 2*** ***Hosted by SOPHiA Genetics***

Accurate detection of CNVs and gene amplifications in tumor samples

Speaker: Emily Paul, PhD

Description: There are incredible challenges faced when looking at the gene amplifications on somatic NGS-based applications as low tumor content weakens the coverage signal and FFPE sample degradation increases coverage noise. Given these criteria, the utmost precision in noise filtering and analysis is required. SOPHiA AI is able to identify Copy Number Variations (CNVs) routinely in a variety of solutions, ranging from targeted, germline applications to large, complex, somatic ones. This presentation will provide an overview of key concepts in CNV detection and explore analytical technologies that allow to overcome limitations and reach advanced performance.

◆**Thursday, November 7**

2:15pm - 2:45pm ***Stage 1*** ***Hosted by Golden Helix***

State of the Art Clinical Copy Number Variant Analysis in Next-Gen Sequencing Data: Gene Panels, Whole Exome, Whole Genome

Copy Number Variations (CNVs) are associated with a variety of genetic disorders, including autoimmune diseases, autism, and cancer. Golden Helix has developed an industry-leading CNV calling solution, called VS-CNV, which enables clinicians and researchers to detect CNVs ranging from small single exon events to large chromosomal deletions

INNOVATION SPOTLIGHT STAGE SCHEDULE

and duplications, removing the need for additional assays such as MLPA. The solution also allows clinicians to annotate CNVs against a wide array of useful data sources and perform filtering based on these annotations to obtain a small set of clinically relevant variations. In this spotlight, Golden Helix President & CEO, Andreas Scherer, Ph.D., and VP of Product & Engineering, Gabe Rudy, will discuss VS-CNV's analysis capabilities with a focus on the application of these various CNV annotations for filtering false positive and clinically irrelevant CNVs. The talk will also include a discussion of CNV interpretation in accordance with the AMP guidelines for the interpretation of somatic variants.

◆**Thursday, November 7**
2:15pm - 2:45pm ***Stage 2*** ***Hosted by New England Biolabs***

Enabling the Next Generation of Diagnostics with Enzyme Design and Control
Nucleic acid enzymes have long powered the chemistries of molecular diagnostics, and as the field moves to rapid POC and field settings, new demands are placed on DNA polymerases, reverse transcriptases, and other key enzymes. Through protein engineering, discovery, and novel mechanisms for control of enzymatic activities, New England Biolabs can provide unique reagents, customizable formats, and solutions to enable this new generation of diagnostic applications. Methods and reagents for isothermal amplification and RT-qPCR can benefit from enzyme innovation, and we will present how our approach to building better tools has benefited both core and developing applications of molecular diagnostics.

◆**Thursday, November 7**
3:00pm - 3:30pm ***Stage 1*** ***Hosted by Illumina***

Comprehensive Genomic Profiling is becoming a new Standard-of-Care in Oncology
Speaker: Phil Febbo, Chief Medical Officer, Illumina
The value behind a comprehensive assessment of the genomic alterations in a tumor has been consistently increasing with the availability of new therapeutic agents and better predictability of response. The regulatory environment and reimbursement for this type of assay evolved drastically over the last few years. We will discuss the value of adopting comprehensive genomic profiling in today's oncology care.

◆**Thursday, November 7**
3:00pm - 3:30pm ***Stage 2*** ***Hosted by Economic Affairs Committee***

Consistent Testing Terminology: Eliminating Patient Confusion and Facilitating Access
Speaker: Nikki Martin, LUNGevity; Lisa Schlager, Facing Our Risk of Cancer Empowered (FORCE)
There are more than 20 terms that can be used to describe comprehensive biomarker testing to patients such as genetic testing, germline testing, somatic testing, genomic testing, molecular testing, molecular profiling, tumor profiling, mutational testing, genotyping, etc. The patient advocacy community has been working with professional societies and industry to align around the use of consistent testing terminology when communicating with patients. These efforts will help eliminate confusion around the testing required after diagnosis. Learn from two patient advocacy groups about the confusion patients face regarding testing terminology, and the collaborative effort to identify one, two or three testing terms to be used consistently across all cancer types.

INNOVATION SPOTLIGHT STAGE SCHEDULE

◆**Friday, November 8**
10:00am - 10:30am ***Stage 1*** ***Hosted by Training & Education Committee***

Resources for the Next Generation of Technologists

The goal of this presentation is to help you to progress in your career by:

- Providing resources for Continuing Education and improvement.
- Outlining paths for Molecular certification.
- Describing opportunities and paths for advancement.

We will highlight the newly updated "Laboratory Careers in Molecular Pathology" page on the AMP website.

◆**Friday, November 8**
10:00am - 10:30am ***Stage 2*** ***Hosted by Novartis Pharmaceuticals Corporation***

Novartis Innovation Spotlight

Join us as Dr Jean Lopategui discusses PIK3CA mutations in HR+/HER2- advanced breast cancer and how to detect them.

◆**Friday, November 8**
12:45pm - 1:15pm ***Stage 1*** ***Hosted by Bayer***

Testing Methods to Identify NTRK Gene Fusions Including NGS, FISH, and IHC

Faculty Presenter Michelle Shiller, DO, AP/CP, MGP Co-Director Cancer Genetics Baylor Sammons Cancer Center Molecular Pathologist-PathGroup/Pathologist Biomedical Laboratories A tumor's underlying genomic profile has become increasingly important in oncology.

One genomic alteration of interest are NTRK gene fusions. This session will cover NTRK gene fusions, the frequency of NTRK gene fusions across many tumor types, and provide an overview of detecting NTRK gene fusions in cancer.

◆**Friday, November 8**
12:45pm - 1:15pm ***Stage 2*** ***Hosted by Clinical Practice Committee***

Meet the Authors: "Recommendations for Clinical CYP2C9 Genotyping Allele Selection: A Joint Recommendation of the Association for Molecular Pathology and College of American Pathologists"

Speakers: Victoria M. Pratt, Larisa H. Cavallari, Andria L. Del Tredici, Houda Hachad, Yuan Ji, Ann M. Moyer, Stuart A. Scott, Michelle Whirl-Carrillo, and Karen E. Weck

The Association for Molecular Pathology in collaboration with Clinical Pharmacogenetics Implementation Consortium and College of American Pathologists has developed and published a manuscript defining key attributes of CYP2C9 alleles and describes a recommended minimum set of variants that should be included in clinical pharmacogenomic genotyping assays. This manuscript appears in the September 2019 edition of JMD. Don't miss a great opportunity to talk to the authors and ask questions.

INNOVATION SPOTLIGHT STAGE SCHEDULE

•Friday, November 8

2:45pm - 3:15pm ***Stage 2*** ***Hosted by Illumina***

Enabling Comprehensive Genomic Profiling from FFPE & liquid biopsy samples on a single high-throughput Sequencing platform

Speakers: Brandon Kocher, Ph.D, Senior Product Manager, Oncology, Illumina; Brandon Selby, Senior Product Manager, Oncology, Illumina

Dr. Kocher will provide an overview of how Illumina plans to enable comprehensive genomic profiling from circulating tumor DNA.

Mr. Selby will discuss how Illumina will enable high-throughput comprehensive genomic profiling.

•Saturday, November 9

10:00am - 10:30am ***Stage 1*** ***Hosted by Golden Helix***

Clinical Variant Analysis: Applying the AMP & ACMG Guidelines in the Clinical Practice

VSClinical enables the interpretation of both somatic and germline variants following the AMP & ACMG Guidelines, respectively. By incorporating new algorithms and annotation sources, detailed variant scoring, classification, and interpretation can occur right within VarSeq without the need for additional, external tools or resources. These capabilities are designed to improved throughput while allowing the lab to maintain consistent quality. Join Golden Helix President & CEO, Andreas Scherer, Ph.D., and VP of Product & Engineering, Gabe Rudy, in this spotlight to learn more about these powerful capabilities:

- Streamline germline variant interpretation using the ACMG scoring guidelines with automatic criteria recommendations and incorporated historical data
- Quickly determine the oncogenicity of somatic mutations using our automated oncogenicity scoring system
- Apply the AMP Tiers to the available clinical evidence for Drug Sensitivity, Drug Response, Prognostics and Diagnostics
- Develop a lab-specific knowledgebase of interpretations that allow maximum re-use of interpretations and descriptions from one patient to the next
- Leverage the built-in Golden Helix CancerKB interpretation knowledgebase that covers many common genes and biomarkers
- Finalize your interpretation for a sample and compose the clinical report with the classified variants and their interpretation

•Saturday, November 9

10:00am - 10:30am ***Stage 2*** ***Hosted by Training & Education Committee***

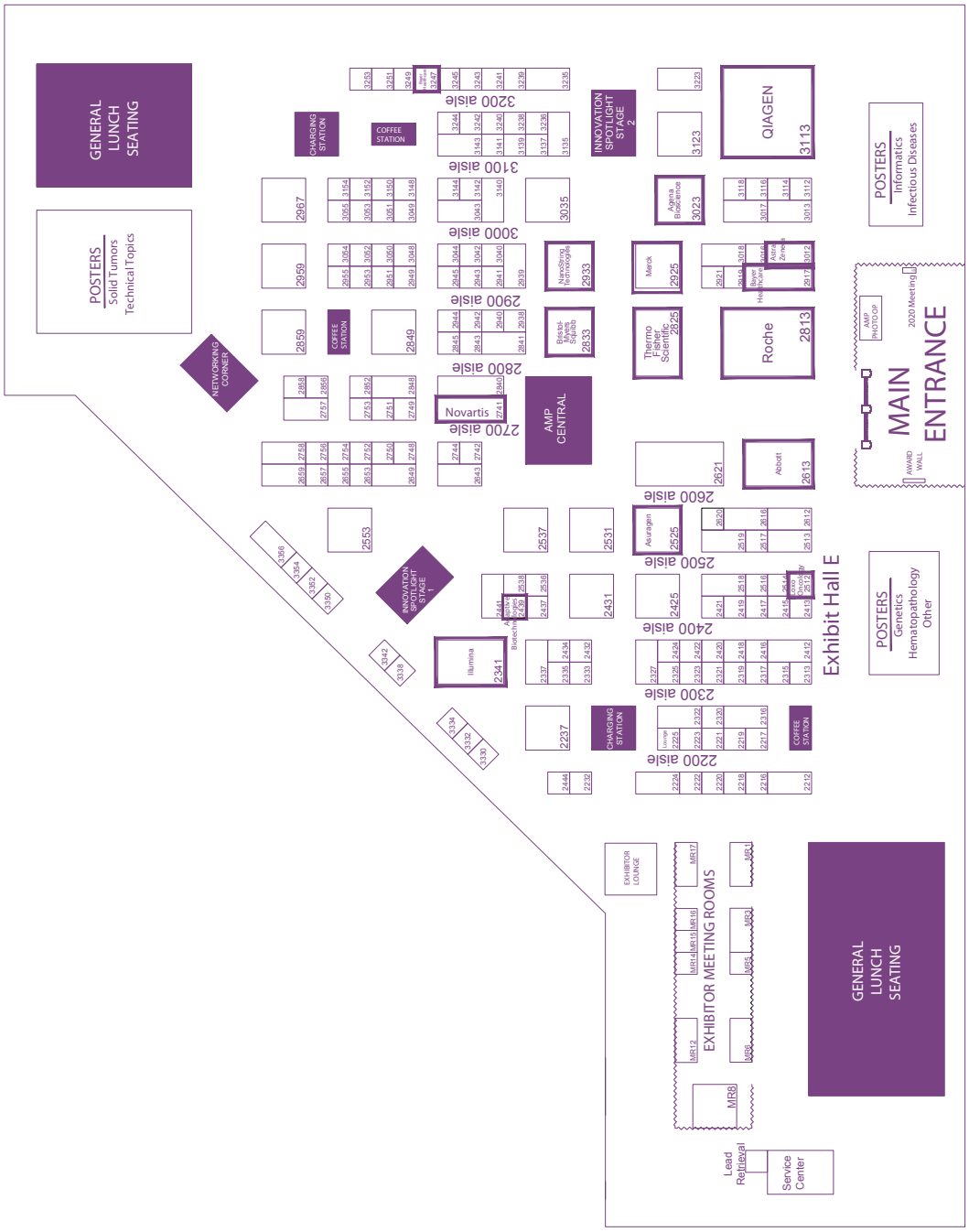
The AMP Educational Needs Survey: A Summation and Discussion

Speaker: Cecilia Yeung, MD, Chair, AMP Training & Education Committee

The AMP Training and Education Committee surveys AMP Membership every two years regarding their needs and preferences for the design and delivery of new educational content. Join the Chair of the AMP Training & Education Committee as she presents the results of the 2018 Educational Needs Survey. We also hope that you will join in on a discussion of your educational goals and ways that AMP Education and the Training and Education Committee can help you meet them.

CONVENTION CENTER

Floorplan



EXHIBITOR LISTING

By Alphabetical Order

10x Genomics	2320
Abbott Miolecular*	**2613**
Adaptive Biotechnologies*	**2439**
Advanced Data Systems Corporation	3354
Agena Bioscience*	**3023**
Agilent	2237
American Proficiency Institute	2538
Amgen	3051
Anpac Biomedical Tecnology, Co. Ltd.	2325
Applied BioCode	2431
Applied Spectral Imaging	3112
Apto-Gen	2218
Arc Bio, LLC	2951
ArcherDX	2553
ARUP Laboratories	3114
AstraZeneca*	**3012**
Asuragen*	**2525**
ATCC	2852
AutoGen, Inc.	2756
B. Braun CeGaT, LLC	2751
Bangs Laboratories	2437
Bayer	3247
Bayer Healthcare*	**2917**
Beckman Coulter Life Sciences	2620
Biocartis	2840
Biocept	3239
BioDot, Inc.	3240
BioID Genomics, Inc.	3236
BIOLYPH LLC	3223
BioMab Inc.	3040
Biomatrica, Inc.	3135
Bionano Genomics	3044
Bio-Rad Laboratories, Inc.	2531
BioView (USA) Inc.	2514
BIT Group	2536
Bristol Myers Squibb*	**2833**
Cancer Genomics Consortium	3142
Caris Life Sciences	2316
Cepheid	2758
Ceres Nanosciences	3332
ChromaCode	2337
Cirrus Dx, inc.	2657
Clinical Omics	2420
Cofactor Genomics	2319
College of American Pathologists	3350
College of American Pathologists Periodicals	2418
COMBiNATi	2417
Contextual Genomics	2653
COPAN Diagnostics, Inc.	3152
Coriell Institute for Medical Research	2317
Covaris Inc	2942
CSI Laboratories	3049
DiaCarta	2333
DiaSorin Molecular	2212
Discovery Life Sciences	2959
EdgeBio	2421
ELITechGroup Inc. Molecular Diagnostics	2753
Elsevier	3055
Endeavor Business Media	2754
EntroGen	2515
Epigenomics	2519
Eppendorf North America	3116
Exact Diagnostics	2416
EZLife Bio Inc.	2516
Fabric Genomics	2224
FluxErgy	3137
FORMULATRIX	2422
Foundation Medicine, Inc	2322
GenapSys Inc.	3244
Genetic Signatures	2222
Genetron Health (Beijing) Co. Ltd.	3251
GENEWIZ	2953
GenMark Diagnostics	2748
GenomeWeb	2413
GenomOncology	2434
Genosity	2517
GenPath Diagnostics, BioReference Laboratories	2219
Golden Helix	2856
GSPMC	2750
Hamilton Company	3143
Health Decisions	3150
Hologic*	**2621**
Horizon Discovery	2327

Corporate Partners

EXHIBITOR LISTING

Illumina*	**2341**
Insilixa	3052
Integrated DNA Technologies	2315
Interpace Diagnostics	2659
Invivoscribe	2849
Karius	2419
LABWARE	2335
LGC, Biosearch Technologies	3330
Loxo Oncology*	**2512**
LRE Medical GmbH	3334
Luminex	2412
Maine Molecular Quality Controls, Inc.	2919
Market Ready Rx	2843
Medical Lab Management	2424
Menarini Silicon Biosystems	2425
Merck*	**2925**
Meridian BioScience Inc.	2757
MetaSystems Group, Inc.	3048
Michigan Medicine Laboratories (MLabs)	3243
Miltenyi Biotec GmbH	3154
Mission Bio	2749
Molecular Health	2323
MolecularMatch, Inc.	3235
MRC-Holland	2845
NanoString Technologies*	**2933**
NeoGenomics Laboratories	2941
NeuMoDx Molecular	2859
New England Biolabs	3342
Norgen Biotek Corp.	3053
Novartis*	**2741**
NovoPath, Inc.	2943
nRichDx	2655
NuProbe	3253
NVIGEN Inc.	2752
Omega Bio-tek	3140
Omni International	2415
Opentrons Labworks	3241
Ovation.io	2232
Oxford Gene Technology	3144
Paragon Genomics	2921
PerkinElmer	2616
Personal Genome Diagnostics	3123
Philips	2537
PierianDx	2441
Pillar Biosciences Inc.	2649
PreAnalytiX	3118
Precision System Science USA, inc.	3338
Promega Corporation	3035
PSOMAGEN, INC.	3054
Purigen Biosystems, Inc.	3139
Q2 Solutions | EA Genomics	2217
QIAGEN*	**3113**
Quidel Corporation	3013
Qvella Corporation	2841
RareCyte, Inc	2949
ResearchDx	2967
Rheonix	2518
Roche*	**2813**
SCC Soft Computer	2432
Seattle Genetics	2742
SeraCare Life Sciences	2612
SmartGene	2955
SoftGenetics	2939
SOPHiA GENETICS	2643
SpeeDx	3148
Staff Icons- A Biotech Recruitment Company	2945
STEMCELL Technologies Inc	2313
Streck	3043
Sunquest Information Systems	3018
Taigen Bioscience Corporation	3141
Takara Bio USA	2216
Texas Children's Hospital	2223
The Jackson Laboratory	3016
The Journal Precision Medicine	3042
The Lab People, Inc.	3238
The Pathologist	2444
Thermo Fisher Scientific*	**2825**
TriLink BioTechnologies	2744
Truckee Applied Genomics LLC	2221
Twist Bioscience	2944
UCSF Center for Next-Gen Precision Diagnostics	3050
UPMC Genome Center	3352
Variantyx Inc	2938
Vela Diagnostics	3356
WellSIM Biomedical Technologies, Inc.	2321
XCR Diagnostics, Inc.	2848
XIFIN, Inc.	2940
YouSeq Ltd	3245
ZeptoMetrix Corporation	3017
Zymo Research Corp.	2858

Corporate Partners

EXHIBITOR DESCRIPTIONS

By Alphabetical Order

10x Genomics
Booth #: 2320
www.10xgenomics.com
10x Genomics builds solutions to interrogate biological systems at a resolution and scale that matches the complexity of biology. Our rapidly expanding suite of products, which include instruments, consumables, and software, have enabled customers to make fundamental discoveries across multiple research areas, including cancer, immunology, and neuroscience.

Abbott Molecular
CORPORATE PARTNER
Booth #: 2613
www.abbott.com
As a leader in molecular diagnostics and the analysis of DNA, RNA, and proteins at the molecular level, Abbott Molecular has over 1000 employees dedicated to manufacturing and marketing more than 450 products worldwide in more than 130 countries. We are committed to advancing molecular testing solutions that guide life's most profound decisions.

AccuGenomics, Inc
Booth #: 2220
AccuGenomics manufactures custom Mixtures of Internal Standards (MIS™) that enable new levels of scientific integrity and eliminates all false positives from any targeted NGS method. Our SNAQ technology provides the best in class Accuracy, Specificity,and Limits of Detection for measuring multiple targets by qPCR (SNAQ-PCR) and NGS (SNAQ-SEQ).

Treat patients right the first time!
Our Standards Your Quality

Adaptive Biotechnologies
CORPORATE PARTNER
Booth #: 2439
www.adaptivebiotech.com
Adaptive Biotechnologies is a commercial-stage biotech company focused on harnessing the inherent biology of the adaptive immune system to transform the diagnosis and treatment of disease. Our proprietary immune medicine platform reveals and translates the massive genetics of the adaptive immune system with scale, precision and speed to develop products in life sciences research, clinical diagnostics, and drug discovery.

Advanced Data Systems Corporation
Booth #: 3354
www.adsc.com/molecular-genetics-laboratory-billing
MedicsRCM for genetics laboratories supports a nearly 100% success rate on first attempt clearinghouse claims. We've coded +100 different CGX/PGX/genetics panels and ensure claims are at maximum value. In/out-of-network EDI/ claim tracking/denial management; proactive denial alerts. PAMA/comprehensive financial/ operational analytics/KPIs. LIS integrations. Sales activity reports/portal. Our MedicsPremier system is available if your own system on your server or in our cloud is preferred.

Agena Bioscience
CORPORATE PARTNER
Booth #: 3023
We Empower Precision Medicine. Agena Bioscience enables clinical laboratories worldwide to deliver affordable targeted genomic testing. Our easy to use mid-plex diagnostic platforms deliver fast, accurate and actionable results, to aid in clinical decision making and improve laboratory economics..

Agilent
Booth #: 2237
www.agilent.com
Agilent is a leader in life sciences, diagnostics and applied chemical markets. The company provides laboratories worldwide with instruments, services, consumables, applications and expertise, enabling customers to gain the insights they seek. Agilent's expertise and trusted collaboration give them the highest confidence in our solutions.

American Proficiency Institute
Booth #: 2538
www.api-pt.com
American Proficiency Institute (API), the leading innovator in proficiency testing programs, serves over 20,000 clinical laboratories. API offers a wide number of proficiency testing programs (including molecular), automated result transmission, and free continuing education. When it comes to proficiency testing, reliability is everything and API is fully committed to supporting you with technical expertise and prompt, personal service.

EXHIBITOR DESCRIPTIONS

Amgen
Booth #: 3051
www.amgen.com
Amgen is committed to unlocking the potential of biology for patients suffering from serious illnesses by discovering, developing, manufacturing, and delivering innovative human therapeutics. A biotechnology pioneer since 1980, Amgen has reached millions of patients around the world and is developing a pipeline of medicines with breakaway potential.

AMP Central
Booth #: See Expo Floorplan
www.amp.org
Visit AMP's booth in the Exhibit Hall, centrally located just past the main entrance to the hall. AMP Central features unique programming including career networking opportunities and the chance to meet current committee members. AMP Central is the best place to learn about all that AMP does and find out how you can get involved! For details on AMP Central Events, see event listings throughout this program.

Anpac Biomedical Tecnology, Co. Ltd.
Booth #: 2325
www.anpacbio.com
Anpac Bio's proprietary "Cancer Differentiation Analysis" (CDA) medical devices and liquid biopsy screening services effectively reinvent early cancer detection. Comprehensive research validity data from 150,000 cases (to date) indicate CDA far exceeds existing revealing a sensitivity and specificity rate range of 80%-95% for over 26 different types of cancer from a single, standard blood test. www.AnpacBio.com.

Applied BioCode
Booth #: 2431
www.apbiocode.com
Applied BioCode® is excited to present Gastrointestinal Pathogen (GPP) syndromic panel for the 17 common pathogenic bacteria, viruses, and parasites tests. The automated high throughput BioCode® MDx 3000 system can process up to 188 GPP samples in an 8-hour shift. The system not only improves laboratory workflow efficiency, but also provide a comprehensive test panel at lower overall cost.

Applied Spectral Imaging
Booth #: 3112
www.spectral-imaging.com/
ASI is a global leader in biomedical imaging with a comprehensive product portfolio and a global distribution footprint. The company's technology, powered by GenASIs, enables Pathology, Cytogenetics and Research laboratories to provide advanced diagnostics to patients. ASI has a wide portfolio of dedicated solutions for Brightfield, Fluorescence and Spectral imaging and analysis.

Apto-Gen
Booth #: 2218
www.apto-gen.com
Apto-Gen develops and provides high-performance, bespoke molecular biology and PCR/qPCR reagents to the healthcare and biotechnology markets to improve detection of DNA and RNA for more accurate diagnoses. For example, we provide oven and freeze-drying compatible enzymes and master-mixes for direct incorporation into molecular tests.

Arc Bio, LLC
Booth #: 2951
www.arcbio.com
Arc Bio is revolutionizing pathogen detection by developing novel NGS solutions that allow for fast, precise, and cost-effective analysis. Our mission is to transform how infectious disease is diagnosed, treated, and managed. The Galileo™ product line arms physicians and laboratorians with an entirely new standard for infectious disease detection through an integrated set of easy-to-use, cutting-edge genomic tools.

ArcherDX
Booth #: 2553
www.archerdx.com
ArcherDX advances molecular pathology with a robust technology platform for NGS-based genetic mutation detection. By combining proprietary Anchored Multiplexed PCR (AMP™) chemistry in an easy-to-use, lyophilized format and powerful bioinformatics software, the Archer® platform dramatically enhances genetic mutation identification and discovery. ArcherDX provides oncology-focused research products and is pursuing regulatory approval for multiple companion diagnostic assays.

ARUP Laboratories
Booth #: 3114
www.aruplab.com
ARUP Laboratories is a national nonprofit and academic reference lab at the forefront of diagnostic medicine. Our forward-thinking community of academic experts and consultants are here to empower our clients with the most current industry knowledge and unparalleled guidance. Visit aruplab.com for more information.

AstraZeneca
CORPORATE PARTNER
Booth #: 3012
AstraZeneca is a global, science-led biopharmaceutical company that focuses on the discovery, development and commercialization of prescription medicines, primarily for the treatment of diseases in three therapy areas – Oncology, Cardiovascular, Renal & Metabolism and Respiratory. The Company also is selectively active in the areas of autoimmunity, neuroscience and infection.

EXHIBITOR DESCRIPTIONS

Asuragen
CORPORATE PARTNER
Booth #: 2525
Asuragen is a molecular diagnostic company changing the way patients are treated in genetics and oncology. The quality, simplicity and sensitivity of its products brings precision medicine within reach. Asuragen's diagnostic systems, composed of proprietary chemistry and software, deliver powerful answers using broadly installed instrument platforms.

ATCC
Booth #: 2852
www.atcc.org
Scientific progress depends on a strong foundation of credibility. As the leading global provider of credible biological products including biological standards and reference materials, ATCC is committed to supporting the AMP community with standards and solutions needed to make incredible achievements in oncology and infectious disease testing, molecular assay development and microbiome research. Visit booth #2852 to discover more. www.atcc.org

AutoGen, Inc.
Booth #: 2756
www.AutoGen.com
AutoGen, a leader in the life sciences marketplace, is an organization that works to understand a lab's full workflow while identifying areas to improve efficiency and reduce costs within their nucleic acid extraction processes.

B. Braun CeGaT, LLC
Booth #: 2751
www.bbrauncegat.com
B. Braun CeGaT - Clinical genetic testing for a broad range of diseases. CAP/CLIA-accredited Laboratory with extensive experience developing next generation sequencing assays and clinical interpretation of genetic variations. Providing hundreds of multi-gene diagnostic panels including epilepsy, oncology, neurodegenerative, neuromuscular and eye diseases to determine molecular causes. Offering whole exome testing, tumor diagnostics and 700+ single-gene tests for targeted analyses.

Bangs Laboratories
Booth #: 2437
www.bangslabs.com
Manufacturer of magnetic, silica and polymer microparticles used as critical raw materials for clinical and molecular biology applications such as sample prep, nucleic acid isolation, sequencing and PCR.

Bayer
Booth #: 3247
www.bayer.us
Bayer is a global Life Sciences leader in cardiopulmonology, hematology, neurology, oncology and women's health. Building on a 150-year legacy in healthcare, Bayer is committed to improving patient lives by developing innovative therapies and delivering first-in-class educational and support programs to meet their needs. For more information, visit www.bayer.us.

Bayer Healthcare
CORPORATE PARTNER
Booth #: 2917
www.bayer.us.com
Bayer is a global Life Sciences leader in cardiopulmonology, hematology, neurology, oncology and women's health. Building on a 150-year legacy in healthcare, Bayer is committed to improving patient lives by developing innovative therapies and delivering first-in-class educational and support programs to meet their needs. For more information, visit www.bayer.us.

Beckman Coulter Life Sciences
Booth #: 2620
Beckman Coulter Life Sciences is dedicated to advancing and optimizing the laboratory. Biomek Genomic Workstations automate and simplify pipetting-intensive genomic workflows including extraction, qPCR/PCR setup, NGS library construction and microarray target prep. Our reagent portfolio, powered by SPRI technology—widely known as the science behind AMPure XP—includes kits for nucleic acid extraction from cells, tissue, blood, cfDNA, and FFPE.

Biocartis
Booth #: 2840
www.biocartis.com/us
Biocartis' proprietary MDx Idylla™ platform is a fully automated sample-to-result, PCR based system that offers accurate, highly reliable molecular information from virtually any biological sample in virtually any setting.
For more information, visit our website at www.biocartis.com/us

Biocept
Booth #: 3239
www.biocept.com
Biocept, Inc. is a molecular diagnostics company with commercialized blood-based assays for lung, breast, gastric, colorectal and prostate, ovarian, pancreatic, and melanoma cancers. Biocept's patented Target Selector™ liquid biopsy technology platform captures and analyzes tumor-associated molecular markers in both circulating tumor cells (CTCs) and in circulating tumor DNA (ctDNA).

EXHIBITOR DESCRIPTIONS

BioDot, Inc.
Booth #: 3240
BioDot develops automated, low volume dispensing systems for immuno-based and molecular diagnostics. The CellWriter Series workstations automate the cell dropping, probe dispensing, and hybridization processes for cytogenetic assays (FISH and Karyotyping). By utilizing our proprietary dispensing technology (the BioJet) to miniaturize traditional assay formats, BioDot maximizes efficiency and reliability while reducing assay costs.

BioID Genomics, Inc.
Booth #: 3236
www.bioidgenomics.com
BioID Genomics is a microbiology sequencing/ software company. RIDI™ 16S Microbial ID Kit is for the Illumina MiSeq. This RUO kit is used for whole blood, stool, wounds, urine or CSF. There is no need for expensive library preparation kits; pre-sequencer time is reduced to 3.5 hours for up to 96 samples. The kit includes library prep and automated bioinformatics.

BIOLYPH LLC
Booth #: 3223
www.BIOLYPH.com
BIOLYPH converts manufacturers' unstable reagents into Room Temperature stable, instantly rehydrating LyoSpheres™, providing years of shelf life and superior ease of use, reducing steps, errors, prep time, and manufacturing costs, and eliminating cold chain dependency. Please visit our booth to learn more about BIOLYPH's LyoSphere™ Technology and Complete Formulation, Stabilization, Lyophilization, and Packaging services.

BioMab Inc.
Booth #: 3040
www.biomabinc.com
BioMab, Inc. is an immune-based precision medicine company based in Taiwan. Our product portfolio features an automated circulating tumor cell (CTC) platform, including CTC enrichment kit , staining kit and instrument with prefilled cartridges to run 12 tests simultaneously. Natural killer cell activation and expansion kit is our pipeline product , targeting market for NK cell immunotherapy.

Biomatrica, Inc.
Booth #: 3135
www.biomatrica.com
As precision medicine becomes standard, Biomatrica provides sample collection products to enable scientific success and help more people find the answers they urgently need. Our products stabilize and protect critical biological material (including blood, saliva, and nucleic acids) at ambient temperature throughout collection, transport and long-term storage.

Bionano Genomics
Booth #: 3044
www.bionanogenomics.com
Bionano Genomics is a life sciences instrumentation company in the genome analysis space. The Company develops and markets the Saphyr system, a platform for ultra-sensitive and ultra-specific structural variation detection that enables researchers and clinicians to accelerate the search for new diagnostics and therapeutic targets and to streamline the study of changes in chromosomes.

Bio-Rad Laboratories, Inc.
Booth #: 2531
www.bio-rad.com
Bio-Rad is a global leader in developing, manufacturing, and marketing a broad range of innovative products for the life science research and clinical diagnostic markets. With a focus on quality and customer service for over 65 years, our products advance the discovery process and improve healthcare.

BioView (USA) Inc.
Booth #: 2514
www.bioview.com
BioView provides automated cell image analysis platforms for clinical and research laboratories. BioView offers capabilities in FISH, Circulating Tumor Cells, whole slide imaging, Digital tissue matching and computer-aided quantitative IHC scoring. Our customers leverage offline analysis and Web-based applications to collaborate and explore new business opportunities. BioView has received FDA clearance and CE Marking for a multitude of applications

BIT Group
Booth #: 2536
www.BIT-Group.com
BIT designs/develops, manufactures and services high-performance IVD and medical devices for our clients. With over 40 years of partnerships with organizations like Beckman, Siemens, and Abbott; BIT has a proven history of success in providing value to our clients. With locations in USA, Europe and China, BIT is the right local solution for your diagnostic automation requirements.

EXHIBITOR DESCRIPTIONS

Bristol Myers Squibb
CORPORATE PARTNER
Booth #: 2833
www.bms.com
Bristol-Myers Squibb is a global biopharmaceutical company focused on discovering, developing and delivering innovative medicines for patients with serious diseases. We are focused on helping patients in disease areas including oncology, cardiovascular, immunoscience and fibrosis. Each day, our employees work together for patients – it drives everything we do.

Cancer Genomics Consortium
Booth #: 3142
www.cancergenomics.org
The Cancer Genomics Consortium (CGC) is a membership-based organization committed to providing high-quality education and promoting best practices in clinical cancer genomics. The CGC has numerous collaborations and initiatives and welcomes new members and ideas. Join us August 2-5, 2020 for the 11th CGC Annual Meeting in Nashville, TN. cancergenomics.org

Caris Life Sciences
Booth #: 2316
www.carislifesciences.com
Caris Life Sciences® is a leading innovator in molecular science focused on fulfilling the promise of precision medicine through quality and innovation. The company's suite of market-leading molecular profiling offerings assess DNA, RNA and proteins to reveal a molecular blueprint that helps physicians and cancer patients make more precise and personalized treatment decisions. To learn more, please visit www.CarisLifeSciences.com.

Cepheid
Booth #: 2758
www.cepheid.com
Cepheid is dedicated to improving healthcare by developing, manufacturing, and marketing accurate yet easy-to-use molecular systems and tests. By automating highly complex and time-consuming manual procedures, the company's solutions deliver a better way to perform sophisticated genetic testing for organisms and genetic-based diseases. The company is focusing on those applications where accurate, rapid, and actionable test results are needed most.

Ceres Nanosciences
Booth #: 3332
Nanotrap® particles are engineered hydrogel particles that capture, concentrate, and preserve low abundance analystes from complex matrices. They are compatible with most downstream measurement or analysis techniques and enable the discovery or detection of analytes like pathogens, nucleic acids, proteins, hormones, extracellular vesicles, and small molecules. They are available in off-the-shelf formats or can be customized for your application.

ChromaCode
Booth #: 2337
www.chromacode.com
ChromaCode is redefining molecular testing through data science. ChromaCode's HDPCR™ multiplexing technology couples widely-used, low-cost chemistries with proprietary software to empower the global installed base of qPCR/dPCR instrumentation to perform multiplex testing at a very low cost. Using HDPCR™, ChromaCode is seeking to expand global access to multiplex testing, reduce healthcare costs, and provide solutions for unmet healthcare needs faster.

Cirrus Dx, inc.
Booth #: 2657
www.cirrusdx.com
The Next Generation of Molecular Infectious Disease Testing Solutions
CirrusDx is bringing diagnostic tools closer to the patient to counteract the challenge presented by antibiotic stewardship and empirical treatment. We are creating vertically integrated diagnostic solutions for UTIs and beyond, proper diagnostic tools that lead to proper treatment. Instrumentation, connectivity, and advanced methods to connect our laboratory to your practice.

Clinical Omics
Booth #: 2420
www.clinicalomics.com
Clinical OMICs is the leading source of practical insights for pathologists, clinicians, researchers, and scientists working to translate important findings across the broad range of "omics" technologies to deliver on the promise of molecular and precision medicine for patients.

Cofactor Genomics
Booth #: 2319
www.cofactorgenomics.com
Cofactor Genomics is a Predictive Immune Modeling company leveraging its experience as one of the first CAP-certified, clinical RNA sequencing laboratories to better characterize disease. Moving beyond isolated, single-analyte biomarkers, Cofactor's products create multidimensional biomarkers using Health Expression Models. Through their molecular, informatic, and database tools, Cofactor enables their partners to deliver more expedient, cost effective, and successful clinical trials.

EXHIBITOR DESCRIPTIONS

College of American Pathologists
Booth #: 3350
www.cap.org
As the world's largest organization of board-certified pathologists and leading provider of laboratory accreditation and proficiency testing programs, the College of American Pathologists (CAP) serves patients, pathologists, and the public by fostering and advocating excellence in the practice of pathology and laboratory medicine worldwide. For more information, read the 2018 CAP Annual Report at CAP.ORG.

College of American Pathologists Periodicals
Booth #: 2418
www.cap.org
The College of American Pathologists offers two monthly publications: CAP TODAY and the Archives of Pathology & Laboratory Medicine. CAP TODAY brings monthly business and medical news in the clinical laboratory. The Archives of Pathology & Laboratory Medicine is one of the best-read journals among pathologists and laboratory directors. Samples are available.

COMBiNATi
Booth #: 2417
www.combinati.com
COMBiNATi believes simplicity shouldn't require sacrificing robustness, quality or rigor – in fact, it should enable it. Our easy-to-use digital PCR platform offers absolute quantification to track disease-relevant biomarkers over time with high accuracy and precision. Comprised of a single instrument and a single consumable, COMBiNATi aims to democratize digital PCR for researchers all over the world.

Contextual Genomics
Booth #: 2653
www.contextualgenomics.com
Contextual Genomics' assays are engineered to detect mutations in cancer, and have been designed to be medically necessary, clinical grade (CAP, CLIA validated), and cost effective. Our tests are embedded with leading, proprietary molecular quality assurance tools, enabling laboratory partners to effectively support their cancer physicians and patients.

COPAN Diagnostics, Inc.
Booth #: 3152
www.copanusa.net
COPAN's collaborative approach to innovation in pre-analytics has resulted in the original FLOQSwabs™, ESwab™, FecalSwab™, eNAT™, MSwab™, UTM™ and full laboratory automation. COPAN's collection and preservation systems have proven to advance the quality of traditional and contemporary microbiology assays, particularly for molecular applications. Our automation includes specimen processing, smart incubation, digital imaging, and algorithms.

Coriell Institute for Medical Research
Booth #: 2317
www.coriell.org
Coriell Institute is a leading biorepository delivering a diverse range of unique biospecimens. The Institute is committed to the highest standard in cell line quality services, as well as unlocking the promise of induced pluripotent stem cells and their role in disease research and drug discovery. For more information, visit catalog.coriell.org.

Covaris Inc
Booth #: 2942
www.covaris.com
Covaris is the recognized industry leader in NGS, utilizing its patented Adaptive Focused Acoustics® (AFA®) technology for DNA fragmentation. AFA-energetics™ is also used for a wide range of sample preparation applications including FFPE and cfDNA extraction, chromatin shearing, proteomics, epigenomics, cell lysis, and compound management. Please visit www.covaris.com for more information.

CSI Laboratories
Booth #: 3049
www.csilaboratories.com
CSI Laboratories provides personalized, patient-focused cancer diagnostic testing for pathologists,community hospitals and oncologists. We offer flow cytometry, cytogenetic analysis, Fluorescence In-Situ Hybridization (FISH), immunohistochemistry, molecular genetics, next generation sequencing, and consultation services to hematopathology and surgical clients. CSI Labs is a CLIA-certified, COGcertified and CAP-accredited cancer reference laboratory based in Atlanta,GA.

DiaCarta
Booth #: 2333
www.diacarta.com
DiaCarta, a translational genomics and precision molecular diagnostics company, was established in 2011 to provide highly sensitive and advanced technologies that will improve the way molecular diagnostics and translational genomics impact healthcare treatment plans and the well-being of individuals around the world.

EXHIBITOR DESCRIPTIONS

DiaSorin Molecular
Booth #: 2212
www.molecular.diasorin.com
DiaSorin Molecular manufactures and distributes molecular diagnostic products worldwide helping laboratories to streamline workflow and improve patient management. Our Simplexa® molecular kits include HSV-1 & 2, Flu A/B & RSV, Bordetella, VZV, Group A Strep, Group B Strep, and C. difficile. Additionally, our menu includes over 60 primer pairs for laboratory developed tests.

Discovery Life Sciences
Booth #: 3049
www.dls.com
Discovery Life Sciences is a global market leader in biospecimen analysis, procurement, and distribution for the pharmaceutical, biotechnology, and diagnostics industries. Driven by science, the Discovery team engages with customers in an innovative, consultative approach to overcoming obstacles and reaching a faster end result. We are Science at your Service™.

Edge BioSystems
Booth #: 2421
www.edgebio.com
EdgeBio is a market leader in Sanger Sequencing workflow consumables. Along with our famous Dye Terminator Removal Kits, we have introduced a drop-in replacement for BigDye: BrilliantDye Sequencing Kits, requiring no changes in protocol, settings, calibration, or dye set. The only adjustment you'll need to make is learning how to deal with the improved value they bring to your lab.

ELITechGroup Inc. Molecular Diagnostics
Booth #: 2753
www.elitechgroup.com
ELITechGroup Inc. provides molecular diagnostic solutions for laboratories focused on specialty testing. With our ELITe InGenius® Sample-to-Result PCR platform, our comprehensive portfolio of assays and reagents and our in-depth technical support, ELITechGroup provides unprecedented efficiency for laboratory developed procedures. The ELITe InGenius combines automated extraction, PCR set up, thermal cycling and results interpretation for unparalleled ease of use and performance.

Elsevier
Booth #: 3055
www.elsevierhealth.com
Elsevier is a world-leading provider of information solutions that enhance the performance of science, health, and technology professionals, empowering them to make better decisions, and deliver better care.

Endeavor Business Media
Booth #: 2754
www.mlo-online.com
Celebrating 50 years, MLO is the premier publication for lab directors and managers. A multimedia resource, MLO delivers peer-reviewed articles, CE courses, lab management tips, regulatory updates, and new product reviews as well as CLR, the annual buyers guide. AMP attendees qualify for a free annual subscription at www.mlo-online.com/subscribe. Come see us at booth 2754!

EntroGen
Booth #: 2515
www.entrogen.com
EntroGen is a Los Angeles-based biotechnology company with a primary focus on molecular diagnostics in the areas of hematology and oncology. EntroGen has a growing commercial portfolio of real-time PCR and NGS based tests, with many of its products being used to guide and monitor targeted therapies for various malignancies.

Epigenomics
Booth #: 2519
www.epiprocolon.com
Epigenomics is a molecular diagnostics company focused on blood-based DNA methylation tests for the early cancer detection. Our lead product, Epi proColon, is the only FDA-approved blood-based test for colorectal cancer screening. For the 23 million unscreened patients, you can add Epi proColon to your rt-PCR. Provider and patient design/messaging available to quick-start your marketing outreach efforts.

Eppendorf
Booth #: 3116
www.eppendorf.com
Eppendorf is a leading life science company that develops and sells instruments, consumables, and services for liquid-, sample-, and cell handling. Its product range includes pipettes and automated pipetting systems, centrifuges, mixers, spectrometers, thermal cyclers, ultra-low temperature freezers, fermentors, bioreactors, CO2 incubators, shakers, cell manipulation systems and all accompanying consumables.

Exact Diagnostics
Booth #: 2416
www.exactdiagnostics.com
Exact Diagnostics is a molecular standards and controls company, utilizing droplet digital PCR for value assignment and sequencing data/information of our standards.

EXHIBITOR DESCRIPTIONS

EZLife Bio Inc.
Booth #: 2516
www.ezlife.bio
Founded in 2016, EZLife Bio rethinks how molecular diagnostics is done with the EFIRM technology. Our platform is user-friendly, with precise and accurate product assertions backed by rigorous scientific data. At EZLife Bio, we hope to transform the landscape of molecular testing.

Fabric Genomics
Booth #: 2224
www.fabricgenomics.com
Fabric Genomics is making precision medicine a reality by facilitating clinical labs, hospital systems, and country-sequencing programs to develop, deploy, and scale genomic testing. Our AI approach to genome interpretation and SOP-based workflows enable rapid generation of physician-ready clinical reports for any genomic test.

FluxErgy
Booth #: 3137
www.fluxergy.com
Run a HIV-1 RNA test, a P24 antigen test and a white blood cell count on the same platform. The Fluxergy Analyzer is a modular point-of-care solution allowing for PCR, chemistry, immunochemistry, and cytometry to be conducted on one portable instrument.

FORMULATRIX
Booth #: 2422
www.formulatrix.com/
At Formulatrix, we simplify laboratory workflows with the most innovative automation to save you time, money, and resources so you can achieve your next breakthrough.
We don't simply upgrade the systems everyone else is making – we push the boundaries of technology, producing the smartest, and most efficient laboratory automation available.

Foundation Medicine, Inc
Booth #: 2322
www.foundationmedicine.com
Foundation Medicine is a molecular information company dedicated to a transformation in cancer care in which treatment is informed by a deep understanding of the genomic changes that contribute to each patient's unique cancer. For more information, visit www.FoundationMedicine.com.

GenapSys Inc.
Booth #: 3244
GenapSys Sequencer, at $10,000, generates data with > 99% accuracy with average read lengths of 150 bp and is highly scalable from 1 to 16 to 144 million sensors. The run cost is projected at $200-$600. The sequencer has a small footprint. Bring the power of NGS to your lab with this compact yet powerful sequencer.

Genetic Signatures
Booth #: 2222
www.geneticsignatures.com
We are the developers of 3base™ technology which is the cornerstone of our EasyScreen™ Pathogen Detection Kits. Our proprietary technology provides hospital and pathology laboratories with the molecular tools to screen for a wide array of infectious pathogens in a rapid high-throughput environment.

Genetron Health (Beijing) Co. Ltd.
Booth #: 3251
www.genetronhealth.com
Genetron Health offers full-cycle cancer molecular diagnostics products and services from prevention to treatment. These include risk assessment, early screening, molecular pathology diagnosis, medication guidance and prognosis monitoring – specially catered to the needs of cancer patients, high-risk groups and the healthy population.

GENEWIZ
Booth #: 2953
www.genewiz.com
GENEWIZ is a leading provider of genomics services to over 4,000 institutional customers worldwide, enabling research scientists to advance their discoveries faster than ever before. Now a Brooks Life Sciences company, GENEWIZ leads the industry with our unique and proprietary technologies backed by specialized experts in Sanger sequencing, gene synthesis, next generation sequencing, and GLP/CLIA regulatory-compliant services.

GenMark Dx
Booth #: 2748
www.genmarkdx.com
GenMark Diagnostics is a leading provider of multiplex molecular diagnostic solutions designed to enhance patient care, improve key quality metrics, and reduce the total cost-of-care. GenMark's ePlex®: The True Sample-to-Answer Solution™ is designed to optimize laboratory efficiency and address a broad range of infectious disease testing needs, including respiratory, bloodstream, and gastrointestinal infections.

EXHIBITOR DESCRIPTIONS

GenomeWeb
Booth #: 2413
www.genomeweb.com
GenomeWeb is an independent online news organization based in New York. Since 1997, GenomeWeb has served the global community of scientists, technology professionals, and executives who use and develop the latest advanced tools in molecular biology research and molecular diagnostics.

GenomOncology
Booth #: 2434
www.genomoncology.com
GenomOncology (GO) enables real-time clinical decision support at the point of care for molecular pathology, oncology, and cancer informatics teams. GO's solutions for molecular pathologists address the full range of requirements for precision medicine, including integrating directly with lab sequencers, annotating detected variants from raw genomic data, recommending potential clinical trials, and producing a comprehensive customizable summary report.

Genosity
Booth #: 2517
www.genosity.com
Genosity is a biotechnology company focused on providing tools and services for clinical and research genomic applications in the healthcare space. Our mission is to unlock the power of precision medicine in improving patient care by providing a technology platform to advance genomics and facilitate collaborative research.

GenPath Diagnostics, BioReference Laboratories
Booth #: 2219
www.genpathdiagnostics.com/oncology
GenPath, a division of BioReference Laboratories, Inc., offers a comprehensive test menu. From routine clinical and special coagulation testing to complex genomic testing for tumor sequencing and hereditary cancers, the full testing spectrum for cancer patients is covered. BioReference Laboratories, Inc. is a wholly owned subsidiary of OPKO Health Inc.

Golden Helix
Booth #: 2856
www.goldenhelix.com
Golden Helix® is a global bioinformatics firm founded in 1998. We develop and sell an industry-leading clinical solution that supports the analysis of sequencing data and the creation of clinical reports.

GSPMC
Booth #: 2750
www.mcw.edu/departments/genomic-sciences-and-precision-medicine-center-gspmc
GSPMC is a precision medicine focused center with services ranging from research to clinical assays.

Hamilton Company
Booth #: 3143
www.hamiltoncompany.com
Hamilton Company specializes in the development, manufacturing and customization of precision measurement devices, automated liquid handling workstations, sample management systems, and OEM solutions.
Hamilton offers fully automated solutions for sample preparation, drugs of abuse testing, toxicology, pain management testing, next-generation sequencing (NGS), ELISA, and more.

Health Decisions
Booth #: 3150
www.healthdec.com
Health Decisions is a full-service CRO with extensive clinical development expertise for bringing therapeutics for women's health indications and diagnostics for all therapeutic areas to market rapidly and with minimal risk. Our service offerings include trial management, monitoring, data management, biostatistics, regulatory, quality, study design and protocol development.

Hologic
CORPORATE PARTNER
Booth #: 2621
An innovative medical technology company primarily focused on improving women's health and well-being, Hologic enables healthier lives everywhere, every day, with clinical superiority that delivers life-changing diagnostic, detection, surgical and medical aesthetic products rooted in science and driven by technology. Hologic: The Science of Sure in action.

Horizon Discovery
Booth #: 2327
www.horizondiscovery.com
From research to therapy, Horizon Discovery drives the application of gene editing and gene modulation. Innovative tools and services enable scientists to gain a greater understanding of the genetic drivers behind disease, develop and validate diagnostic workflows, and deliver new therapies for precision medicine.

EXHIBITOR DESCRIPTIONS

Illumina
CORPORATE PARTNER
Booth #: 2341
www.illumina.com
Serving customers in the clinical, research, and applied markets, Illumina technology is responsible for generating more than 90% of the world's sequencing data.* Illumina is fueling groundbreaking advancements in oncology, reproductive health, genetic disease, and beyond. By empowering large-scale analysis of genetic variation and function, Illumina is enabling studies that were not imaginable just a few years ago.

InSilixa
Booth #: 3052
www.insilixa.com
InSilixa enables high-performance, affordable, and easy-to-use molecular diagnostics (MDx) for applications in infectious disease and oncology. InSilixa's integrated detection platforms guide personalized drug treatments at the point-of-care (POC) or near patient settings. Using an integrated CMOS biochip, dedicated informatics and unique modular instrument platform approach, InSilixa provides assays for your chosen molecular targets and applications.

Integrated DNA Technologies
Booth #: 2315
www.idtdna.com
Integrated DNA Technologies (IDT) is the world leader in delivering custom nucleic acid products for life sciences and medical research, serving academic, clinical, biotechnology, pharmaceutical development, and agricultural research communities. IDT product applications include qPCR, gene construction, CRISPR genome editing, next generation sequencing, and functional genomics.

Interpace Diagnostics
Booth #: 2659
www.interpacediagnostics.com
Interpace Diagnostics Group, Inc. is a fully integrated commercial and bioinformatics company that provides evidence-based, clinically beneficial molecular diagnostic tests and pathology services. We develop and commercialize molecular diagnostic tests that deliver cutting-edge genetic and mutational analysis. Our tests help risk-stratify patient samples for thyroid, pancreatic, lung, and other cancers to better inform treatment decisions.

Invivoscribe
Booth #: 2849
www.invivoscribe.com
Invivoscribe® is an ISO13485 compliant cGMP manufacturer of standardized reagents and bioinformatics software used by LabPMM clinical labs and >700 customers. Products include the FDA-approved LeukoStrat® CDx FLT3 Mutation Assay, RUO, and CE-marked assays for capillary and NGS platforms. Kits, gene panels, and MRD assays (Ig, TCR, FLT3, NPM1) are used to stratify/enroll subjects and track malignancies in clinical trials.

Karius
Booth #: 2419
www.kariusdx.com
Karius is focused on generating genomic insights for infectious diseases with the non-invasive Karius Test that helps clinicians make rapid treatment decisions. The Karius Test is a blood test based on NGS of microbial cell-free DNA. The Karius laboratory is CLIA-certified and CAP-accredited to perform high-complexity clinical laboratory testing.

LABWARE
Booth #: 2335
www.labware.com
LabWare is recognized as the global leader in providing enterprise-scale Laboratory Information Management Systems and electronic laboratory notebook solutions. Our Enterprise Laboratory Platform combines the award-winning LabWare LIMS™ solution with LabWare ELN™, a comprehensive Electronic Laboratory Notebook application, enabling companies to optimize compliance, improve quality, increase productivity and reduce costs.

LGC, Biosearch Technologies
Booth #: 3330
www.biosearchtech.com
Biosearch Technologies is the comprehensive genomics portfolio from LGC, providing products and services for genomic analysis that support mission critical applications in molecular diagnostics. We enable our customers from assay development to commercialisation through our expertise in sample preparation, oligo synthesis, enzymes, and components for PCR and NGS.

Loxo Oncology
CORPORATE PARTNER
Booth #: 2512
Loxo Oncology is dedicated to developing highly-selective medicines for patients with genomically defined cancers. Our pipeline is focused on purpose-built medicines designed to selectively and potently inhibit oncogenic drivers of cancer. We believe that this approach, combined with tumor genomic testing to identify appropriate patients, will allow us to develop medicines that deliver on the promise of precision medicine.

EXHIBITOR DESCRIPTIONS

LRE Medical GmbH
Booth #: 3334
www.lre.de
LRE Medical is a leading contract Developer and Contract Manufacturer of Medical and In-Vitro-Diagnostic and Life Sciences Instrumentation. LRE offers "One Stop shopping" Solutions (Engineering, Manufacturing, After Sales Service, Lifetime Product Support)

Luminex
Booth #: 2412
WWW.LUMINEX.COM
Luminex Corporation is committed to creating innovative, breakthrough solutions to help our customers improve health and advance science worldwide. Our goal is to transform global healthcare and life science research through the development, manufacturing, and marketing of proprietary instruments and assays that deliver cost-effective, rapid results to clinicians and researchers.

Maine Molecular Quality Controls, Inc.
Booth #: 2919
www.mmqci.com
MMQCI designs and markets unique quality controls for molecular testing for inherited disease, pharmacogenetics and infectious disease. Easy-to-use controls contain multiple targets and can be extracted like patient samples, are non-infectious, stable and provide consistent results. INTROL CF Panel I is the first FDA-cleared quality control for genetic testing. Custom orders are welcome at our cGMP facility in Saco, Maine.

Market Ready Rx
Booth #: 2843
www.marketreadyrx.com
Market Ready Rx is a premium IVD marketing consultancy supporting diagnostic marketing professionals to create commercial strategies and execute seamless commercial programs. We support global diagnostic companies with market entry strategic roadmaps, voice-of-the-customer research and full commercial launch programs. Market Ready Rx accelerates the introduction of world changing personalized diagnostics to market by bridging diagnostics and pharma commercial launch knowhow.

Medical Lab Management
Booth #: 2424
www.medlabmag.com
MedicalLab Management, a print and digital publication, is a peer-to-peer information source for clinical laboratory management. It provides clinical laboratory managers and directors with unbiased articles, practical, actionable, real-world examples, purchasing research, decision-making processes and new products in the marketplace.

Menarini Silicon Biosystems
Booth #: 2425
www.siliconbiosystems.com
A biotech company with a passion to advance healthcare and personalized medicine with its DEPArray™ system and, the CELLSEARCH® Circulating Tumor Cell System - only clinically validated blood test cleared by the FDA for detecting and enumerating CTCs to help manage patients with metastatic breast, prostate, and colorectal cancers.

Merck
CORPORATE PARTNER
Booth #: 2925
www.keytruda.com
For more than a century, Merck has been inventing for life, bringing forward medicines and vaccines for many of the world's most challenging diseases. Today, Merck continues to be at the forefront of research to deliver innovative health solutions and advance the prevention and treatment of diseases that threaten people and animals around the world.

Meridian BioScience Inc.
Booth #: 2757
www.meridianbioscience.com
For more than 40 years, Meridian Bioscience has helped healthcare providers in early diagnosis and proper patient management by providing a line of trusted solutions so that patients can get back to living. The Meridian platforms provide established testing technologies with accurate results. Meridian's comprehensive line of testing options deliver results with speed, accuracy and simplicity.

MetaSystems Group, Inc.
Booth #: 3048
www.metasystems.org
MetaSystems is a leading manufacturer of genetic imaging (high throughput) slide scanning systems and high quality DNA FISH probes for clinical laboratories. We offer innovative solutions for automated interphase FISH spot counting with RapidScore technology, TissueFISH and TMA analysis in fluorescence and brightfield, pathology whole slide imaging, metaphase search, and automatic karyotyping.

Michigan Medicine Laboratories (MLabs)
Booth #: 3243
As a full-service reference laboratory, Michigan Medicine Laboratories (MLabs) combines the scientific rigor and infrastructure investment of a top academic research institution with the efficiency, flexibility and responsiveness of a private reference lab. Partnering with MLabs means gaining access to one of the largest, most productive pathology enterprises in academic medicine.

EXHIBITOR DESCRIPTIONS

Miltenyi Biotec GmbH
Booth #: 3154
www.miltenyibiotec.com
Miltenyi Biotec provides products that advance biomedical research and cellular therapy. Our innovative tools support research from basic research to translational research to clinical application. Our 30 years of expertise includes immunology, stem cell biology, neuroscience, and cancer. Miltenyi Biotec has 2,500 employees in 28 countries.

Mission Bio
Booth #: 2749
www.missionbio.com
Mission Bio delivers targeted solutions for high impact applications with the Tapestri Platform. The Tapestri Platform is the industry's first single-cell DNA sequencing platform, enabling precise detection of heterogeneity in disease progression and treatment response. Application areas include blood cancers, solid tumors, and genome editing validation. The platform includes an instrument, consumables and software, plugging seamlessly into existing NGS workflows.

Molecular Health
Booth #: 2323
www.molecularhealth.com/us
Molecular Health is a computational biomedicine company focused on big-data curation, integration and analytics to enable precision medicine. Its technology Dataome™ integrates clinico-molecular drug and disease databases to generate novel and actionable insights for stakeholders across the healthcare ecosystem. Molecular Health's scientific and commercial teams are based in Heidelberg, Germany and Boston, MA in the US.

MolecularMatch, Inc.
Booth #: 3235
www.molecularmatch.com
MolecularMatch is a genomics software company that provides real-time information on the best-targeted drugs, literature, trials along with evidence-based guidelines. We match therapeutic options for patients from their electronic medical record in real-time, providing us with patient outcomes data, providing a rich data asset in which we can monetize for new verticals such as real world clinical trial data.

MRC-Holland
Booth #: 2845
www.mlpa.com
Multiplex Ligation-dependent Probe Amplification (MLPA®) is the gold standard for DNA copy number quantification and is used worldwide to study both hereditary disorders and tumours. MLPA can also be applied to investigate the methylation status of DNA sequences. Up to 60 DNA sequences can be analysed in a single reaction in high-throughput manner, with results being available within 24h.

NanoString Technologies
CORPORATE PARTNER
Booth #: 2933
www.nanostring.com
NanoString® is a leading provider of life science tools for translational research and diagnostics. Cited in over 2,500 peer-reviewed publications, the nCounter® Analysis System measures gene and protein expression to profile novel biomarkers. The company's GeoMx™ Digital Spatial Profiler enables highly-multiplexed spatial profiling of RNA and protein targets in a variety of sample types, including FFPE tissue sections.

NeoGenomics Laboratories
Booth #: 2941
www.neogenomics.com
NeoGenomics specializes in cancer genetics testing and information services with the most comprehensive oncology-focused testing menus globally to diagnose and treat cancer. NeoGenomics operates CLIA certified laboratories serving the needs of pathologists, oncologists, academic centers, hospital systems, Pharma, and managed care organizations. Visit neogenomics.com/ to learn more about our global locations.

NeuMoDx Molecular
Booth #: 2859
www.neumodx.com
NeuMoDx Molecular has developed a novel molecular diagnostic system for clinical laboratory customers. The Company's patented 'sample-to-result' platforms offer market-leading ease of use, true continuous random-access, rapid turnaround time, and lower total cost of ownership. Initial test menu is focused on women's health and quantitative tests for blood born viruses along with the ability to efficiently perform Laboratory Developed Tests.

New England Biolabs
Booth #: 3342
www.neb.com
For over 40 years, New England Biolabs, Inc. has led the industry in the supply of molecular biology reagents. In addition to products for genomics, NEB continues to expand its offering into areas related to PCR and qPCR, gene expression, sample preparation for next gen sequencing, synthetic biology, glycobiology, genome editing, epigenetics and RNA analysis.

EXHIBITOR DESCRIPTIONS

Norgen Biotek Corp.
Booth #: 3053
Norgen Biotek provides researchers with innovative kits for Sample Collection/ Preservation [DNA/RNA including cf-DNA/cf-RNA/exo-RNA from Blood/Plasma/Serum, Urine, Saliva, Stool, Swab], Molecular Diagnostics (MDx), and microRNA/RNA/DNA/Protein Purification. Our kits feature exceptional quality, ease-of-use and sensitivity. Norgen Biotek also offers full in-house isolation and Next Generation Sequencing (NGS) Services in an Illumina Propel and ISO Certified Facility.

Novartis
CORPORATE PARTNER
Booth #: 2741
www.novartis.com
At Novartis, our mission is to discover new ways to improve and extend people's lives. We use science-based innovation to address some of society's most challenging health care issues. We discover and develop breakthrough treatments and find new ways to deliver them to as many people as possible.

NovoPath, Inc.
Booth #: 2943
www.novopath.com
NovoPath is a leading U.S.-based Lab Information Systems (LIS) company serving the Anatomic and Clinical Pathology, Molecular and Genetic Testing, and Clinical Trials markets. NovoPath's clients include national/ regional reference labs, university and teaching hospitals, regional and community hospitals, and specialty labs. NovoPath's mission is to provide unique and unparalleled solutions and services to improve laboratory costs and patient safety.

nRichDx
Booth #: 2655
www.nrichdx.com
Unleash the power of liquid biopsies with nRichDx's cfDNA sample prep system and yield up to 75X more DNA in a single, scalable sample prep compatible with any downstream PCR or NGS system.

NuProbe
Booth #: 3253
www.nuprobe.com
NuProbe develops innovative solutions for ultra-sensitive and noninvasive nucleic acid profiling.

NVIGEN Inc.
Booth #: 2752
www.nvigen.com
NVIGEN is a nanotechnology empowered personalized medicine innovator. Our pipeline of solutions are enabled by the state-of-the-art engineered nanoparticles to efficiently capture and identify information from proteins, cells, nucleic acids and other target molecules. We are developing a comprehensive circulating bio-marker biopsy technology, Nanopsy™, to predict cancer recurrence at the earliest possible time and guide the most effective personalized therapy.

Omega Bio-Tek, Inc.
Booth #: 3140
Since its founding in 1998, Omega Bio-tek has been at the forefront of nucleic acid purification by offering products for clinical and basic research, biotechnology, and agricultural applications. DNA and RNA extraction is the first step for so many downstream analyses, and our goal is to offer high quality products to help improve your workflows.

Omni International
Booth #: 2415
www.omni-inc.com
Omni International, Inc is a leading global manufacturer and distributor of laboratory homogenizers. Omni sets the industry standard with an unmatched commitment to outstanding product design, reliable performance, and a uniquely diversified solution based product line.

Opentrons Labworks
Booth #: 3241
www.opentrons.com
We make robots for biologists. Our mission is to provide the scientific community with a common platform to easily share protocols and reproduce each other's results. Automate time consuming NGS Library Prep, PCR/qPCR, plate filling, or anything else you can dream of with our open-source OT-2, starting at only $4,000 (no joke!). Come meet your personal pipetting robot today!

Ovation.io
Booth #: 2232
www.ovation.io/
Ovation is a scientific data company transforming the way a LIMS supports the critical functions of molecular diagnostic laboratories because it is not enough to just track samples and manage workflows. To be successful, labs have to attend to physicians, patients, sales teams, lab operations, revenue cycle management, and business performance. Ovation is here to help with all of it.

EXHIBITOR DESCRIPTIONS

Oxford Gene Technology
Booth #: 3144
www.ogt.com
Oxford Gene Technology (OGT) provides world-class genetics research solutions to leading institutions worldwide. Our integrated product portfolio enables accurate identification of variation to facilitate understanding of genetic disease. Visit the OGT booth to learn more about our focus on customised solutions and high-quality Cytocell® FISH probes, SureSeq™ next generation sequencing (NGS) panels, and CytoSure™ array products.

Paragon Genomics
Booth #: 2921
www.paragongenomics.com
Paragon Genomics, Inc. specializes in sample preparation for targeted next-generation sequencing (NGS). We develop and commercialize reagents and molecular diagnostic tools for genomic analysis of clinically-relevant samples. Our CleanPlex® and CleanPlex® UMI NGS panels combine superior primer design and innovative library preparation chemistry to eliminate non-specific PCR products, incorporate molecular identifiers, and achieve superior target enrichment and variant detection performance.

PerkinElmer
Booth #: 2616
PerkinElmer, Inc. offers automated solutions which improve the efficiency of genomic and proteomics workflows. With our nucleic acid isolation technology, liquid handlers, library preparation kits, automated nucleic acid and protein analysis systems, and solutions for single cell genetic analysis, PerkinElmer is eliminating the challenges associated with genomic and proteomic analysis.

Personal Genome Diagnostics
Booth #: 3123
www.pgdx.com
Personal Genome Diagnostics (PGDx) is empowering the fight against cancer by unlocking actionable information from the genome. We are committed to developing a portfolio of regulated tissue-based and liquid biopsy genomic products for laboratories worldwide.

Philips
Booth #: 2537
www.philips.com/genomics
Philips Intellispace Precision Medicine empowers next NGS workflow. Our comprehensive and customizable architecture provides the pathologist, oncologist and bioinformatician with intuitive workflow tools to help rapidly sift through the information to make informed decisions. Access cases whenever and wherever, select and prioritize treatment recommendations for molecular tumor boards. Focus on patient care while we provide a secure and scalable infrastructure.

PierianDx
Booth #: 2441
www.pieriandx.com
PierianDx empowers progressive health institutions and diagnostic laboratories to build world-class precision medicine programs. Our industry-leading clinical genomics technologies, CAP and CLIA accredited laboratory, and expertise deliver the most integrated, trusted, and collaborative approach across the clinical care spectrum. We drive the adoption of genomics in clinical care and accelerate the fight against cancer and other diseases. www.pieriandx.com

Pillar Biosciences Inc.
Booth #: 2649
www.pillar-biosciences.com
Pillar Biosciences develops and manufactures targeted next-generation sequencing-based assays and software for NGS laboratories. Utilizing proprietary SLIMamp target enrichment technology and PiVAT bioinformatics pipeline, Pillar offers catalog and custom panels with simplified workflow and robust automatable solutions to deliver highly sensitive results from low input DNA samples including liquid biopsy.

PreAnalytiX
Booth #: 3118
www.PreAnalytiX.com
PreAnalytiX, a joint venture between BD and QIAGEN, develops, manufactures and sells integrated and standardized systems for collection, stabilization and purification of RNA, microRNA, DNA and cfDNA from blood, bone marrow and tissue specimens. The company provides a broad array of manual and automated products.

Precision System Science USA, inc.
Booth #: 3338
www.pssbio.com
Precision System Science, for over 20 years an OEM leader in automated, self-contained instrumentation meeting the rigors of today's IVD market. We provide clinical diagnostic laboratories with solutions for extraction, purification as well as versatile sample-to-answer instruments. Complete systems with user friendly software interface, consumables and reagents. Simple, fast solutions for improving the healthcare around the world.

EXHIBITOR DESCRIPTIONS

Promega Corporation
Booth #: 3035
www.promega.com
Promega is a global leader in providing solutions and technical support to life scientists in academic, industrial and government settings. Promega products are used by life scientists asking fundamental questions about biological processes and those applying their knowledge to diagnose and treat diseases, discover new therapeutics, and use genetics and DNA testing for human identification.

PSOMAGEN, INC.
Booth #: 3054
www.psomagen.com
Psomagen, Inc., formerly Macrogen Corp., has been the genomic sequencing service provider of choice for many academic and commercial organizations for over 15 years. We provide quality driven services to researchers and clinicians alike. The new name, Psomagen, reflects the intersection of "mind, body and genomics" and our commitment to personalized medicine.

Purigen Biosystems, Inc.
Booth #: 3139
www.purigenbio.com
Purigen Biosystems' transformative platform provides a hands-free solution for extracting, enriching and quantifying DNA and RNA from biological samples. Our proprietary approach uses isotachophoresis (ITP), an electric-field-driven technique for purifying, focusing, and/or separating species. Purigen's system is compatible with a range of samples. This includes mammalian cells, FFPE and FNA tissue biopsies, plasma, blood, and buccal swabs.

Q2 Solutions | EA Genomics
Booth #: 2217
www.q2labsolutions.com/
We are a global clinical trials laboratory services organization that helps biopharmaceutical, medical device and diagnostics customers improve human health through innovation that transforms science and data into actionable medical insights. With comprehensive end-to-end anatomic pathology and genomic services to support drug discovery, precision medicine and clinical development, we provide solutions for smarter clinical studies.

QIAGEN
CORPORATE PARTNER
Booth #: 3113
QIAGEN is known to more than 500,000 customers around the world for our innovation, engagement, integrity, quality and passion. Our mission is to deliver Sample to Insight solutions enabling QIAGEN customers to unlock valuable molecular insights faster, better and more efficiently – from the raw biological sample to the final interpreted result.

Quidel Corporation
Booth #: 3013
www.quidel.com
Quidel® is committed to enhancing health and well-being through innovative diagnostic solutions. Assays use lateral-flow, direct fluorescent antibody, molecular and other technologies to improve patient outcomes and give economic benefits to healthcare providers. Leading brands - QuickVue®, Solana®, Sofia®, Triage®, Virena®, AmpliVue®, Lyra®, Thyretain®, InflammaDry®, AdenoPlus®, MicroVue™, and D3® Direct Detection™, aid in detection and diagnosis of critical diseases/conditions.

Qvella Corporation
Booth #: 2841
www.qvella.com
Qvella was founded with a vision to dramatically reduce time to actionable results.
Qvella's FAST-ID™ BSI Panel* is a transformative product designed for fully-automated detection of multiple pathogens directly from whole blood in minutes instead of hours.
* The FAST-ID BSI Panel is in development and not approved for sale. The performance characteristics of this product have not been established.

RareCyte, Inc
Booth #: 2949
www.rarecyte.com
RareCyte provides next generation technology for liquid biopsy and digital pathology. The portfolio of instruments, consumables and software enable deep phenotyping, cell retrieval and molecular analysis for rare cells in blood and multiplex tissue imaging for immuno-oncology and more. Pharma Programs enable CTC-based CDx development from RUO through IVD.

ResearchDx
Booth #: 2967
www.researchdx.com
ResearchDx is the leading provider of Diagnostic Development Services. We build diagnostic assays for a multitude of applications, including Biomarker Discovery, Laboratory Developed Testing (LDT's), and in vitro Diagnostic Devices (IVD's). Additionally, we perform a wide array of diagnostic testing in our CAP/CLIA accredited and GxP compliant facility.

EXHIBITOR DESCRIPTIONS

Rheonix
Booth #: 2518
www.rheonix.com
The Rheonix Encompass Optimum™ workstation is a fully automated liquid handling system that now integrates and automates nucleic acid purification and NGS library preparation directly from raw samples, enabling labs to begin same shift sequencing with very limited technician time. Rheonix workstations, technologies, and multiplexed sample-to-answer molecular assays are used throughout the world in clinical, food safety and brewing industries.

Roche
CORPORATE PARTNER
Booth #: 2813
www.roche.com
Roche provides innovative PCR and next generation sequencing-based solutions to empower your lab with flexible, scalable and integrated solutions. Our diverse portfolio for clinical diagnostics and research increases lab productivity and enables faster, more confident clinical decisions in virology, infectious diseases, sexually transmitted infections, women's health, genomics, and oncology.

SCC Soft Computer
Booth #: 2432
www.softcomputer.com
SCC Soft Computer's laboratory and genetics information system solutions accommodate clinical laboratory and anatomic pathology test ordering and reporting. Our fully integrated systems eliminate the need for costly add-ons providing a seamless interface that links all clinical laboratory departments. Tremendous flexibility is provided to allow the distribution of data and results from the laboratory to the entire care provider network.

Seattle Genetics
Booth #: 2742
www.seattlegenetics.com
Seattle Genetics, an emerging multi-product, global biotechnology company, develops and commercializes transformative cancer-targeting therapies. ADCETRIS® (brentuximab vedotin) utilizes the company's industry-leading antibody-drug conjugate (ADC) technology and is currently approved for the treatment of multiple CD30-expressing lymphomas. Beyond ADCETRIS, the company has established a robust pipeline of novel targeted therapies, including three in late-stage development to address significant unmet needs.

SeraCare Life Sciences
Booth #: 2612
www.seracare.com
SeraCare is a leading partner to global IVD manufacturers and clinical testing laboratories. Our expanding portfolio of clinical genomics QC products and technologies includes reference materials for TMB, liquid biopsy, tumor sequencing, germline mutation testing, NIPT, and infectious disease. Today, SeraCare is advancing data integration with products for better QC and regulatory compliance.

SmartGene
Booth #: 2955
www.smartgene.com
SmartGene is a bio-informatics application service provider (ASP), facilitating analysis of both Sanger and NGS data. We deliver secure, integrated, software solutions for the management and interpretation of genetic sequences and related data, such as HIV HCV and Microbiome. SmartGene provides specific applications for medical, clinical research and molecular epidemiology purposes, focusing on rapid identification, typing and analysis of pathogens.

SoftGenetics
Booth #: 2939
www.softgenetics.com
Featuring NextGENe software for analysis of NGS data including Variations – SNVs/Indels/ Somatics/Structural/Copy Number and HLA; Geneticist Assistant NGS Workbench, a knowledge-base for your samples and variant predictions; GeneMarker software with new Repeat Expansion (HTT, DMPK, ALS...) module; ChimerMarker, Chimerism Analysis software and Mutation Surveyor software for the analysis of Sanger Sequences. SoftGenetics is providing no cost trials of each program

SOPHiA GENETICS
Booth #: 2643
www.sophiagenetics.com
At SOPHiA GENETICS, we believe in building a more sustainable global healthcare system. That's why we developed SOPHiA AI, the advanced technology for Data-Driven Medicine, enabling healthcare institutions around the world make sense of genomic and radiomic data. By empowering clinical researchers to leverage their expertise and work as a community, we democratize Data-Driven Medicine together.

EXHIBITOR DESCRIPTIONS

SpeeDx
Booth #: 3148
www.plexpcr.com
SpeeDx develop molecular diagnostics with identification and therapeutic guidance capabilities. Clinical trials are nearing completion for FDA submission of ResistancePlus MG - for Mycoplasma genitalium and macrolide resistance markers. FDA recently designated breakthrough status for ResistancePlus GC - for gonorrhoea testing with ciprofloxacin susceptibility markers. See www.plexpcr.com for more information.

Staff Icons- A Biotech Recruitment Company
Booth #: 2945
WWW.STAFFICONS.COM
Staff Icons is a National Recruitment Firm. NO CHARGE TO USE OUR SERVICES UNLESS YOU HIRE ONE OF OUR CANDIDATES. We do full cycle recruiting in the Biotech/Pharma/Healthcare Industry and service direct hire, short & long term staffing needs. We represent both clients and candidates. Call 1-888-452-0102 or email at info@stafficons.com or visit our website: WWW.STAFFICONS.COM.

STEMCELL Technologies Inc
Booth #: 2313
www.stemcell.com
STEMCELL Technologies offers cell isolation products to enhance the sensitivity of molecular assays for multiple myeloma, CLL, and other hematological malignancies by enriching for cells of interest. RoboSep™automates immunomagnetic cell separation from whole blood or bone marrow and offers a true walk-away solution. RoboSep™ minimizes sample handling, eliminates cross-contamination, and reduces hands-on time - ideal for busy routine labs. www.robosep.com

Streck
Booth #: 3043
www.streck.com
Streck develops and manufactures hematology, immunology and molecular biology products for clinical and research laboratories. Innovative products include the Zulu RT™, a 20 minute real-time PCR platform; real-time PCR test kits for the detection of Gram-negative Beta-lactamase gene families and PhilisaFAST®, a hot-start PCR enzyme specifically formulated for rapid thermal cycling.

Sunquest Information Systems
Booth #: 3018
www.sunquestinfo.com
Sunquest Information Systems provides enterprise laboratory information solutions for clinical, anatomic and molecular pathology, enabling interoperability for world-class labs, including multi-site, multi-disciplinary support for complex anatomic, molecular and genetic testing. Since 1979, Sunquest has helped over 1,700 labs and healthcare organizations across the world enhance efficiency, patient care and financial results. For more information go to www.sunquestinfo.com

Taigen Bioscience Corporation
Booth #: 3141
www.labturbo.com
Taigen Bioscience Corporation is specialized in the automation of DNA/RNA related applications and sample preparation. We provide sample-to-result solutions for liquid-handling, DNA/RNA purification, PCR setup, and qPCR. Our LabTurbo systems are part of the FDA-approved nucleic acid testing for infectious disease screening in US blood supply. Complete automation includes the detection of cancer, methylated DNA, circulating DNA, NIPD, HIV/HBV/HCV/HPV, etc.

Takara Bio USA
Booth #: 2216
www.takarabio.com
Takara Bio USA, Inc., (TBUSA; formerly Clontech Laboratories, Inc.) is a wholly owned subsidiary of Takara Bio Inc. that manufactures and distributes kits, reagents, and instruments for life sciences research applications, including NGS, PCR, gene delivery, genome editing, stem cell research, nucleic acid and protein purification, and automated sample preparation.

Texas Children's Hospital
Booth #: 2223
www.texaschildrens.org
Texas Children's Hospital offers superior care and specialized pediatric testing capabilities to hospitals across the United States. Our goal is to provide a precise diagnosis, prognosis and assist in disease monitoring through our unrivaled consultative services. We specialize in pediatric anatomic and clinical pathology. Including molecular and genomic pathology, blood banking, clinical chemistry, coagulation, hematology, medical microbiology, neuropathology and hematopathology.

EXHIBITOR DESCRIPTIONS

The Jackson Laboratory
Booth #: 3016
www.jax.org
The Jackson Laboratory (www.jax.org) is an independent, nonprofit biomedical research institution with a National Cancer Institute-designated Cancer Center, with facilities in Bar Harbor, ME, Sacramento, CA and a new genomic medicine institute in Farmington, CT. Its mission is to discover precise genomic solutions for disease, empowering the global biomedical community in the shared quest to improve human health.

The Journal Precision Medicine
Booth #: 3042
www.thejournalofprecisionmedicine.com
Through the medium of print, digital media, video and live event portfolio we examine the whole spectrum of precision medicine from discovery to diagnostics to clinical implementation. Visit our booth for your FREE subscription and to learn more about our Precision Medicine Leaders Summits.

The Lab People, Inc.
Booth #: 3238
The Lab People, Inc. is an A2LA Accredited ISO 17025 certified laboratory and industrial equipment service company. We help customer maintain quality programs for critical measurement equipment including pipettes, balances, test weights and temperature. In addition, we are a premium distributor for the laboratory equipment and supplies.

The Pathologist
Booth #: 2444
www.thepathologist.com
We are The Pathologist, a global magazine focused on pathology and laboratory medicine. We feature articles on all aspects of the field – news, views, personal profiles, practical tips and tricks, new and upcoming developments, training, education, and career development.

Thermo Fisher Scientific
CORPORATE PARTNER
Booth #: 2825
Thermo Fisher Scientific is the world leader in serving science. Through our trusted Thermo Scientific, Applied Biosystems and Ion Torrent research and diagnostic solutions, services and support, we help molecular laboratories uncover and interpret relevant genetic insights across oncology, pharmacogenomics, and infectious disease areas using technologies such as next-generation sequencing, real-time PCR, Sanger sequencing, and bioinformatics.

TriLink BioTechnologies
Booth #: 2744
www.trilinkbiotech.com
TriLink BioTechnologies specializes in the synthesis and production of complex and highly-modified nucleic acids for research, diagnostics, pre-clinical therapeutic and pharmaceutical applications. Since 1996, TriLink has been developing and manufacturing custom oligonucleotides, mRNA transcripts, nucleotides, PCR & RT-PCR reagents, NGS library preparation kits, bioconjugation, custom chemistry, and other small molecules.

Truckee Applied Genomics LLC
Booth #: 2221
Truckee Applied Genomics LLC is a molecular pathology company who has developed a novel technology for the replacement of formalin for the stabilization of tumor tissue for molecular analysis. The TAG-1 technology eliminates the challenges that formalin fixed tumor tissues present in a novel patented formulation. TAG-1 represents a non toxic product that delivers stabilized tissue and nuclear contents.

Twist Bioscience
Booth #: 2944
www.twistbioscience.com
Twist Bioscience, the leader in synthetic DNA with unparalleled precision at scale, is redefining targeted sequencing performance with superior NGS target enrichment solutions. Whether you need library preparation and enrichment components or specific custom panels, Twist can help you achieve higher depth of coverage across target regions with uncompromising quality.

UCSF Center for Next-Gen Precision Diagnostics
Booth #: 3050
www.nextgendiagnostics.ucsf.edu
Metagenomic next-generation sequencing (mNGS) is a single, clinically validated test that identifies thousands of pathogens, including novel infectious agents and rare variants. By testing for all organisms in an unbiased, hypothesis-free process, mNGS data can tell a fact-based story in a clinical context.

UPMC Genome Center
Booth #: 3352
www.ipm.pitt.edu/UGC
The UPMC Genome Center is a high-throughput, CAP/CLIA certified sequencing center located in Pittsburgh, PA. We focus on providing the highest quality lab services for both clinical and research needs to support the pursuit of understanding DNA and RNA sequence variation in relation to phenotypic variability in human disease.

EXHIBITOR DESCRIPTIONS

Variantyx Inc
Booth #: 2938
www.variantyx.com
Variantyx provides Genomic Unity™ whole genome testing services to clinicians for diagnosis of rare inherited disorders. We also enable hospitals and labs to profitably expand their test menu with validated genomic diagnostic solutions using our automated Genomic Intelligence® platform for simplified NGS data analysis, interpretation and clinical reporting.

Vela Diagnostics
Booth #: 3053
www.veladx.com
Vela Diagnostics is a leading provider of an automated IVD Next Generation Sequencing (NGS) workflow in the global diagnostics market. Our sample-to-result NGS and real-time PCR solutions standardize testing, improve workflows, and help to reduce cost for optimal efficiency across laboratories of all sizes.

WellSIM Biomedical Technologies, Inc.
Booth #: 2321
www.wellsimbiotech.com
WellSIM Biomedical Technologies has developed innovative high-throughput exosome isolation technologies that enable the highest yield and purity of exosomes from clinical specimens such as urine, plasma, CSF and tears, and cell culture media. Our Label-free Exosome Automatic Purification (LEAP) System is the first fully automatic platform for exosome preparation in the world. Visit us to learn more or visit www.wellsimbiotech.com.

XCR Diagnostics, Inc.
Booth #: 2848
www.xcrdiagnostics.com
XCR Diagnostics utilizes the patented amplification technology - Xtreme Chain Reaction (XCR(r)) on the Pyramid system to provide rapid, quality results in as few as 7 minutes in the near patient testing environment. XCR(r) is also adaptable to most existing PCR instruments, reagents and probe technologies increasing their speed and therefore providing greater throughput.

XIFIN, Inc.
Booth #: 2940
www.xifin.com
XIFIN is a health information technology company that leverages diagnostic information to improve the quality and economics of healthcare. The XIFIN technology platform facilitates connectivity and workflow automation for accessing and sharing clinical and financial diagnostic data, linking healthcare stakeholders in the delivery and reimbursement of care.

YouSeq Ltd
Booth #: 3245
www.youseq.com
YouSeq is an expert organisation, specialising in the design, development and manufacture of Next Generation Sequencing (NGS) kits, panels and reagents.

ZeptoMetrix Corporation
Booth #: 3017
www.zeptometrix.com
ZeptoMetrix™ is a leader in the design, development, and delivery of innovative, quality solutions to the Infectious Disease Diagnostics Market. Our expertise and abilities in Molecular Diagnostics, including External Quality Controls, Verification Panels, Proficiency Panels, Customized and OEM Products/Services has set the industry standard for performance and reliability and made us the preferred choice for independent 3rd party QC materials.

Zymo Research Corp.
Booth #: 2858
www.zymoresearch.com
Since 1994, Zymo Research has been offering innovative, quality and easy-to-use tools for nucleic acid purification and Epigenetics research. Our innovative products and services simplify complex processes while at the same time improving results. All of our products are supported by unparalleled customer support. Zymo Research – Innovation. Quality. Simplicity.

NOTES

NOTES

PICKING UP PIK3CA MUTATIONS

Learn about the most common mutation in HR+/HER2- advanced breast cancer (aBC) and how to detect it at **BOOTH 2741**[1-4]

INNOVATION SPOTLIGHT

with Jean Lopategui, MD

Associate Professor of Pathology
Director of Translational Genomics
Program Director of Molecular Genetic Pathology Fellowship
Cedars-Sinai Medical Center
Los Angeles, California

Friday, November 8, 2019
10:00 AM - 10:30 AM
at STAGE 2

Join us as Dr Jean Lopategui discusses PIK3CA mutations in HR+/HER2- aBC and how to detect them.

References: 1. The Cancer Genome Atlas Network. Comprehensive molecular portraits of human breast tumours. *Nature*. 2012;490(7418):61-70. 2. Tolaney S, Toi M, Neven P, et al. Presented at: 2019 American Association for Cancer Research (AACR) Annual Meeting; March 29-April 3, 2019; Atlanta, GA. 3. Di Leo A, Johnston S, Seok Lee K, et al. *Lancet Oncol*. 2018;19(1):87-100. 4. Moynahan ME, Chen D, He W, et al. *Br J Cancer*. 2017;116(6):726-730.

NOVARTIS

Novartis Pharmaceuticals Corporation
East Hanover, New Jersey 07936-1080

10/19 BST-1222219

Bristol-Myers Squibb: at the forefront of Immuno-Oncology research

Precision Medicine Starts with Pathology

At Bristol-Myers Squibb (BMS), we recognize pathologists play a crucial role in furthering advancements that may help predict which patients are likely to benefit from Immuno-Oncology (I-O) therapies.

Bristol-Myers Squibb is looking at multiple I-O biomarkers to help identify new ways to understand a patient's immune response to a tumor. These biomarkers may have the potential to change how cancer is treated through personalized I-O therapy selection. BMS is dedicated to discovering predictive I-O biomarkers that can help pathologists support better patient outcomes.

To learn more, visit us at the Association for Molecular Pathology Annual Meeting in Baltimore, November 7–9, 2019

The sponsor of this ad verifies that they had no input into decision making regarding selection of educational programs, content, or faculty for this 2019 Annual Meeting.

For more information, please visit **IOHCP.com** and our YouTube channel at **youtube.com/bmsIOresearch**.

Bristol-Myers Squibb

Immuno-Oncology