



AMP 2020

ANNUAL MEETING & EXPO

November 16-20, 2020

**A Virtual Education &
Networking Experience**

Program Book

amp20.amp.org

 **AMP** ASSOCIATION
FOR MOLECULAR
PATHOLOGY

The power to **react**. The potential to **grow**.

In these uncertain times, consolidate your molecular testing today on a platform that offers scalability, growth and confidence for tomorrow.

VISIT THE **HOLOGIC® VIRTUAL BOOTH** TO LEARN MORE.

AVAILABLE TODAY



PANTHER®

CT/NG
Mycoplasma genitalium
Trichomonas vaginalis
 Bacterial vaginosis
 Candida vaginitis/*Trichomonas vaginalis*
 HSV 1 & 2



ADD ON PANTHER FUSION®

§ The Aptima and Panther Fusion SARS-CoV-2 assays:
 • These tests have not been FDA cleared or approved;
 • These tests have been authorized by FDA under an EUA for use by authorized laboratories;
 • These tests have been authorized only for the detection of nucleic acid from SARS-CoV-2, not for any other viruses or pathogens; and
 • These tests are only authorized for the duration of the declaration that circumstances exist justifying the authorization of emergency use of in vitro diagnostic tests for detection and/or diagnosis of COVID-19 under Section 564(b)(1) of the Act, 21 U.S.C. § 360bbb-3(b)(1), unless the authorization is terminated or revoked sooner.



ADD ON PANTHER® PLUS

HPV
 HPV 16 18/45
 Group B Strep
 Zika Virus[†]
 HIV-1 Quant
 HIV-1 Qual Claim*[‡]



ADD ON PANTHER® LINK

HCV Quant Dx
 HBV Quant
 CMV*
 Flu A/B/RSV
 Paraflu
 Adv/hMPV/RV



ADD ON PANTHER® TRAX*

SARS-CoV-2[§]
 SARS-CoV-2/Flu/A/B*
 Bordetella*
 GI Panel*

GROW ON PANTHER

* In development and not for sale.

[†] 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 under section 564(b)(1) of the Act, 21 U.S.C. § 360bbb-3(b)(1), unless the authorization is terminated or revoked sooner.

[‡] Seeking dual claim for the HIV-1 Quant assay.

§ The Aptima and Panther Fusion SARS-CoV-2 assays:
 • These tests have not been FDA cleared or approved;
 • These tests have been authorized by FDA under an EUA for use by authorized laboratories;
 • These tests have been authorized only for the detection of nucleic acid from SARS-CoV-2, not for any other viruses or pathogens; and
 • These tests are only authorized for the duration of the declaration that circumstances exist justifying the authorization of emergency use of in vitro diagnostic tests for detection and/or diagnosis of COVID-19 under Section 564(b)(1) of the Act, 21 U.S.C. § 360bbb-3(b)(1), unless the authorization is terminated or revoked sooner.



KITTED



BIOINFORMATICS



REPORTING



PGDx^{elio}™ tissue complete

**OUR TEST.
YOUR LAB.
FAST RESULTS.**

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.



Break Through Your SARS-CoV-2 Testing Bottleneck

**Secure a Reliable Supply of Testing Materials
Under \$10 Per Sample**

SARS-CoV-2 Testing on the MassARRAY® System



- Immediate availability of instruments and reagents
- Mitigate supply chain risks with reliable supply
- Test 1000s of samples per day on a single instrument
- Perform testing at under \$10 per sample

Alleviate testing material shortages with the MassARRAY® SARS-CoV-2 Panel. With a secure supply of instruments and reagents, Agena Bioscience® can help to quickly increase your SARS-CoV-2 testing capacity. Laboratories can process 1000s of samples in less than 24 hours on a single MassARRAY System, helping them keep pace with increased volumes.

Get Started Now

Ask us about our solutions for combined detection of Flu A/B and SARS-CoV-2.

Visit agenabio.com or call 1-858-882-2800



The assay is available for *in vitro* diagnostic use under the U.S. FDA's Emergency Use Authorization and is CE-IVD marked in Europe.

KEYTRUDA[®]
(pembrolizumab) Injection 100 mg

Visit **keytruda.com/hcp**
to learn more about **KEYTRUDA:**

- Approved indications
- Resources for health care professionals
- The Merck Access Program
- KEY+YOU Support Program for patients



Copyright © 2018 Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc.
All rights reserved. ONCO-1246949-0000 02/18 keytruda.com

Table of Contents

General Information

Code of Conduct.....	7
Highlights & General Information.....	9
Award for Excellence 2020 Recipient.....	12
Jeffrey A. Kant Leadership Award 2020 Recipient.....	13
Meritorious Service Award 2020 Recipient.....	14
2020 Registration Support Award Recipients.....	15

Continuing Education

Continuing Education Information.....	17
Continuing Education Tracker.....	18

Program

Full Program Listing.....	21
---------------------------	----

Posters

Poster Information.....	51
Poster Listing.....	52
Author Index.....	73

Exhibits

Exhibitor Listing.....	86
Exhibitor Descriptions.....	88

~~~

# Virtual Meeting Code of Conduct

## Policy:

The Association for Molecular Pathology (AMP) is committed to providing a friendly, comfortable, and welcoming virtual event 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, vendors/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, messages, posts within a virtual or social media platform, 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, vendors/contractors, 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 virtual platform, we expect all participants at AMP virtual events and meetings to abide by this Code of Conduct in all venues, including whatever virtual platform being used, 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.

## Expected Behaviors

- AMP holds 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, written text and actions.
- Abstain from all demeaning, discriminatory, or harassing behavior and language when communicating with others.
- Respect the fact that slides and e-posters may include unpublished work so if a speaker or author requests that slides or posters not be “photographed,” do not download, take a screen shot, photograph or video your screen, or otherwise retain them.
- Do not video, audio, or otherwise record presentations.
- Slides and/or handouts available within the virtual platform may be downloaded for non-commercial use. Scientific integrity mandates that speakers and authors be acknowledged.
- Registrations are for individual access. Please do not share or broadcast the meeting to a group or share your platform login access with anyone else.
- Be mindful of your fellow participants. Alert the AMP Meetings Department at [meetings@amp.org](mailto:meetings@amp.org) or at the Virtual Meeting Help Desk if you notice behavior that violates this Code of Conduct.

## **Unacceptable Behaviors**

Unacceptable Behaviors at AMP Virtual Events Include:

- Intimidating, harassing, abusive, discriminatory, derogatory or demeaning speech, written text, 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, posts within a virtual or social media platform, and in exhibit booths
- Intimidation in any form, such as virtual stalking
- Unwelcome or uninvited attention or contact
- Real or implied threat of harm of any type, including physical, professional, or financial
- Retaining, by any means, slides, presentations, or posters when the presenter/author requests “no photography” or otherwise indicates this directive.
- Disruption of sessions or other events
- Failure to follow the directives of the session moderators or AMP staff

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

- Anyone who is the recipient of unacceptable behavior should feel free to speak up without any fear of retaliation.
- Please contact the AMP Meetings Department at [meetings@amp.org](mailto:meetings@amp.org) or at the Virtual Meeting Help Desk if you notice behavior that violates this Code of Conduct. All reports will be kept confidential to the extent possible while allowing for effective investigation and response.
- AMP Staff will help participants contact relevant authorities, and otherwise assist those experiencing conduct that violates this Code of Conduct. We value your participation with AMP, and want your experience to be professionally rewarding and personally enjoyable.



# Highlights & General Information

For the most up to date information please visit:

<https://amp20.amp.org/program/attendee-information/>

## General Information

- The **AMP Virtual Platform** will be accessible to registered meeting attendees **starting Monday, November 16, 2020 at 10:00 AM Eastern** through Monday, February 15, 2021 at 11:59 PM. *Note: You will NOT be able to login/access the event until that time.*
- The AMP virtual platform will give you access to scientific sessions, corporate workshops, eposters, the expo hall and several other exciting features!
- All sessions and events are listed in US Eastern time.
- Please make sure you login/logout each day so your account is updated with important announcements.
- Live Hours For Technical/Program Questions: Will be available for the following times, just email: [amp20@getvfairs.io](mailto:amp20@getvfairs.io)

Mon: 10am – 7pm  
Tues: 9am – 7pm  
Wed: 10am – 7pm  
Thurs: 10am – 7pm  
Fri: 10am – 5pm

## Virtual Platform User Guides

Please refer to the following "User Guides" as you navigate your way through the virtual platform!

- [Getting Started/Setting Up Your Profile](#)
- [Technical Support](#)
- [Scientific Sessions](#)
- [Corporate Workshop Theater](#)
- [Poster Hall](#)
- [Expo Hall](#)
- [Chat with Exhibitors](#)
- [Networking & Social Events](#)
- [Continuing Education](#)
- [AMP Leaderboard](#)
- [Expo Hall Scavenger Hunt](#)

## Program Information

The full scientific program can be found on the meeting [website](#). Please be sure to check out all the areas of the virtual platform, including the Auditorium (scientific sessions), Poster Hall, Expo Hall, and Corporate Workshop Theater.

## Continuing Education

Included in your attendee registration, you will be eligible to apply for continuing education credit! Unlike previous years, you will be able to apply for significantly more credits because you will

have the ability to watch the sessions onDemand through February 15th! Please wait to submit for CE until you've watched all of the sessions for which you want to claim credit! Please click [here](#) for more information.

## Code of Conduct

Please make sure you review [AMP's Code of Conduct](#).

## Social Media

Follow AMP on Twitter, Facebook and LinkedIn, and use the #AMPath20 and #AMPlifier hashtags to join the conversation! We encourage you to share insights from the meeting, but ask that all attendees refrain from taking/sharing photos of slides or posters without permission. Please be respectful and courteous to your colleagues, and most importantly, have fun!

### Social Media Guidelines

We encourage the use of social media for professional networking purposes before, during and after AMP 2020. To ensure that everyone has a positive social media experience, please adhere to these guidelines:

Do:

- Follow AMP on Twitter (@AMPath), like us on Facebook (facebook.com/AMPathology), and/or join our LinkedIn group (linkedin.com/groups/2681654)
- Use the #AMPath20 hashtag to join the conversation and get the latest annual meeting updates
- Post about what you discover at the meeting, but be mindful of requests for confidentiality or attribution
- Share your knowledge and insights
- Be respectful and courteous to your colleagues
- Have fun!

Don't:

- Post inflammatory, disrespectful or otherwise inappropriate comments
- Take/share photos of slides or posters without permission
- Post copyrighted/trademarked/embargoed materials

## AMP Central

Visit AMP Central to view AMP Documents, access the Chat Rooms and be connected to AMP's Social Media platforms.

## Expo Hall

Be sure not to miss the Virtual Expo Hall - whether you're searching for the latest products and services, are just browsing, or want to connect with one of your current vendors, the AMP Expo Hall has it all! Once in the Virtual Platform, please enter the "Expo Hall" You'll be able to search the "exhibitor index" or scroll through to see booths from AMP Corporate Partners and exhibiting companies.

### DON'T MISS THESE EXCITING FEATURES OF THE VIRTUAL EXPO HALL:

- Reserve you "Chat Slot" with Premium Exhibitors during the designated Expo Hall hours.

- Save exhibitor documents to your "Virtual Meeting Bag" and email them to yourself later.
- Participate in the "Scavenger Hunt" in the Expo Hall and the "AMP Leaderboard" throughout the virtual platform! We have some really cool prizes - check them out on the "Leaderboard" menu tab in the Lobby!

We have have designated Expo Hall hours (schedule below), but please visit the hall throughout the day and connect with with all of our exhibitors!

**Monday, November 16, 2020**

10:30am - 11:15am

2:00pm - 3:00pm - includes demos & drawings

**Tuesday, November 17, 2020**

11:00am - 11:45am

2:00pm - 3:00pm - includes demos & drawings

**Wednesday, November 18, 2020**

11:00am - 11:45am

2:30pm - 3:30pm - includes demos & drawings

**Thursday, November 19, 2020**

11:00am - 11:45am

2:00pm - 3:00pm - includes demos & drawings

**Friday, November 20, 2020**

11:00am - 11:45am

2:30pm - 3:30pm - includes demos & drawings

**Thank You Sponsors!** Thank you to our exhibitors and sponsors for their support of the 2020 Annual Meeting & Expo! Click [here](#) to see the current listing of exhibitors & sponsors!

**Corporate Workshops**

Corporate Workshop Day has been re-imagined to better accommodate a virtual format. In the past, time constraints or flight schedules limited how many events you could attend. Now, with complimentary OnDemand access to recorded sessions through February 15, 2021 you can catch all of your "must-see" content on *your* schedule. Please view the [Corporate Workshop Program](#) and visit the Corporate Workshop Theater to view these workshops!

**Innovation Spotlights**

This year's Innovation Spotlight Stages will include exhibitor spotlights as well as two presentations from AMP's Training & Education Committee. You can view the Exhibitor Spotlight in the Corporate Workshop Theater and the Training & Education Committees presentations in the Auditorium. Schedules for this program are available on the website, please [click here](#) to view the schedule.

**Networking & Social Events**

Check out the [website](#) for information on some exciting networking events - including some of our favorites like the trainee and technologist mixers and the AMP Talent Show! Also, if you like beer and wine, please check out those social events as well!

**ASSOCIATION FOR MOLECULAR PATHOLOGY**

**AMP Award for Excellence  
in Molecular Diagnostics 2020**



**Dennis Lo, FRS**  
The Chinese University of Hong Kong

**ASSOCIATION FOR MOLECULAR PATHOLOGY**

**Jeffrey A. Kant Leadership Award 2020**

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



**Karen P. Mann, MD, PhD**

Grady Health System  
Emory University School of Medicine  
Atlanta, GA

**ASSOCIATION FOR MOLECULAR PATHOLOGY**

**AMP Meritorious Service Award 2020**



**Ronald M. Przygodzki, MD**

Department of Veterans Affairs, Veterans Health  
Administration, Office of Research & Development,  
Washington, DC

# ASSOCIATION FOR MOLECULAR PATHOLOGY

## Registration Support Awards 2020

### Trainees

Sara Akhavanfard, MD, PhD - Nationwide Children's Hospital, Columbus, OH  
Erica Kay Barnell - Washington University School of Medicine, Saint Louis, MO  
Isabel Betancor Fernández - Hospital Universitario de Canarias, San Cristóbal de La Laguna, Santa Cruz de Tenerife, Spain  
Kelly E. Craven, MD, PhD - Johns Hopkins University School of Medicine, Baltimore, MD  
Pratik Deb, MD, PhD - Rutgers New Jersey Medical School, Newark, NJ  
Ryan DeCoste, MD - QEII Health Sciences Centre, Nova Scotia Health Authority, Halifax, Nova Scotia, Canada  
Samreen Fathima, MD - Baylor University Medical Center, Dallas, TX  
Matthew Gayhart, MD - Cedars-Sinai Medical Center, Los Angeles, CA  
Lisa Lansdon, PhD - Children's Mercy Kansas City, Kansas City, MO  
Cullen M. Lilley, MA - Loyola University Chicago Stritch School of Medicine, Maywood, IL  
Andres G. Madrigal, MD, PhD - Oregon Health & Science University, Portland, OR  
Marilena Melas, PhD - Institute for Genomic Medicine/ Nationwide Children's Hospital, Columbus, OH  
Vamsi Parini - The Johns Hopkins University School of Medicine, Baltimore, MD  
Vanessa Smith, MD - Duke University Health System, Durham, NC  
Yian Wang - Coder School, Irvine, CA

### Technologists

Ayah Abdulhamid - Children's Mercy Hospital, Kansas City, MO  
Diana Gerrard - University of Vermont Medical Center, Burlington, VT  
Egiebade Iriabho - The University of Alabama at Birmingham, Birmingham, AL  
Krupa Jani - Memorial Sloan Kettering Cancer Center, New York, NY  
Brittany Jones - St. Jude Children's Research Hospital, Memphis, TN  
Julie Joyce - Children's Mercy Hospital, Kansas City, MO  
Melissa Rimmel - Inflammatrix, Burlingame, CA  
Jeffery Schubert - Children's Hospital of Philadelphia, Philadelphia, PA  
Susan Shumaker - St. Jude Children's Research Hospital, Memphis, TN  
Patricia L. Stow - St. Jude Children's Research Hospital, Memphis, TN  
Rebecca Wallace - St. Jude Children's Research Hospital, Memphis, TN

# ASSOCIATION FOR MOLECULAR PATHOLOGY

## Registration Support Awards 2020

### Individuals Underrepresented in Medicine

Adewole Adegboruwa, MS - Magnolia Diagnostics LLC, Dallas, TX  
David O. Henriquez Ticas, MD - Baylor College of Medicine, Houston, TX  
Patricia Hernandez, MD - Institute for Systems Biology, Tucson, AZ  
Peter Louis, MD, JD, MT (ASCP) - Vanderbilt University Medical Center, Nashville, TN  
Jude Noel, MS – Virginia Commonwealth University Health, Richmond, VA  
Veronica Ortega, BS, BA – UTHealth, San Antonio, TX

### Residents of Lower-middle- and Lower-income Countries

Zeeshan Ahmed, MBBS - Aga Khan University Hospital, Karachi, Pakistan  
Vincent Francis P. Castillo, MD - St. Luke's Medical Center - Global City, Taguig City, Metro Manila, Philippines  
Gauri Deshpande, MD - Tata Memorial Hospital, Mumbai, Maharashtra, India  
Vivek Gupta, MD, PhD - Government Institute of Medical Sciences, Greater Noida, Uttar Pradesh, India  
Zahra Hasan, PhD - Aga Khan University, Karachi, Pakistan  
Sawsan Ismail, MD - Tishreen University Hospital, Lattakia, Syria  
Sudha S. Murthy, MD - Datar Cancer Genetics Ltd, Nashik, Maharashtra, India  
Shano Naseem, MD - Postgraduate Institute of Medical Education and Research, Chandigarh, India  
Ruhul Quddus, MBBS - Aga Khan University Hospital, Karachi, Pakistan



# Continuing Education

## Physicians

In support of improving patient care, this activity has been planned and implemented by Amedco LLC and 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.

## Physicians

Amedco LLC designates this live streamed activity for a maximum of **59.50 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 Amedco and the joint provider-ship of the ASC and the Association for Molecular Pathology (AMP) and has been approved for 59.50 Credits of CMLE Hours.

## American Board of Pathology (ABPath) MOC

This activity is registered with the American Board of Pathology Maintenance of Certification Program for Self-Assessment Module (SAM) for **13.00 credit hours**. Participant information will be uploaded to the ABPath MOC Board 30 days post activity.

**\*IMPORTANT: The ABPath MOC/SAM Program will end 12/31/2020. All credits must be claimed by that date.**

For any questions, contact [ampeducation@amp.org](mailto:ampeducation@amp.org).

## AMP 2020 ANNUAL MEETING & EXPO CREDIT TRACKER

<https://amp20.amp.org/program/virtual-program/>

| Session Date                            | Session Title                                                                                      | Faculty                                                                                                            | CME/CMLE Eligible Hours<br>(Available through 2/15/21) | SAMs Eligible Hours (Available<br>through 12/31/2020) | Number of hours attended of<br>session | Session Notes and Comments |
|-----------------------------------------|----------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------|-------------------------------------------------------|----------------------------------------|----------------------------|
| Monday November 16<br>11:30am - 1:00pm  | AMP Award for Excellence in Molecular Diagnostics: Presentation and Lecture                        | Dennis Lo, FRS                                                                                                     | 1.5                                                    | -                                                     |                                        |                            |
| Monday November 16<br>1:00pm - 2:00pm   | Molecular Methods for Discovery of Novel Pathogens                                                 | Ilan Schwartz, MD, PhD and Lea Starita                                                                             | 1.0                                                    | -                                                     |                                        |                            |
| Monday November 16<br>1:00pm - 2:00pm   | Transitioning to hg38                                                                              | Justin Zook, PhD and Sabah Kadri, PhD                                                                              | 1.0                                                    | 1.0                                                   |                                        |                            |
| Monday November 16<br>1:00pm - 2:00pm   | Integrative Analysis of the Tumor Microenvironment                                                 | Thomas Gajewski, MD, PhD and Scott Rodig, MD, PhD                                                                  | 1.0                                                    | 1.0                                                   |                                        |                            |
| Monday November 16<br>1:00pm - 2:00pm   | Targeted Therapies for Constitutional Genetic Disorders                                            | Garry Cutting, MD                                                                                                  | 1.0                                                    | 1.0                                                   |                                        |                            |
| Monday November 16<br>1:00pm - 2:00pm   | Case Studies in Infectious Diseases and Solid Tumors                                               | Eun Kim, MSC; Debbie Walley, MD; William Webster, DO; Adam Fisch, MD, PhD; and Matthew Gayhart, MD                 | 1.0                                                    | -                                                     |                                        |                            |
| Monday November 16<br>3:00pm - 4:00pm   | Implementation of Molecular Infectious Diagnostics Test at the Point-of-Care                       | Omai Garner, PhD and Raquel M. Martinez, MBA, PhD                                                                  | 1.0                                                    | -                                                     |                                        |                            |
| Monday November 16<br>3:00pm - 4:00pm   | Laboratory Assurance Compliance Solutions                                                          | Justin Hammerling, MBA                                                                                             | 1.0                                                    | -                                                     |                                        |                            |
| Monday November 16<br>3:00pm - 4:00pm   | Guidance for Reevaluation and Reanalysis of Genomic Test Results                                   | Josh Deignan, PhD                                                                                                  | 1.0                                                    | -                                                     |                                        |                            |
| Monday November 16<br>3:00pm - 4:00pm   | Case Studies in Hematopathology and Solid Tumors                                                   | Jessica Ziemba, MD; Jonathan Tsai, MD, PhD; Audrey Jajosky, MD, PhD; Sara Akhavanfard, MD, PhD; and Eric Goold, MD | 1.0                                                    | -                                                     |                                        |                            |
| Monday November 16<br>3:00pm - 4:00pm   | Epigenetics in Malignant Hematology                                                                | Maria Figueroa, MD                                                                                                 | 1.0                                                    | 1.0                                                   |                                        |                            |
| Tuesday November 17<br>12:00pm - 1:00pm | Single Cell Insights into Myeloid Neoplasia                                                        | Koichi Takahashi, MD, PhD                                                                                          | 1.0                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>1:00pm - 2:00pm  | Platform Presentations of Selected Genetics Abstracts                                              | Elan Hahn, MD; Diana Mandelker, MD, PhD; Ozge Ceyhan-Birsoy, PhD; and Dale Muzey, PhD                              | 1.0                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>1:00pm - 2:00pm  | Platform Presentations of Selected Hematopathology Abstracts                                       | Eitan Halper-Stromberg, MD, PhD; Miguel Cantu, MD; Mia Donna Dabrowski, MT(ASCP); and Lu Wang, MD, PhD             | 1.0                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>1:00pm - 2:00pm  | Platform Presentations of Selected Infectious Diseases Abstracts                                   | Michael Tomasek, Priya Velu, MD, PhD; Rossio Kersey, PhD; and Timothy Blauwkamp, PhD                               | 1.0                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>3:00pm - 4:00pm  | Practical Approaches to Diagnostic Stewardship of Advanced Molecular Tests                         | Daniel Diekema, MD, Neil Anderson MD, Amanda Harrington, PhD, and D. Jane Hata, PhD                                | 1.0                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>3:00pm - 4:00pm  | Single-cell Sequencing/Slide-Seq: A Scalable Method for Spatially Resolved Gene Expression Studies | Orit Rozenblatt-Rosen, PhD                                                                                         | 1.0                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>3:00pm - 4:00pm  | Moving Towards Clinical-grade HGVS Nomenclature                                                    | Birgit Funke, PhD, Reece Hart, PhD, Somak Roy, MD, and Ryan Schmidt, MD, PhD                                       | 1.0                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>3:00pm - 4:00pm  | Case Studies in Genetics and Hematopathology                                                       | Kelly Rafferty, PhD, MS; Diana Toledo, PhD, MS; Sjjawal Ahmad, MSc; Marilena Melas, MSc; and Won Sok Lee, MD, MPH  | 1.0                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>3:00pm - 6:00pm  | Next-generation Sequencing Assay Development and Validation                                        | Ryma Benayed, PhD, Eric Konnick, MD, MS, Kurt Davies, PhD, Dara Aisner, MD, PhD, and Jeremy Segal, MD, PhD         | 3.0                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>4:00pm - 5:30pm  | Variant Review and Classification Workshop                                                         | Laura Tafe, MD, Somak Roy, MD, Mark Routbort, MD, PhD                                                              | 1.5                                                    | -                                                     |                                        |                            |

| Session Date                              | Session Title                                                                                        | Faculty                                                                                                           | CME/CMLE Eligible Hours<br>(Available through 2/15/21) | SAMs Eligible Hours (Available<br>through 12/31/2020) | Number of hours attended of<br>session | Session Notes and Comments |
|-------------------------------------------|------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------|-------------------------------------------------------|----------------------------------------|----------------------------|
| Tuesday November 17<br>4:00pm - 5:30pm    | High-Throughput Functional and Genomic Approaches for Understanding Germline and Somatic             | Collin Tokheim, PhD and Jay Shendure, MD, PhD                                                                     | 1.5                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>4:00pm - 5:30pm    | COVID-19 Molecular Testing: Experiences from the Field                                               | Teresa Karre, MD, Anthony Tran, DrPH, MPH, Beth Marlowe, PhD, Michael Bachman, MD, PhD                            | 1.5                                                    | -                                                     |                                        |                            |
| Tuesday November 17<br>4:00pm - 5:30pm    | Laboratory Economics During a Public Health Emergency: Lessons Learned (and still learning) from the | Erika Miller, JD, Samuel Caughron, MD, Pranil Chandra, DO, and Jay Patel, MD, MBA                                 | 1.5                                                    | -                                                     |                                        |                            |
| Wednesday November 18<br>12:00pm - 1:00pm | Coronavirus Pandemic Updates                                                                         | Carlos del Rio, MD                                                                                                | 1.0                                                    | -                                                     |                                        |                            |
| Wednesday November 18<br>1:00pm - 2:30pm  | Distributed Laboratories and Third Party Interpretation Services                                     | Gail Javitt, MD, PhD, Matthew Lebo, PhD, and Rakesh Nagarajan, PhD, MD                                            | 1.5                                                    | -                                                     |                                        |                            |
| Wednesday November 18<br>1:00pm - 2:30pm  | Point-Counter Point: Clinical Metagenomics Is Worth the Juice                                        | Steve Miller, MD, PhD, William Muller, MD, PhD, Stephanie Mitchell, PhD, and Debra Palazzi, MD                    | 1.5                                                    | -                                                     |                                        |                            |
| Wednesday November 18<br>1:00pm - 2:30pm  | Early Detection and Characterization of Cancer Using cfDNA and Distinction from                      | Pedram Razavi, MD, PhD and Victor Velculescu, MD, PhD                                                             | 1.5                                                    | -                                                     |                                        |                            |
| Wednesday November 18<br>1:00pm - 2:30pm  | Bridging the Gap: Molecular Tumor Boards, Clinical Trials Matching, and the                          | Marios Giannakis, MD, PhD, and Mia Levy, MD, PhD                                                                  | 1.5                                                    | -                                                     |                                        |                            |
| Thursday November 19<br>12:00pm - 1:00pm  | Machine Learning in Health Care                                                                      | Stephen Kingsmore, MD, DSc                                                                                        | 1.0                                                    | 1.0                                                   |                                        |                            |
| Thursday November 19<br>1:00pm - 2:00pm   | Platform Presentations of Selected Informatics Abstracts                                             | Jagadshwar Balan, Andrew Skol, PhD, Andrea Sboner, PhD, and Egiebade Iriabho, MSc                                 | 1.0                                                    | -                                                     |                                        |                            |
| Thursday November 19<br>1:00pm - 2:00pm   | Platform Presentations of Selected Solid Tumors Abstracts                                            | Cameron Beech, MD; Ryan DeCoste, MD; Fumin Lin, PhD; and Erica Barnell, PhD                                       | 1.0                                                    | -                                                     |                                        |                            |
| Thursday November 19<br>1:00pm - 2:00pm   | Platform Presentations of Selected Technical Topics Abstracts                                        | Xiaotian Wang, PhD; Chris Karlovich, PhD; Lei Zhang, and Ernest Lam                                               | 1.0                                                    | -                                                     |                                        |                            |
| Thursday November 19<br>3:00pm-4:00pm     | True or False: Interpretation Challenges of Blood Culture Identification                             | Richard Davis, PhD, and Susan Butler-Wu, PhD                                                                      | 1.0                                                    | 1.0                                                   |                                        |                            |
| Thursday November 19<br>3:00pm-4:00pm     | Addressing the Clinical Laboratory Workforce Shortage - Automation and Robotics                      | Jose Manuel Collados, ABB and Susanne Norris-Zanto                                                                | -                                                      | -                                                     |                                        |                            |
| Thursday November 19<br>3:00pm-4:00pm     | Next-generation Sequencing Assay Development and Validation Q&A                                      | Dara Aisner, MD, PhD; Ryma Benayed, PhD; Kurt Davies, PhD; Eric Konnick, MD, MS; and Jeremy Segal, MD, PhD        | 1.0                                                    | -                                                     |                                        |                            |
| Thursday November 19<br>3:00pm-4:00pm     | Tissue Stewardship: Maximizing the Information That Can Be Provided by Small                         | Sinchita Roy Chowdhuri, MD, PhD, and Christopher Gilbert, DO                                                      | 1.0                                                    | 1.0                                                   |                                        |                            |
| Thursday November 19<br>3:00pm-4:00pm     | Next Generation Guidelines for Clinical Sequencing: Translating Regulations into                     | Birgit Funke, PhD and Annette Leon, PhD, MS                                                                       | -                                                      | -                                                     |                                        |                            |
| Thursday November 19<br>4:00pm-5:30pm     | What Do All These Mutations Mean?                                                                    | Kelly Bolton, MD, PhD and Amy Dezern, MD, MHS                                                                     | 1.5                                                    | 1.5                                                   |                                        |                            |
| Thursday November 19<br>4:00pm-5:30pm     | Genomics in Children: Coming of Age                                                                  | Sharon Plon, MD, PhD and Jinghui Zhang, PhD                                                                       | 1.5                                                    | -                                                     |                                        |                            |
| Thursday November 19<br>4:00pm-5:30pm     | Enhanced Molecular Diagnosis Through Structural Variant Detection                                    | Madhuri Hegde, PhD, Stephen Lincoln and Nicole Hoppman, PhD                                                       | 1.5                                                    | 1.5                                                   |                                        |                            |
| Thursday November 19<br>4:00pm-5:30pm     | The Roadmap to Recognition of Molecular Professionals as Qualified Healthcare                        | Charles Matthews, MPP; Andrea Ferreira-Gonzalez, PhD; Elaine Lyon, PhD; Tina Lockwood, PhD; and John Schmitz, PhD | 1.5                                                    | -                                                     |                                        |                            |
| Thursday November 19<br>4:00pm-5:30pm     | Strain Typing in Clinical and Public Health Laboratory: Migration to Whole Genome                    | William Glover, PhD and Sanchita Das, MD                                                                          | 1.5                                                    | -                                                     |                                        |                            |
| Friday November 20<br>12:00pm - 1:00pm    | DepMap: The Cancer Dependency Map Project                                                            | William Hahn, MD, PhD                                                                                             | 1.0                                                    | -                                                     |                                        |                            |
| Friday November 20 1:00pm - 2:30pm        | Genomically-informed Lymphoma Classification                                                         | Sandeep Dave, MD and Javeed Iqbal, MS, PhD                                                                        | 1.5                                                    | -                                                     |                                        |                            |

| Session Date                          | Session Title                                                              | Faculty                                                 | CME/CMLE Eligible Hours<br>(Available through 2/15/21) | SAMs Eligible Hours (Available<br>through 12/31/2020) | Number of hours attended of<br>session | Session Notes and Comments |
|---------------------------------------|----------------------------------------------------------------------------|---------------------------------------------------------|--------------------------------------------------------|-------------------------------------------------------|----------------------------------------|----------------------------|
| Friday November 20 1:00pm<br>- 2:30pm | Whole Genome Sequencing for Antimicrobial Resistance Testing               | Matthew Binnicker, PhD and Kimberlee Musser, PhD        | 1.5                                                    | 1.5                                                   |                                        |                            |
| Friday November 20 1:00pm<br>- 2:30pm | Emerging Testing Paradigms and Insights                                    | Steven Bleyl, MD, PhD, Scott Topper, PhD, James Lu, PhD | 1.5                                                    | 1.5                                                   |                                        |                            |
| Friday November 20 1:00pm<br>- 2:30pm | Tumor Evolution and Therapeutic Resistance                                 | Noam Auslander, PhD and Peter Van Loo, PhD              | 1.5                                                    | -                                                     |                                        |                            |
| Friday November 20 1:00pm<br>- 2:30pm | Next Generation Data: Integration and Dissemination of Molecular Pathology | Ahmet Zehir, PhD and Cihan Kaya, PhD                    | 1.5                                                    | -                                                     |                                        |                            |
| Friday November 20 3:30pm<br>- 4:30pm | Gene Therapy for Retinal Disorders                                         | Elias I. Traboulsi, MD                                  | 1.0                                                    | -                                                     |                                        |                            |
|                                       |                                                                            | <b>TOTAL HOURS</b>                                      | <b>59.5</b>                                            | <b>13.0</b>                                           |                                        |                            |



---

## Award for Excellence Lecture

Monday, November 16, 11:30 am – 1:00 pm

**Session Type:** Live

**CE Credit:** 1.5

### **Award for Excellence Lecture: Plasma DNA Based Molecular Diagnostics - From Dream to Reality**

*Dennis Lo, FRS, The Chinese University of Hong Kong, Hong Kong, China*

**Session Description:** In this lecture, Dennis Lo will share with the audience regarding his journey from the discovery of fetal DNA in maternal plasma to the development of non-invasive prenatal testing (NIPT). He will also discuss the application of plasma DNA analysis to early cancer detection. Finally, he will discuss recent understanding of the biology of circulating DNA in blood.

**Session Objectives:**

- To appreciate the basic biology of circulating DNA in plasma.
- To obtain an overview of the clinical applications of noninvasive prenatal testing (NIPT).
- To obtain some insight about the use of liquid biopsies for cancer screening.

---

## Case Studies in Infectious Diseases and Solid Tumors

Monday, November 16, 1:00 pm – 2:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Infectious Diseases, Oncology

**Moderators:** *Erin H. Graf, PhD, Mayo Clinic Arizona, Phoenix, AZ, USA and Christian Kunder, MD, PhD, Stanford University, Stanford, CA, USA*

### **Molecular Characterization of *Aspergillus Fumigatus* by Next-generation Sequencing in Neonates Diagnosed with Invasive Fungal Dermatitis at a Tertiary Care Hospital – Florida, 2019**

*Eun a Kim, MSc, IDbyDNA, Draper, UT, USA*

### **SARS-CoV-2 and Cytomegalovirus Co-infection in Patients Over 45: A Case Series**

*Debbie Rigney Walley, MD, Houston Methodist Hospital, Houston, TX, USA*

### **Disseminated Histoplasmosis with Concomitant *Mycobacterium Haemophilum* and *Anncaliia Algerae* Myositis in a Polymyositis Patient: A Diagnostic Approach**

*William Webster, DO, University of South Carolina School of Medicine-Prisma Health, Columbia, SC, USA*

### **Papillary Thyroid Carcinoma with Hashimoto Thyroiditis: Detecting the Driver Signal in the Inflammatory Noise**

*Adam Fisch, MD, PhD, Massachusetts General Hospital, Boston, MA, USA*

## Next Generation Sequencing Catches a Cytopathology Pitfall

*Matthew Gayhart, MD, Cedars-Sinai Medical Center, Los Angeles, CA, 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.

---

## Integrative Analysis of the Tumor Microenvironment

Monday, November 16, 1:00 pm – 2:00 pm

**Session Type:** Live

**CE Credit:** 1 | **SAM:** 1

**Path:** Oncology

**Moderator:** *Raj Emmadi, MD, University of Illinois, Chicago, IL, USA*

## Integrative Analysis of the Tumor Microenvironment

*Thomas Gajewski, MD, PhD, The University of Chicago, Chicago, IL, USA*

## Immune Cell Characterization via Multiplexed Digital Imaging

*Scott Rodig, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA*

**Session Description:** The rapidly expanding use of immunotherapy has significantly altered the landscape of cancer therapeutics. However, as our understanding of the tumor immune microenvironment grows, it is increasingly likely that multimodal interrogation of this environment will be needed to guide optimal therapeutic selection. This session will explore how current and emerging novel methods are expanding our knowledge of how tumor cells restructure their microenvironment to avoid immune attacks and how we can diagnose the alterations of the tumor-immune system interactions to implement precision medicine.

### Session Objectives:

- Learn how state-of-art multiplex immunostaining, digital imaging, and computational algorithms can define and quantify anti-tumor immunity in a spatially-resolved manner in situ.
- Diagnose how the tumor-immune system interaction has broken down, so we can choose the proper interaction to fix it.

---

## Molecular Methods for Discovery of Novel Pathogens

Monday, November 16, 1:00 pm – 2:00 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Infectious Diseases, Molecular Methodologies & Technologies

**Moderator:** *Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

## The Use of Molecular Tests in the Discovery and Characterization of Emerging Fungal Pathogens

*Ilan Schwartz, MD PhD, University of Alberta, Edmonton, Alberta, Canada*

## Molecular Methods for Discovery of Novel Pathogens

Lea M. Starita, PhD, University of Washington, Seattle, WA, USA

**Session Description:** Describe and discuss the use of novel and established molecular methods for the discovery of new pathogens of clinical importance.

**Session Objectives:**

- Discuss the use of molecular tests for discovery of new fungal pathogens.
- Discuss the use of molecular tests for discovery of new vector-borne pathogens.

---

## Targeted Therapies for Constitutional Genetic Disorders

Monday, November 16, 1:00 pm – 2:00 pm

**Session Type:** Live

**CE Credit:** 1 | **SAM:** 1

**Path:** Inherited Conditions

**Moderator:** Hyunseok Kang, MD, MS, Natera, Inc., Los Altos Hills, CA, USA

## Molecular Therapies for Cystic Fibrosis

Garry Cutting, MD, Johns Hopkins University, Baltimore, MD, USA

**Session Description:** In the last several years, there have been significant advances in the area of targeted therapies for constitutional genetic disorders. This session will review the targeted molecular therapies for cystic fibrosis, their mechanisms of action, and their impact on patient care.

**Session Objectives:**

- Upon completion, participant will be able to describe novel targeted therapies for various genetic disorders.
- Upon completion, participant will be able to describe the mechanisms of targeted therapies and patient prognosis.

---

## Transitioning to hg38

Monday, November 16, 1:00 pm – 2:00 pm

**Session Type:** Live

**CE Credit:** 1 | **SAM:** 1

**Path:** Informatics

**Moderator:** Ahmet Zehir, PhD, Memorial Sloan Kettering Cancer Center, Department of Pathology, New York, NY, USA

## GRCh38/hg38 and Transitioning to hg38

Justin M. Zook, PhD, National Inst of Standards & Tech, Gaithersburg, MD, USA

### Look Before You Leap: How to Systematically Move Clinical Diagnostic Testing from hg19 to hg38

Sabah Kadri, PhD, Lurie Children's Hospital of Chicago, Chicago, IL, USA

**Session Description:** Human genome reference GRCh38 (hg38) has been around for years but its implementation into existing NGS assays has been very slow due to various reasons. This session aims to discuss the main differences between hg19 and hg38, and identify the challenges in transitioning into hg38 in clinical NGS assays

**Session Objectives:**

- Describe the main differences between hg19 and hg38.
  - Describe various of effects of moving a clinical NGS assay from hg19 to hg38 at various levels of test design and implementation.
  - Define the effects of genome assembly change at sequence level, gene annotation level and variant annotation level.
- 

## Interactive Expo Hall with Demos and Drawings

Monday, November 16, 2:00 pm – 3:00 pm

---

## Chat Room Discussion – Meet a Membership Affairs Committee (MAC) Member

Monday, November 16, 2:30 pm – 3:00 pm

---

## Case Studies in Hematopathology and Solid Tumors

Monday, November 16, 3:00 pm – 4:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Oncology

**Moderators:** *Kristin Hunt Karner, MD, Department of Pathology, University of Utah, Salt Lake City, UT, USA and Christian Kunder, MD, PhD, Stanford University, Stanford, CA, USA*

### Recurrent Mediastinal Neoplasm of Unknown Origin

*Jessica B. Ziemba, MD, Beth Israel Deaconess Medical Center, West Roxbury, MA, USA*

### Fortuitous Detection of a NUP214-ABL1 Fusion Through Copy Number Changes

*Jonathan M. Tsai, MD, PhD, Brigham and Women's Hospital, Brookline, MA, USA*

### Targeted RNA Sequencing Reveals a Cryptic t(9;11) Leading to KMT2A-MLL3 Fusion in Accelerated Phase Primary Myelofibrosis Evolving into Acute Myeloid Leukemia

*Audrey N. Jajosky, MD, PhD, University of Michigan, Cleveland, OH, USA*

### Undifferentiated Neuroblastoma with Unique Molecular Features

*Sara Akhavanfard, MD, PhD, Nationwide Children's Hospital, Beachwood, OH, USA*

### A Compound EGFR Exon 21 Mutation in a Metastatic Liver Mass

*Eric A. Goold, MD, University of Utah/ARUP laboratories, Salt Lake City, UT, 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.



---

## Epigenetics in Malignant Hematology

Monday, November 16, 3:00 pm – 4:00 pm

**Session Type:** On Demand

**CE Credit:** 1 | **SAM:** 1

**Path:** Oncology

**Moderator:** Noah Brown, MD, University of Michigan, Ann Arbor, MI, USA

### Epigenetics in Malignant Hematology

*Maria E. Figueroa, MD, Sylvester Comprehensive Cancer Center, University of Miami Health System, Miami, FL, USA*

**Session Description:** In this session we will review how epigenetic deregulation contributes to the development of hematological malignancies, with a focus on myeloid malignancies.

**Session Objectives:**

- To recognize epigenetic modifiers that contribute to malignant transformation.
- To recognize the amplifying effect of epigenetic mutations by reprogramming the epigenome.

---

## Guidance for Reevaluation and Reanalysis of Genomic Test Results

Monday, November 16, 3:00 pm – 4:00 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Inherited Conditions

**Moderator:** Ryan Schmidt, MD, PhD, Children's Hospital Los Angeles, Los Angeles, CA, USA

### Guidance for Reevaluation and Reanalysis of Genomic Test Results

*Josh Daignan, PhD, University of California - Los Angeles, Los Angeles, CA, USA*

**Session Description:** The evidence supporting the classification of variants detected during genomic testing, such as exome sequencing, is constantly accumulating. Additionally, new patient phenotypes may be recognized that impact variant interpretation. Thus, the diagnostic yield of genomic testing may be increased by reevaluation of variant classifications or case-level reanalysis. This session will provide guidance for laboratories seeking to perform reanalysis of genomic testing results.

**Session Objectives:**

- Recognize the considerations surrounding the reevaluation and reanalysis of genomic test results.
- Design and implement strategies for the reevaluation and reanalysis of genomic test results.

---

## Implementation of Molecular Infectious Diagnostic Tests at the Point-of-Care

Monday, November 16, 3:00 pm – 4:00 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Infectious Diseases, Lab Management

**Moderator:** Erin McElvania, PhD, NorthShore University HealthSystem, Evanston, IL, USA

### Triumphs and Challenges Surrounding Implementation of Point-of-care Molecular Assays Outside of the Microbiology Laboratory

Omai Garner, PhD, UCLA, Los Angeles, CA, USA

### Implementation of Molecular Infectious Diagnostic Tests at the Point-of-Care

Raquel M. Martinez, MBA, PhD, Geisinger, Danville, PA, USA

**Session Description:** Describe and discuss approaches to successful implementation of molecular infectious disease tests at the point-of-care (e.g. emergency room or outpatient laboratories).

**Session Objectives:**

- Discuss challenges in implementation of molecular identification testing at the point-of-care.
- Discuss triumphs in implementation of molecular identification testing at the point-of-care.

---

## Laboratory Assurance Compliance Solutions

Monday, November 16, 3:00 pm – 4:00 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Molecular Methodologies & Technologies

**Moderator:** Jennifer Bergendahl, MT(ASCP), Michigan Medicine, Northville, MI, USA

### Digital Transformation: What Does It Mean for Compliance?

Justin Hammerling, M.B.A., Kapios Health, Toledo, OH, USA

**Session Description:** Introduction to a compliance solution for clinical laboratories. Laboratory Assured Compliance Solutions (LACS) replaces paper logs in clinical laboratories with tablets to track scheduled instrument activity and notifies technologists with a chain of alerts until a required task is completed. LACS provides a centralized database to record and review equipment status, access records and run audit reports, all in real-time. Learn about a solution that was created in a laboratory just like yours, by people who really know the pains of regulatory audit obligations.

**Session Objectives:**

- Learn the benefits of Laboratory Assured Compliance Solutions (LACS).
- Gain an understanding of the platform that provides a centralized database to record and review equipment status, access records, and run audit reports, all in real-time.

---

## Corporate Workshops

Monday, November 16, 4:00 pm – 5:00 pm

---

## Trainee Virtual Happy Hour & Mixer

Monday, November 16, 5:00 pm – 5:45 pm

---

## Social Event – Beer Tasting Event

Monday, November 16, 5:45 pm – 6:30 pm

---

## Interactive Expo Hall

Tuesday, November 17, 11:00 am – 11:45 am

---

## Chat with the 2020 Program Chair (Dr. Jane Gibson) & the 2021 Program Chair (Dr. Laura Tafe)

Tuesday, November 17, 11:45 am – 12:00 pm

---

## Single Cell Insights into Myeloid Neoplasia

Tuesday, November 17, 12:00 pm – 1:00 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Oncology

**Moderator:** Noah Brown, MD, University of Michigan, Ann Arbor, MI, USA

### Clonal Heterogeneity and Evolution of Myeloid Neoplasia with Single-cell Genomics

*Koichi Takahashi, MD, PhD, UT MD Anderson Cancer Center, Houston, TX, USA*

**Session Description:** The session will cover the recent updates on how single-cell genomics is unveiling the clonal heterogeneity of myeloid neoplasia and how this information can guide clinical decisions.

**Session Objectives:**

- Understand the technology and potential uses of single cell sequencing.
  - Understand current findings from single cells sequencing in myeloid neoplasms and their implications for how myeloid neoplasms first arise, how they involve and the potential implications for patient management.
- 

## Platform Presentations of Selected Genetics Abstracts

Tuesday, November 17, 1:00 pm – 2:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Inherited Conditions

**Moderators:** *Hyunseok Kang, MD, MS, Natera, Inc., Los Altos Hills, CA, USA and Ryan Schmidt, MD, PhD, Children's Hospital Los Angeles, Los Angeles, CA, USA*

Note: these sessions are On Demand and have been pre-recorded, you can view them in the Auditorium. If you would like to “chat” with the authors, please do so during the designated poster times in the Poster Hall.

- Even-numbered posters must be attended on Tuesday, November 17, 1:00pm – 2:00pm
- Odd-numbered posters will be attended on Thursday, November 19, 1:00pm – 2:00pm

### G02 - Copy Number Variant Analysis Improves the Diagnostic Yield in a Cohort of Pediatric Patients with Previously Negative Constitutional Exome Sequencing Results

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

### G11 - Mosaicism in Cancer Susceptibility Genes in Unselected Cancer Patients

*Diana Mandelker, MD, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

### **G13 - Comparison of Universal versus Traditional Genetic Testing Models for Cancer Patients**

*Ozge Ceyhan-Birsoy, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

### **G23 - High-throughput Fetal-fraction Amplification Increases Analytical Performance of Noninvasive Prenatal Screening**

*Dale Muzzey, PhD, Myriad Women's Health, Inc., South San Francisco, CA, 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**

Tuesday, November 17, 1:00 pm – 2:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Oncology

**Moderator:** *Noah Brown, MD, University of Michigan, Ann Arbor, MI, USA*

Note: these sessions are On Demand and have been pre-recorded, you can view them in the Auditorium. If you would like to "chat" with the authors, please do so during the designated poster times in the Poster Hall.

- Even-numbered posters must be attended on Tuesday, November 17, 1:00pm – 2:00pm
- Odd-numbered posters will be attended on Thursday, November 19, 1:00pm – 2:00pm

### **H14 - Cloneretriever: An Automated Algorithm to Identify Clonal Immunoglobulin Gene Rearrangements by Next-generation Sequencing**

*Eitan Halper-Stromberg, MD PhD, JHU, Baltimore, MD, USA*

### **H21 - Validation of MYD88 L265P Ddpcr Assay and Application in Assessment of Primary CNS Lymphoproliferative Disorders**

*Miguel D. Cantu, MD, New York Presbyterian-Weill Cornell, New York, NY, USA*

### **H28 - Chromosome Arm Gain or Loss by Next Generation Sequencing**

*Mia Donna Dabrowski, MT(ASCP), AdventHealth Orlando, Orlando, FL, USA*

### **H44- Comparison of Whole Genome Sequencing (WGS) with Conventional Cytogenetics in Profiling Genome-Wide Large-Scale Copy Number and Structural Variations in Pediatric and Adolescent AML**

*Lu Wang, MD, PhD, St. Jude Children's Research Hospital, Memphis, TN, 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**

Tuesday, November 17, 1:00 pm – 2:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Infectious Diseases

**Moderator:** *Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

Note: these sessions are On Demand and have been pre-recorded, you can view them in the Auditorium. If you would like to “chat” with the authors, please do so during the designated poster times in the Poster Hall.

- Even-numbered posters must be attended on Tuesday, November 17, 1:00pm – 2:00pm
- Odd-numbered posters will be attended on Thursday, November 19, 1:00pm – 2:00pm

### **ID07 - Evaluation of an automated rRNA quantitation system for rapid AST in clinical lab diagnostics**

*Dakai Liu, PhD, NewYork-Presbyterian Queens Hospital, Flushing, NY, USA*

### **ID27 - Evaluating the Clinical Utility of Next-Generation Sequencing of Nasopharyngeal Specimens for SARS-CoV-2 in the COVID-19 Pandemic**

*Priya Velu, MD, PhD, New York Presbyterian-Weill Cornell Medicine, New York, NY, USA*

### **ID52 - Design and Optimization of Novel ITS2-28s rRNA Gene Primers for Fungal Species Detection from Formalin-Fixed Paraffin-Embedded Tissues with a Targeted Next-Generation Sequencing Assay**

*Rossio K. Kersey, PhD, Joint Pathology Center, Bethesda, MD, USA*

### **ID53 - Non-invasive Microbial Cell-free DNA Sequencing Detects Invasive Mold Infections in Immunocompromised Patients with Pneumonia**

*Tim 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.

---

## **Interactive Expo Hall with Demos and Drawings**

Tuesday, November 17, 2:00 pm – 3:00 pm

---

## **Chat Room Discussion - Meet a Membership Affairs Committee (MAC) Member**

Tuesday, November 17, 2:30 pm – 3:00 pm

---

## **Case Studies in Genetics and Hematopathology**

Tuesday, November 17, 3:00 pm – 4:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Inherited Conditions, Oncology

**Moderators:** *Alanna J. Church, MD, Boston Children's Hospital, Boston, MA, USA and Kristin Hunt Karner, MD, Department of Pathology, University of Utah, Salt Lake City, UT, USA*

## Persistent High Levels of Donor Cells Following Solid Organ Transplant Confirm Diagnosis of Graft versus Host Disease

Kelly A. Rafferty, PhD, MS, Virginia Commonwealth University, Richmond, VA, USA

## Co-occurrence of Mosaic Turner Syndrome and Mosaic Spinal Muscular Atrophy Carrier Status in an Adult Female

Diana M. Toledo, PhD, MS, CGC, Dartmouth-Hitchcock Medical Center, Lebanon, NH, USA

## A Rare Occurrence of Three Compound Heterogeneous Mutations of HBB Gene Leading to B-thalassemia Major in a Pakistani Family

Sjjawal Ahmad, Msc, Aga Khan University, Hospital Pakistan, Karachi, Pakistan

## When Old Meets New: Sophisticated Interplay of Multiple Technologies to Diagnose a Case of SOPH Syndrome

Marilena Melas, MSc, PhD, The Steve and Cindy Rasmussen Institute for Genomic Medicine, Nationwide Children's Hospital, Columbus, OH, USA

## Identification of Targetable NUP214-ABL1 Fusion in T-lymphoblastic Leukemia

Won Sok Lee, MD, Virginia Commonwealth University, Richmond, VA, 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.

---

## Moving Towards Clinical-grade HGVS Nomenclature

Tuesday, November 17, 3:00 pm – 4:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Inherited Conditions

**Moderator:** Hyunseok Kang, MD, MS, Natera, Inc., Los Altos Hills, CA, USA

### Moving Towards Clinical-grade HGVS Nomenclature

Birgit Funke, PhD, FACMG, Sema4, Newton, MA, USA

Reece Hart, PhD, Reece Hart Consulting, San Francisco, CA, USA

Somak Roy, MD, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, USA

Ryan Schmidt, MD, PhD, Children's Hospital Los Angeles, Los Angeles, CA, USA

**Session Description:** HGVS nomenclature is an essential vocabulary that allows for consistent description of sequence variants. However, HGVS nomenclature usage is highly variable across laboratories in proficiency testing surveys, and different software annotation tools frequently generate discordant HGVS nomenclature outputs. This session seeks to engage the diagnostic testing community in order to improve the consistency of HGVS nomenclature usage. Ongoing work by the CAP Genomic Medicine Committee on this topic will be presented.

**Session Objectives:**

- Identify sources of discrepancy in the usage of HGVS nomenclature.
- Compare potential solutions for improving the usage of HGVS nomenclature by laboratories.

---

## Practical Approaches to Diagnostic Stewardship of Advanced Molecular Tests

Tuesday, November 17, 3:00 pm – 4:00 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Infectious Diseases

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

### Practical Approaches to Diagnostic Stewardship of Advanced Molecular Tests

*Neil Anderson, MD, Washington University in St. Louis, Saint Louis, MO, USA*

*Daniel Diekema, MD, MS, University of Iowa, Iowa City, IO, USA*

*Amanda Harrington, PhD, D(ABMM), Loyola University Medical Center, Maywood, IL, USA*

*D. Jane Hata, PhD, Mayo Clinic Florida, Jacksonville, FL, USA*

**Session Description:** In a round table/panel format, describe and discuss various approaches taken by laboratory to ensure best utilization by clinicians, of advanced molecular testing, particularly as it applies to next generation, metagenomics sequencing for infectious disease diagnosis.

**Session Objectives:**

- Identify challenging areas that can benefit from diagnostic stewardship.
- Describe real world approaches that have been implemented to direct appropriate laboratory testing.
- Discuss the effectiveness of different diagnostic stewardship approaches.

---

## SHORT COURSE: Next-generation Sequencing Assay Development and Validation

Tuesday, November 17, 3:00 pm – 6:00 pm

**Session Type:** On Demand

**CE Credit:** 3

**Path:** Informatics, Molecular Methodologies & Technologies

**Moderator:** *Ahmet Zehir, PhD, Memorial Sloan Kettering Cancer Center, Department of Pathology, New York, NY, USA*

### Targeted Molecular Profiling using NGS Based Assays: A Clinical Journey

*Ryma Benayed, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

### Amplicon NGS Sequencing – Considerations and Applications

*Eric Konnick, MD, MS, University of Washington Department of Laboratory Medicine and Pathology, Seattle, WA, USA*

### RNA-Based NGS: Technical Considerations for Assay Validation

*Kurtis Davies, PhD, University of Colorado Anschutz Medical Campus, Aurora, CO, USA*

### **Nuts and Bolts: Details about NGS that You Need to Know**

*Dara Aisner, MD, PhD, University of Colorado Hospital, Aurora, CO, USA*

### **Bioinformatics Pipeline Development for NGS Oncology Laboratory Developed Tests**

*Jeremy Segal, MD, PhD, University of Chicago, Chicago, IL, USA*

**Session Description:** NGS-based genomic assays continue to evolve regarding methodologies and clinical applications. This short course from experts in genomic diagnostics aims to provide practical guidelines on the different aspects of designing NGS assays including assay design principles, wet-bench validation, and bioinformatics validation and implementation. Speakers will be available at a 1 hr live Q&A session for an interactive discussion.

#### **Session Objectives:**

- Describe best practices for designing panels for DNA and RNA sequencing applications.
- Recognize steps in designing and implementing bioinformatics pipelines from aligning sequencing reads to detecting various genomic alterations.
- List the principles of validation and implementation of NGS based assays.

---

## **Single-cell Sequencing**

Tuesday, November 17, 3:00 pm – 4:00 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Molecular Methodologies & Technologies, Oncology

**Moderator:** *Renee Webb, BS, MT (ASCP), Texas Children's Hospital, Houston, TX, USA*

### **Cell Atlases as Roadmaps to Understand and Treat Disease**

*Orit Rozenblatt-Rosen, PhD, Broad Institute, Cambridge, MA, USA*

**Session Description:** Cells are the basic unit of life, yet we know surprisingly little about them. They vary immensely within the body, and express different sets of genes. Without maps of different cell types and where they are located in the body, we cannot describe all their functions and understand the biological networks that direct their activities. Recent advances in single-cell genomic analysis of cells and tissues have put systematic, high-resolution and comprehensive reference maps of all human cells within reach. We can now realistically envision a human cell atlas to serve as a basis for both understanding human health and diagnosing, monitoring, and treating disease. This is an ambitious but achievable goal, and requires an international community of biologists, clinicians, technologists, physicists, computational scientists, software engineers, and mathematicians. A complete Human Cell Atlas (HCA) would give us a unique ID card for each cell type, a three-dimensional map of how cell types work together to form tissues, knowledge of how all body systems are connected, and insights into how changes in the map underlie health and disease.

#### **Session Objectives:**

- Discuss the need for a human cell atlas in understanding human health and disease.
- Discuss the utility of single-cell sequencing in molecular diagnostics.
- Understand the role of single-cell sequencing and HCA play in understanding and treating diseases.

---

## **COVID-19 Molecular Testing: Experiences from the Field**

Tuesday, November 17, 4:00 pm – 5:30 pm



**Session Type:** Live

**CE Credit:** 1.5

**Path:** Infectious Diseases

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

### **COVID-19 Molecular Testing: Experiences from the Field**

*Teresa A. Karre, MD, Nebraska Methodist Hospital and Children's Hospital and Medical Center, Omaha, NE, USA  
Anthony Tran, DrPH, MPH, D(ABMM), District of Columbia Department of Forensic Sciences, Bethesda, MD, USA*

*Beth M. Marlowe, PhD, D(ABMM), Quest Diagnostics, San Juan Capistrano, CA, USA*

*Michael Bachman, MD PhD, University of Michigan/Michigan Medicine, Ann Arbor, MI, USA*

**Session Description:** In a discussion based format, four expert clinical microbiologists from academic, reference, and public health laboratories will discuss challenges and triumphs associated with SARS-CoV-2 molecular testing during the COVID-19 pandemic.

#### **Session Objectives:**

- Discuss the evolution of SARS-CoV-2 molecular testing from the beginning of the COVID-19 pandemic to current day.
- Describe challenges of molecular SARS-CoV-2 testing, including but not limited to government regulation and supply shortages.
- Identify ways in which the laboratory medicine has triumphed and grown stronger as a result of the COVID-19 pandemic.

---

## **High-throughput functional and genomic approaches for understanding germline and somatic variants**

Tuesday, November 17, 4:00 pm – 5:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Oncology

**Moderators:** *Jonathan A. Nowak, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA and Ryan Schmidt, MD, PhD, Children's Hospital Los Angeles, Los Angeles, CA, USA*

### **Saturation Genome Editing for Variant Effect Prediction**

*Jay A. Shendure, MD, PhD, University of Washington, Seattle, WA, USA*

### **Validating Oncogenic Somatic Mutations: A Computational and Functional Approach**

*Collin Tokheim, PhD, Dana-Farber Cancer Institute, Boston, MA, USA*

**Session Description:** Variants of uncertain significance are routinely detected during diagnostic testing for constitutional genetic disorders. This session will describe high throughput methods for functional validation that can provide evidence for or against the pathogenicity of these variants.

#### **Session Objectives:**

- Describe approaches for high throughput functional and genomic characterization of variants.
  - Compare methods for high throughput functional validation.
  - Apply high throughput functional validation results to variant classification.
-

## Laboratory Economics During a Public Health Emergency: Lessons Learned (and still learning) from the COVID-19 Pandemic

*(Sponsored by the AMP Economic Affairs Committee)*

Tuesday, November 17, 4:00 pm – 5:15 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Advocacy, Lab Management

**Moderator:** Erika Miller, CRD Associates, Washington, D.C., USA

### Laboratory Economics During a Public Health Emergency: Lessons Learned (and still learning) from the COVID-19 Pandemic

*Samuel K. Caughron, MD, MAWD Pathology Group, Lenexa, KS, USA*

*Pranil Chandra, DO, FCAP, FASCP, PathGroup, Nashville, TN, USA*

*Jay L. Patel, MD, MBA, University of Utah and ARUP Laboratories, Salt Lake City, UT, USA*

**Session Description:** The Economic Affairs Committee (EAC) invites you to participate in a dynamic discussion about the lessons we learned and are still learning about reimbursement policies for, needs of, and issues faced by laboratories during the COVID-19 public health emergency. While the Federal government endeavored to create new policies and adapt to the needs for diagnostic tests during the pandemic, some policies have created confusion for patients and laboratories. Looking forward, it is unclear how reimbursement policies will be maintained once the public health emergency is declared over. These uncertainties have resulted in great concerns within the laboratory community about maintaining COVID-19 testing capacity throughout the entire pandemic. Proper and flexible coverage and reimbursement policies need to be in place during a pandemic so that laboratories can continue to support the U.S. population's public health needs and so that patients are able to easily access these crucial tests. The AMP EAC has worked avidly throughout 2020 to help elicit such an outcome. Please join us for an in-depth discussion about the road-blocks that were encountered throughout coverage, coding, and pricing of COVID-19 diagnostic tests, and explore ideas that could help avoid these problems to quickly get high quality diagnostic tests to patients in future health emergencies.

#### Session Objectives:

- Understand process of coding, coverage and pricing during the pandemic.
- Explain the concerns that resulted from this unusual coding and pricing process.
- Discuss difficulties that your laboratory has had with coverage and reimbursement for COVID-19 diagnostic tests.
- Provide input on policies that AMP EAC is advocating for to develop a coding and reimbursement pathway within CMS during future public health emergencies.

---

## Variant Review and Classification Workshop

Tuesday, November 17, 4:00 pm – 5:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Informatics, Oncology

**Moderator:** Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA

### Variant Review and Classification Workshop

*Mark Routbort, MD, PhD, M. D. Anderson Cancer Center, Houston, TX, USA*

*Somak Roy, MD, Cincinnati Children's Hospital Medical Center, Mason, OH, USA*

*Laura Tafe, MD, Dartmouth-Hitchcock Medical Center, Lebanon, NH, USA*

**Session Description:** Genomic variants of different classes have distinct characteristics, error profiles, and classification challenges. Allied to this are challenges related to context-specific interpretation. Variant data visualization and review can be critical in resolving and interpreting complex alterations. In this hands-on workshop, the expert speakers will be doing a live interactive session demonstrating the use of Integrative Genomics Viewer (IGV) for viewing and interpreting different types of variants in DNA sequencing and discuss practical strategies for variant classification and interpretation.

**Session Objectives:**

- Learn basic features and functionalities in IGV.
  - Understand the importance of variant visualization in resolving complex alterations.
- 

## Technologist Mixer: Navigating Opportunities for Career Advancement and Certification for Molecular Technologists

Tuesday, November 17, 5:30 pm – 6:15 pm

---

## International Affairs Committee Networking Meet-up

Wednesday, November 18, 10:15 am – 11:00 am

---

## Interactive Expo Hall

Wednesday, November 18, 11:00 am – 11:45 am

---

## Chat with the 2020 Program Chair (Dr. Jane Gibson) & the 2021 Program Chair (Dr. Laura Tafe)

Wednesday, November 18, 11:45 am – 12:00 pm

---

## Coronavirus Pandemic Updates

Wednesday, November 18, 12:00 pm – 1:00 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Infectious Diseases

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

### Coronavirus Pandemic Updates

*Carlos del Rio, MD, Emory School of Medicine, Decatur, GA, USA*

**Session Description:** The COVID-19 pandemic has changed life as we know it worldwide. Molecular diagnostics are the backbone of diagnosis and prevention efforts surrounding this deadly virus. This lecture will give an evolution from where we started to what we know now focusing on the impact of molecular diagnostics.

**Session Objectives:**

- Provide an a history and update on the COVID-19 pandemic.
- Identify the impact of molecular diagnostics on SARS-CoV-2 diagnosis, tracking, and prevention efforts.

---

## Bridging the Gap: Molecular Tumor Boards, Clinical Trials Matching, and the Pathologist-oncologist Interface

Wednesday, November 18, 1:00 pm – 2:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Oncology

**Moderator:** *Jonathan A. Nowak, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA*

### Precision Oncology Through a Molecular Tumor Board: Hype or Reality?

*Marios Giannakis, MD, PhD, Dana-Farber Cancer Institute, Boston, MA, USA*

### Cancer Clinical Decision Making Tools in the Era of Precision Medicine & Big Data

*Mia Levy, MD, PhD, Rush University Medical Center, Chicago, IL, USA*

**Session Description:** Next-generation sequencing provides an increasing wealth of information that can be helpful to improve patient care. However, optimal use of this information requires not only a detailed understanding of tumor biology, but also standard of care therapeutic recommendations, clinical trial options and a patients' individual situation. Molecular tumor boards offer an opportunity to address this challenge by bridging the gap between molecular pathologists and medical oncologists. This session will explore different models for molecular tumor function and will highlight opportunities to improve patient care by bridging the pathology-oncology gap.

#### Session Objectives:

- Understand the elements and operational considerations of a molecular tumor board.
- Describe the role of the molecular tumor board in guiding precision oncology.
- Understand how shared genomic resources and knowledgebases can contribute to precision oncology.

---

## Distributed Laboratories and Third Party Interpretation Services

Wednesday, November 18, 1:00 pm – 2:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Lab Management

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

### Distributed Laboratories and Third Party Interpretation Services

*Hyunseok Kang, MD, MS, Natera, Inc., Los Altos Hills, CA, USA*

*Gail Javitt, Hyman, Phelps & McNamara, Washington, D.C., USA*

*Matthew Lebo, PhD, Lab for Molecular Medicine, Mass General Brigham Personalized Medicine, Cambridge, MA, USA*

*Rakesh Nagarajan, MD, PhD, PierianDx, Creve Coeur, MO, USA*

**Session Description:** In the last several years, some laboratories have started providing isolated wetlab or interpretation services. This session will explore the practice and regulation of such distributed laboratory services.

**Session Objectives:**

- Upon completion, participant will be able to describe the workflow of distributed testing and interpretation services.
- Upon completion, participant will be able to describe the regulatory issues related to distributed testing and interpretation.

---

## Early Detection and Characterization of Cancer Using cfDNA and Distinction from Clonal Hematopoiesis

Wednesday, November 18, 1:00 pm – 2:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Informatics, Oncology

**Moderator:** Noah Brown, MD, University of Michigan, Ann Arbor, MI, USA and Ahmet Zehir, PhD, Memorial Sloan Kettering Cancer Center, Department of Pathology, New York, NY, USA

### Clonal Hematopoiesis Detected from cfDNA Testing

*Pedram Razavi, MD, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*

### cfDNA to Detect and Characterize Cancer at Early Stages

*Victor Velculescu, MD, PhD, John Hopkin's Medicine, Baltimore, MD, USA*

**Session Description:** Cell free DNA has great potential as a biomarker for early detection of cancer as well as monitoring response to therapy in patients in a minimally invasive way. However, there are technical challenges that need to be considered before utilizing this technology in practice. This session aims to discuss novel methodologies in early detection of cancer. This session will also address the frequency of clonal hematopoiesis inadvertently detected during cell-free DNA intended for solid tumor cancer patients, the importance evaluating matched white blood cells and the appropriate next steps when clonal hematopoiesis is detected as an incidental finding.

**Session Objectives:**

- Describe ways in which cfDNA can be used for early cancer detection and challenges involved.
- Understand the frequency of clonal hematopoiesis inadvertently detected during cell-free DNA testing for solid tumors.
- Understand how clonal hematopoiesis can be distinguished from oncogenic mutations within cfDNA from solid tumor cancer cells.

---

## Point-Counter Point: Clinical Metagenomics Is It Worth the Juice

Wednesday, November 18, 1:00 pm – 2:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Infectious Diseases

**Moderator:** Erin H. Graf, PhD, Mayo Clinic Arizona, Phoenix, AZ, USA

### **Point-counter Point: Clinical Metagenomics Is It Worth the Juice**

*Steve Miller, MD PhD, University of California San Francisco, San Francisco, CA, USA*

*Stephanie L. Mitchell, PhD, D(ABMM), University of Pittsburgh, Pittsburgh, PA, USA*

*William J. Muller, MD, PhD, Lurie Children's Hospital of Chicago; Northwestern University Feinberg School of Medicine, Chicago, IL, USA*

*Debra Palazzi, MD, MEd, Baylor College of Medicine, Texas Children's Hospital, Houston, TX, USA*

**Session Description:** In a point/counter point format, the utility of clinical metagenomics to impact patient outcomes will be discussed. Two teams, each with an infectious disease physician and a Micro director from opposite side of this issue.

#### **Session Objectives:**

- Discuss the advantages and clinical utility of metagenomics for use in patient care.
- Describe the downsides or harm that metagenomics can cause to patient care.
- Identify clinical situations in which metagenomics is or is not appropriate.

---

### **Interactive Expo Hall with Demos and Drawings**

Wednesday, November 18, 2:30 pm – 3:30 pm

---

### **Chat Room Discussion - Meet a Membership Affairs Committee (MAC) Member**

Wednesday, November 18, 2:30 pm – 3:30 pm

---

### **Corporate Workshops**

Wednesday, November 18, 3:30 pm – 5:30 pm

---

### **Business Meeting**

Wednesday, November 18, 5:30 pm – 6:15 pm

---

### **Social Event – Wine Tasting Event**

Wednesday, November 18, 6:15 pm – 7:00 pm

---

### **Interactive Expo Hall**

Thursday, November 19, 11:00 am – 11:45 am

---

### **Chat with the 2020 Program Chair (Dr. Jane Gibson) & the 2021 Program Chair (Dr. Laura Tafe)**

Thursday, November 19, 11:45 am – 12:00 pm

---

### **Machine Learning in Health Care**

Thursday, November 19, 12:00 pm – 1:00 pm

**Session Type:** Live

**CE Credit:** 1 | **SAM:** 1

**Path:** Informatics, Inherited Conditions

**Moderator:** *Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA and Ahmet Zehir, PhD, Memorial Sloan Kettering Cancer Center, Department of Pathology, New York, NY, USA*

## Machine Learning in Genomic Medicine

Stephen F. Kingsmore, MD DSc FRCPath, Rady Children's Institute for Genomic Medicine, San Diego, CA, USA

**Session Description:** One of the critical bottlenecks in implementing genomics in the critical care setting remains the availability of rapid analytic platforms. In this plenary session, the speaker will describe ultra-rapid whole genome sequencing (urWGS) for diagnosis and management of children in intensive care units. You will learn about the application of machine learning and clinical natural language processing algorithms to perform urWGS as well as the indications, clinical utility of WGS in ICUs, and the impact of urWGS on healthcare utilization in children's hospital systems.

### Session Objectives:

- Understand the indications and clinical utility of urWGS.
- Understand the role of machine learning algorithms in urWGS.

---

## Platform Presentations of Selected Informatics Abstracts

Thursday, November 19, 1:00 pm – 2:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Informatics

**Moderator:** Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA

Note: these sessions are On Demand and have been pre-recorded, you can view them in the Auditorium. If you would like to "chat" with the authors, please do so during the designated poster times in the Poster Hall.

- Even-numbered posters must be attended on Tuesday, November 17, 1:00pm – 2:00pm
- Odd-numbered posters will be attended on Thursday, November 19, 1:00pm – 2:00pm

### I08 - Microhaplotype Locus-based Workflow for Sample Contamination Detection in Multiplexed Next Generation Sequencing (NGS) Assays

Jagadheshwar Balan, MS, Mayo Clinic, Rochester, MN, USA

### I14 - ReGe: A Toolkit for Moving Clinical Panels to hg38

Andrew Skol, PhD, Ann & Robert H. Lurie Children's Hospital of Chicago, Chicago, IL, USA

### I23 - Many NGS-based Assays, One Platform: Ensuring a High-quality Case Review and Sign-out Process with NGS Reporter (NGSR)

Andrea Sboner, PhD, Weill Cornell Medicine, New York, NY, USA

### I28 - Building a Comprehensive Teaching Repository of Whole Slide Images

Egiebade E. Iriabho, MSc, The University of Alabama at Birmingham, Birmingham, AL, 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

Thursday, November 19, 1:00 pm – 2:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Oncology

**Moderator:** Jonathan A. Nowak, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA

Note: these sessions are On Demand and have been pre-recorded, you can view them in the Auditorium. If you would like to "chat" with the authors, please do so during the designated poster times in the Poster Hall.

- Even-numbered posters must be attended on Tuesday, November 17, 1:00pm – 2:00pm
- Odd-numbered posters will be attended on Thursday, November 19, 1:00pm – 2:00pm

### **ST48 - Tumor Microbiome in Colorectal Carcinoma: Bacterial Enrichment Is Associated with Oncogenic Variants Within Specific Signaling Pathways**

Cameron Beech, MD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

### **ST50 - Comprehensive Genomic Profiling of Different Subsets of Merkel Cell Carcinoma: Insights on Pathogenetic Pathways**

Ryan C. DeCoste, MD, QEII Health Sciences Centre, Nova Scotia Health Authority, Halifax, Nova Scotia, Canada

### **ST58 - Genomic Profiling Uncovers Mutation Signatures That Differentiate Pediatric Rhabdomyosarcoma (RMS) Subgroups and Predict Clinical Outcomes**

Fumin Lin, PhD, Children's Hospital of Philadelphia, Philadelphia, PA, USA

### **ST80 - Prospective Study Using Virtual Enrollment to Assess an RNA-FIT Assay for Non-invasive Detection of Colorectal Cancer, Advanced Adenomas, and Other Precancerous Adenomas**

Erica K. Barnell, PhD, Geneoscopy Inc., Saint Louis, MO, USA

**Session Description:** Platform presentations of selected Solid Tumors abstracts.

#### **Session Objectives:**

- Analyze platform 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**

Thursday, November 19, 1:00 pm – 2:00 pm

**Session Type:** On Demand

**CE Credit:** 1

**Path:** Molecular Methodologies & Technologies

**Moderator:** Jennifer Bergendahl, MT(ASCP), Michigan Medicine, Northville, MI, USA

Note: these sessions are On Demand and have been pre-recorded, you can view them in the Auditorium. If you would like to "chat" with the authors, please do so during the designated poster times in the Poster Hall.

- Even-numbered posters must be attended on Tuesday, November 17, 1:00pm – 2:00pm
- Odd-numbered posters will be attended on Thursday, November 19, 1:00pm – 2:00pm

### **TT04 - Performance Validation of Magnis BR: A Full-automatic Capture-based Library Preparation Platform for Next-generation Sequencing (NGS)**

Xiaotian Wang, PhD, Burning Rock Dx, Shanghai, China

### **TT06 - Concordance of Variant Detection Between the MoCha ctDNA Assay and Matched Tissue Biopsy in Non-Small Cell Lung Cancer**

Chris Karlovich, PhD, Frederick National Laboratory for Cancer Research, Frederick, MD, USA



## TT10 - Comparative Study of Three Assays: Target Capture Sequencing, MassARRAY and Real-Time qPCR for Testing Somatic Mutations in Plasma Cell-Free Circulation Tumour DNA of Non-Small Cell Lung Cancer

Lei Zhang, PhD, University of Alberta, Edmonton, Alberta, Canada

## TT34 - Optical Mapping Enables High-throughput Analysis of Pathogenic Repeats

Ernest Lam, PhD, Bionano Genomics, San Diego, CA, USA

**Session Description:** Platform presentations of selected Technical Topics abstracts.

**Session Objectives:**

- Analyze platform presentations of abstracts highlighted by the Technical Topics Subdivision leadership as particularly significant.
- Evaluate the scientific merit and significance of these selected studies through further discussion with the authors.

---

## Interactive Expo Hall with Demos and Drawings

Thursday, November 19, 2:00 pm – 3:00 pm

---

## Addressing the Clinical Laboratory Workforce Shortage

Thursday, November 19, 3:00 pm – 4:00 pm

**Session Type:** Live

**CE Credit:** 0

**Path:** Infectious Diseases, Informatics, Inherited Conditions, Lab Management, Molecular Methodologies & Technologies, Oncology

**Moderators:** Jennifer Bergendahl, MT(ASCP), Michigan Medicine, Northville, MI, USA and Renee Webb, BS, MT (ASCP), Texas Children's Hospital, Houston, TX, USA

### Addressing the Clinical Laboratory Workforce Shortage

Susanne Norris-Zanto, MPH, Laboratory SolutionZ, Helena, MT, USA

### Addressing the Clinical Laboratory Workforce Shortage - Automation and Robotics

Jose Manuel Collados, Industrial Engineer, ABB, Houston, TX, USA

**Session Description:** Effects of the current shortage of qualified clinical laboratory professionals are being felt throughout the laboratory community. This session will describe recent data on the workforce shortage, reasons for the shortage, and the impact on laboratories, patient care, and educational facilities. New solutions for addressing the workforce shortage will also be presented, highlighting new partnerships between healthcare and robotics and the roadmap for robotics implementation in the clinical laboratory.

**Session Objectives:**

- Understand the drivers behind the current laboratory workforce shortage.
- Gain insight on the impact of staffing shortages on clinical laboratories, patients and academics.
- Learn of newly-developed laboratory-specific robotics that could alleviate the workforce deficit in the clinical laboratory.

---

## Next Generation Guidelines for Clinical Sequencing: Translating Regulations into Practical Implementation Frameworks

Thursday, November 19, 3:00 pm – 4:00 pm

**Session Type:** On Demand  
**CE Credit:** 1

### **Next Generation Guidelines for Clinical Sequencing: Translating Regulations into Practical Implementation Frameworks**

*Birgit Funke, PhD, FACMG, Sema4, Newton, MA, USA*  
*Annette Leon, PhD, MS, FACMG, Color, Burlingame, CA, USA*

**Session Description:** Clinical NGS is going mainstream and its applications are increasing. A growing number of guidelines and recommendations have been issued but generally do not provide sufficient concrete instructions on how to translate them into laboratory practice. This course will cover an effort by the Clinical Laboratory Standards Institute (CLSI) to introduce practical guidance for clinical applications of NGS.

**Session Objectives:**

- Enable laboratory professionals to develop and operate high complexity sequencing tests.

---

### **Next-generation Sequencing Assay Development and Validation Q&A**

Thursday, November 19, 3:00 pm – 4:00 pm

**Session Type:** Live  
**CE Credit:** 1

**Path:** Informatics, Molecular Methodologies & Technologies

**Moderators:** *Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA* and *Ahmet Zehir, PhD, Memorial Sloan Kettering Cancer Center, Department of Pathology, New York, NY, USA*

### **Next-generation Sequencing Assay Development and Validation Q&A**

*Dara Aisner, MD, PhD, University of Colorado Hospital, Aurora, CO, USA*  
*Ryma Benayed, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA*  
*Eric Konnick, MD, MS, University of Washington Department of Laboratory Medicine and Pathology, Seattle, WA, USA*  
*Jeremy Segal, MD, PhD, University of Chicago, Chicago, IL, USA*

**Session Description:** Please join us for a live Q&A session and interactive discussion with experts in genomic diagnostics. This will be a highly anticipated follow-up to the Short Course held earlier in the week. Please check on the onDemand recording in the sessions listings for Tuesday, November 17th to watch the session ahead of the Q&A.

**Session Objectives:**

- Describe best practices for designing panels for DNA and RNA sequencing applications.
- Recognize steps in designing and implementing bioinformatics pipelines from aligning sequencing reads to detecting various genomic alterations.
- List the principles of validation and implementation of NGS based assays.

---

### **Tissue Stewardship: Maximizing the Information That Can Be Provided by Small Specimens**

Thursday, November 19, 3:00 pm – 4:00 pm

**Session Type:** Live

**CE Credit:** 1 | **SAM:** 1

**Path:** Oncology

**Moderator:** *Jonathan A. Nowak, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA*

### **Optimal Assay Design for Small Specimens**

*Christopher Gilbert, DO, MS, Swedish Cancer Institute, Seattle, WA, USA*

### **Best Practices for Tissue Allocation**

*Sinchita Roy-Chowdhuri, MD, PhD, The University of Texas MD Anderson, Houston, TX, USA*

**Session Description:** Across tumor types, the expanding use of molecular profiling and biomarker analysis places increased demands on often limited amounts of tissue. As targeted therapies move into first-line settings, as the use of neoadjuvant therapy increase, and as biopsy size shrinks, optimized and comprehensive testing from small biopsy specimens is increasingly necessary. This session will explore how recently released joint AMP and CAP guidelines regarding optimal tissue allocation and testing strategies that can maximize the amount of information which can be gleaned from small tissue samples.

#### **Session Objectives:**

- Describe the role of the pathologist in triaging small specimens to maximize diagnostic utility.
- Understand how appropriate assay design and selection can reduce tissue requirements for testing.

---

## **True or False: Interpretation Challenges of Blood Culture Identification Panels**

Thursday, November 19, 3:00 pm – 4:00 pm

**Session Type:** Live

**CE Credit:** 1 | **SAM:** 1

**Path:** Infectious Diseases

**Moderator:** *Erin McElvania, PhD, NorthShore University HealthSystem, Evanston, IL, USA*

### **True or False: Interpretation Challenges of Blood Culture Identification Panels**

*Susan Butler-Wu, PhD, LA County and USC Medical Center, Los Angeles, CA, USA*

### **Pitfalls in Interpretation of Blood Culture Molecular ID Panels**

*Richard E. Davis, PhD, D(ABMM), MLS(ASCP)CM, Providence Sacred Heart Medical Center, Spokane, WA, USA*

**Session Description:** In a case format, the speakers will describe the advantages and limitations of molecular panels used for identification of pathogens and resistance markers from positive blood cultures.

#### **Session Objectives:**

- Understand the complexities and challenges associated with diagnosis and biomarker testing in small biopsy and cytology samples.
- Learn judicious ways to triage and optimize the use of small specimens for diagnostic and molecular/biomarker testing.
- Discuss approaches for optimal tissue collection and processing to maximize chances of ensuring successful molecular testing in non small-cell lung cancer specimens.

---

## **Enhanced Molecular Diagnosis Through Structural Variant Detection**

Thursday, November 19, 4:00 pm – 5:30 pm

**Session Type:** Live

**CE Credit:** 1.5 | **SAM:** 1.5

**Path:** Inherited Conditions

**Moderator:** *Ryan Schmidt, MD, PhD, Children's Hospital Los Angeles, Los Angeles, CA, USA*

### **Mate Pair Sequencing as a Tool to Increase Diagnostic Yield for Constitutional Genetic Disorders**

*Nicole Hoppman, PhD, Mayo Clinic, Rochester, MN, USA*

### **Application of New Methods of Structural Variant Detection in the Clinical Laboratory**

*Madhuri Hegde, PhD, PerkinElmer, Duluth, GA, USA*

### **Simple and Complex Variants Detected by Short and Long Read Sequencing**

*Stephen Lincoln, Invitae, Potomac, MD, USA*

**Session Description:** Technological advancements have increased the ability to detect structural variants. These new tools are now being applied by laboratories for the diagnosis of constitutional disorders in affected individuals. This session seeks to highlight the potential for new structural variant detection methods to impact clinical diagnosis and provide practical guidance for clinical laboratories interested in adopting these methods.

#### **Session Objectives:**

- Recognize the contribution of structural variants to constitutional genetic disorders.
- Evaluate new technologies for the high-resolution detection of structural variants.

---

## **Genomics in Children: Coming of Age**

Thursday, November 19, 4:00 pm – 5:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Informatics, Inherited Conditions, Oncology

**Moderator:** *Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA*

### **The Current State of the Field in Pediatric Cancer Genomics and Rare Disorders**

*Sharon E. Plon, Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA*

### **Utility of WGS in Molecular Analysis Pediatric Cancers Discussing the Pro's and Con's Within the Question of Clinical Utility**

*Jinghui Zhang, PhD, St. Jude Children's Research Hospital, Memphis, TN, USA*

**Session Description:** Genomic disorders manifesting during childhood are distinct in terms of clinical spectrum and genetic etiology. The clinical application of genomic technologies and interpretation of genomic results require careful and unique considerations. In this session, the two speakers will describe the current state of the application of clinical genome-scale technologies to childhood Mendelian disorders and pediatric cancers.

#### **Session Objectives:**

- Choose correct genome-scale technology and test for the different clinical applications.
  - Explain the different types of genomic technologies and the different variants reported with such technologies.
  - Define the evidence for the correct classification of germline variants.
-

## Strain Typing in Clinical and Public Health Laboratories: Migration to Whole Genome Sequencing for Epidemiology Purposes

Thursday, November 19, 4:00 pm – 5:30 pm

**Session Type:** On Demand

**CE Credit:** 1.5

**Path:** Infectious Diseases, Informatics, Molecular Methodologies & Technologies

**Moderator:** Erin McElvania, PhD, NorthShore University HealthSystem, Evanston, IL, USA

### Transitioning from Conventional Typing to Whole Genome Sequencing (WGS) for Public Health Epidemiology

*William A. Glover, PhD, North Carolina State Laboratory of Public Health, Raleigh, NC, USA*

### Strain Typing in Clinical and Public Health Laboratory: Migration to Whole Genome Sequencing for Epidemiology Purposes

*Sanchita Das, MD, D(ABMM), NIH, Bethesda, MD, USA*

**Session Description:** Whole genome sequencing has the greatest discriminatory power for establishing pathogens relatedness. With the decreased cost of WGS, many laboratories (clinical and public health) have abandoned traditional molecular methods in favor of WGS.

#### Session Objectives:

- Describe basic concepts of WGS and subtyping methods currently being utilized in hospital and public health microbiology laboratories.
- Identify the advantages and challenges of moving from conventional typing methods to WGS.
- Discuss the requirements and infrastructure required to switch from conventional typing to WGS.

---

## The Roadmap to Recognition of Molecular Professionals as Qualified Healthcare Professionals *(Sponsored by the AMP Professional Relations Committee)*

Thursday, November 19, 4:00 pm – 5:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Advocacy

**Moderator:** Charles Mathews, Clearview Healthcare Partners, New York, NY, USA

### The Roadmap to Recognition of Molecular Professionals as Qualified Healthcare Professionals

*Andrea Ferreira-Gonzalez, PhD, VCU Heath, Richmond, VA, USA*

*Elaine Lyon, PhD, HudsonAlpha Institute for Biotechnology, Huntsville, AL, USA*

*Christina Lockwood, PhD, University of Washington, Seattle, WA, USA*

*John Schmitz, PhD, D(ABHI, ABMLI), F(AAM), UNC School of Medicine, Chapel Hill, NC, USA*

**Session Description:** The Professional Relations Committee (PRC) invites you to participate in a conversation about the past, present and future advocacy efforts focused on the ability of Board-certified doctoral clinical laboratory professionals to bill CMS under the physician fee schedule (PFS) for their role in performing, interpreting, and reporting individual results for molecular diagnostic tests. AMP has long been an advocate for qualified doctoral clinical laboratory professionals to bill on the PFS and in late 2018, AMP reignited our advocacy in this area through the creation of the Professional Reimbursement Workgroup (a joint workgroup of the PRC and the Economic Affairs Committee, EAC). The workgroup is charged with developing and proposing potential coding solutions for the interpretive work involved with molecular tests as well as ensuring that qualified doctoral

clinical laboratory professionals will also be able to bill for this work. This year, the workgroup launched a landscape analysis of the interpretive work that is performed by both molecular pathologists and clinical laboratory professionals. During the session, the workgroup will report on the results of this study and their next advocacy steps. Additionally, the AMP workgroup will be joined by representatives from the American College of Medical Genetics and Genomics (ACMG), who also reignited their advocacy in this area by releasing a statement on “PhDs as Qualified Healthcare Professionals” in late 2019. Please join us for an in-depth discussion about AMP and ACMG’s current advocacy activities in this area and to learn how AMP members can get more involved in furthering this mission.

**Session Objectives:**

- Understand the CMS billing for professional and interpretive work and explain previous efforts by AMP and others on this topic.
- Gain a clear perspective of AMP’s landscape analysis and understand the gaps between the interpretive work involved with molecular pathology testing and the current reimbursement structure.
- Comprehend the history on this issue and concerns for various professional organizations.
- Learn key ways one can get more involved in this issue.

---

## What Do All These Mutations Mean?

Thursday, November 19, 4:00 pm – 5:30 pm

**Session Type:** Live

**CE Credit:** 1.5 | **SAM:** 1.5

**Path:** Oncology

**Moderator:** Mark D. Ewalt, MD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

### How Do I Manage a Patient with CH?

Kelly Bolton, MD PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

### How Can I Use Mutation Data to Diagnose MDS in a Patient with Cytopenia and No Morphologic Dysplasia?

Amy E. Dezern, MD, MHS, The Johns Hopkins University School of Medicine, Baltimore, MD, USA

**Session Description:** Over the last several years, we have come to recognize that healthy individuals often harbor somatic alterations which are detectable in the peripheral blood but are not specifically diagnostic for a hematologic neoplasm, which has been named Clonal Hematopoiesis (CH). In addition, some patients show evidence of clonal hematopoiesis and a cytopenia but no overt evidence of morphologic dysplasia. This session aims to review our understanding of the impact of CH on health and how the presence of multiple clonal mutations may impact diagnosis of a hematologic neoplasm.

**Session Objectives:**

- Understand the effects of CH on health and clinical management strategies.
- Review, in the context of unexplained cytopenia, the diagnostic value of a somatic mutation analysis.

---

## Innovation Spotlights

Thursday, November 19, 5:30 pm – 6:30 pm

---

## Social Event – AMP Talent Show

Thursday, November 19, 6:00 pm – 7:00 pm

---

## Interactive Expo Hall

Friday, November 20, 11:00 am – 11:45 am

---

## Chat with the 2020 Program Chair (Dr. Jane Gibson) & the 2021 Program Chair (Dr. Laura Tafe)

Friday, November 20, 11:45 am – 12:00 pm

---

## DepMap: The Cancer Dependency Map Project

Friday, November 20, 12:00 pm – 1:00 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Oncology

**Moderators:** Raj Emmadi, MD, University of Illinois, Chicago, IL, USA and Jonathan A. Nowak, MD, PhD, Brigham and Women's Hospital, Boston, MA, USA

### Depmap: The Cancer Dependency Map Project

William C. Hahn, MD, PhD, Dana-Farber Cancer Institute, Boston, MA, USA

**Session Description:** Applying precision cancer medicine requires an understanding of somatic alterations and their consequences in tumors. This presentation will describe our efforts to comprehensively map genes required for the fitness of human cancers using genome scale genetic approaches.

### Session Objectives:

- Understand the concept of a cancer dependency.
- Understand genome-scale approaches to study gene function.
- Define different types of cancer targets to enable cancer precision medicine.

---

## Emerging Testing Paradigms and Insights

Friday, November 20, 1:00 pm – 2:30 pm

**Session Type:** Live

**CE Credit:** 1.5 | **SAM:** 1.5

**Path:** Inherited Conditions

**Moderator:** Hyunseok Kang, MD, MS, Natera, Inc., Los Altos Hills, CA, USA

### Experience from Proactive Whole Genome Sequencing in 400 Newborn Children

Steven B. Bleyl, PHD, MD, Genome Medical Services, S. San Francisco, CA, USA

### Genetic Testing as an Employee Benefit

Scott Topper, PhD, Color, Burlingame, CA, USA

### Translational Research Approaches to Large-scale Population Genomics

James Lu, MD, PhD, Helix, San Mateo, CA, USA

**Session Description:** Genetic testing models have proliferated beyond the traditional clinical setting. This session will explore some of the non-traditional models and insights that have arisen from them.

**Session Objectives:**

- Upon completion, participant will be able to describe some of the services that do not fit into a traditional CLIA testing framework.
- Upon completion, participant will be able to describe the advantages and disadvantages of some emerging testing services.

---

## Genomically-informed Lymphoma Classification

Friday, November 20, 1:00 pm – 2:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Oncology

**Moderator:** Mark D. Ewalt, MD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

### Molecular Updates in Classification of B-cell Lymphomas

Sandeep Dave, MD, Duke University, Durham, NC, USA

### Molecular Updates in Classification of T-cell Lymphomas

Javeed Iqbal, MS PhD, Department of Pathology and Microbiology, University of Nebraska Medical Center, Omaha, NE, USA

**Session Description:** The past several years have seen an explosion in genomic information in lymphoid neoplasms. This information has helped to refine our classification systems of B- and T-cell lymphoproliferative disorders. This session aims to review major updates to the molecular classification of lymphoid neoplasms and suggestions for how to incorporate this into molecular hematopathology practice.

**Session Objectives:**

- Describe how gene expression profiling and molecular classification can delineate novel subtypes of T-cell lymphoma.
- Discuss novel classifications of B-cell lymphoma based on genetic information.

---

## Next Generation Data: Integration and Dissemination of Molecular Pathology Data

Friday, November 20, 1:00 pm – 2:30 pm

**Session Type:** On Demand

**CE Credit:** 1.5

**Path:** Informatics

**Moderator:** Angshumoy Roy, MD, PhD, Baylor College of Medicine, Houston, TX, USA

### Modern Application Deployment Strategies for NGS Testing and Integration with Molecular Pathology Data

Cihan Kaya, PhD, Molecular and Genomic Pathology Lab, University of Pittsburgh Medical Center, Pittsburgh, PA, USA

### Next Generation Data: Integration and Dissemination of Molecular Pathology Data

Ahmet Zehir, PhD, Memorial Sloan Kettering Cancer Center, Department of Pathology, New York, NY, USA



**Session Description:** Molecular pathology generates multitude of data points for each specimen received. With increasing adoption of NGS assays, managing and sharing data has become harder but more important than ever. This session will discuss best practises around managing, reviewing, integrating and disseminating molecular pathology data. Participants will discuss their experiences and tools developed/used for this process.

**Session Objectives:**

- Best practices for developing software tools for molecular pathology applications.
- Integrating data from disparate data sources; not only from molecular tests but from across all pathology.

---

## Tumor Evolution and Therapeutic Resistance

Friday, November 20, 1:00 pm – 2:30 pm

**Session Type:** Live

**CE Credit:** 1.5

**Path:** Oncology

**Moderator:** Raj Emmadi, MD, University of Illinois, Chicago, IL, USA

### In-silico Modeling of Tumor Evolution

Noam Auslander, PhD, National institute of Biotechnology Information, NIH, Bethesda, MD, USA

### Molecular Archeology of Cancer

Peter Van Loo, PhD, The Francis Crick Institute., London, England, United Kingdom

**Session Description:** The cancer genome contains an evolutionary record of the tumor's past. Mining this record can show us the timelines of tumor evolution. Studying this mutational landscape through neural nets and other computational modeling allows for a more comprehensive view of mutational process, burdens and hierarchical sequence, allowing for clearer definitions of tumor progressions and therapeutic implications. It also opens up opportunities for future early diagnostic approaches.

**Session Objectives:**

- Understand how methods of massively parallel sequencing and computational modeling can be used to elucidate and model the temporal sequence of tumor progression and evolution.
- Investigate tumor progression and construct clinically relevant mutational profiles.
- Understand how characterization of tumor evolution can impact clinical care and identify opportunities for future early diagnosis of cancer.

---

## Whole Genome Sequencing for Antimicrobial Resistance Testing

Friday, November 20, 1:00 pm – 2:30 pm

**Session Type:** Live

**CE Credit:** 1.5 | **SAM:** 1.5

**Path:** Infectious Diseases, Informatics, Molecular Methodologies & Technologies

**Moderator:** Esther Babady, PhD, Memorial Sloan Kettering Cancer Center, New York, NY, USA

### Detection of Resistance-associated Mutations in Cytomegalovirus Through the Use of Next-generation Sequencing

Matthew Binnicker, PhD, Mayo Clinic, Rochester, MN, USA

## Clinical Whole-genome Sequencing and Drug Resistance Reporting for mycobacterium tuberculosis in New York: A 5 Year Summary

Kimberlee Musser, PhD, Wadsworth Center, New York Department of Health, Wadsworth Center, Loudonville, NY, USA

**Session Description:** Describe and discuss the use of WGS for the routine detection and monitoring of antimicrobial resistance of pathogens of clinical importance.

### Session Objectives:

- Understand the basic design of a Next generation sequencing (NGS) whole-genome sequencing (WGS) approach to detect mutations of clinical significance.
- Discuss the application of next-generation sequencing for the detection and identification of resistance-associated mutations for Mycobacterium tuberculosis and cytomegalovirus.
- Be familiar with interpretation and reporting of NGS WGS testing.

---

## Interactive Expo Hall with Demos and Drawings

Friday, November 20, 2:30 pm – 3:30 pm

---

## Gene Therapy for Retinal Disorders

Friday, November 20, 3:30 pm – 4:30 pm

**Session Type:** Live

**CE Credit:** 1

**Path:** Inherited Conditions

**Moderator:** Hyunseok Kang, MD, MS, Natera, Inc., Los Altos Hills, CA, USA

### Gene Therapy for Retinal Disorders

Elias Traboulsi, MD, MEd, Cleveland Clinic, Cleveland, OH, USA

**Session Description:** In the last several years, there have been significant advances in the area of targeted therapies for constitutional genetic disorders. In 2017, the FDA approved its first gene therapy, Luxturna, for the treatment of RPE65-associated retinal dystrophy. As a result of this breakthrough, gene therapy trials are underway for a variety of other retinal disorders. Retinal disorders exemplify the emerging paradigm that links molecular diagnostic testing for constitutional genetic disorders to targeted therapies.

### Session Objectives:

- Upon completion, participant will be able to describe novel targeted therapies for various genetic disorders.
- Upon completion, participant will be able to describe the mechanisms of targeted therapies and patient prognosis.

---

## Closing Remarks

Friday, November 20, 4:30 pm – 4:45 pm

---

## Poster Information

### General Poster Information

- All poster will be on display in the “Poster Hall” of the AMP Virtual Platform. There, you’ll be able...
  - View the ePosters (PDF File)
  - View Video Presentations (if submitted by author)
  - Chat with and ask the authors questions during the designated Poster Presentations times (see below). You will do this by using the “Chat” Function within each poster listing.
- Please note that poster-viewing is not eligible for Continuing Education credit.
- Abstracts can be viewed online here: [https://www.jmdjournal.org/issue/S1525-1578\(19\)X0018-5](https://www.jmdjournal.org/issue/S1525-1578(19)X0018-5)
- Posters are arranged by category and listed in sequential order by number in the following format:

**Poster Number**      **Abstract Title**  
*First Author’s Name*

- Key to poster categories:

|                                 |                              |
|---------------------------------|------------------------------|
| <b>G</b> = Genetics             | <b>I</b> = Informatics       |
| <b>HP</b> = Hematopathology     | <b>OTH</b> = Other           |
| <b>ID</b> = Infectious Diseases | <b>ST</b> = Solid Tumors     |
|                                 | <b>TT</b> = Technical Topics |

### Award Applicant Information

- All Award Applicant posters display in Poster Number order in the areas of their subject category. They are identified as Technologist or YIA Award Applicant within the Poster Title Listing.
- All Award Applicants must attend their posters on Tuesday, November 17, 1:00pm – 2:00pm for interviews with members of the poster reviewing committees via the chat function within the virtual platform.

### Author/Presenter Information

- All First/Presenting Authors, including Award Applicants, must attend their posters either Tuesday afternoon (even-numbered posters) or Thursday morning (odd-numbered posters):
  - Even-numbered posters must be attended on Tuesday, November 17, 1:00pm – 2:00pm
  - Odd-numbered posters will be attended on Thursday, November 19, 1:00pm – 2:00pm
- 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 type a message in the chat function alerting attendees that they will attend the poster in the alternate session.

## Poster Listing

**Even numbered ePosters** will be attended by their authors on Tuesday, November 17, 1:00pm – 2:00pm Eastern

**Odd numbered ePosters** will be attended by their authors on Thursday, November 19, 1:00pm – 2:00pm Eastern.

---

### GENETICS

**G01. Development and Validation of a High-Throughput Next-Generation Sequencing Assay from Buccal Cell DNA as a Cost-Effective Screening Method for Celiac Genetic Risk**

*S. Gunn*

**G02. Copy Number Variant Analysis Improves the Diagnostic Yield in a Cohort of Pediatric Patients with Previously Negative Constitutional Exome Sequencing Results**

*E. Hahn*

**G03. A Retrospective Study of Products of Conception with More Than 44,000 Specimens in 27 Years at a National Cytogenetic Reference Laboratory**

*H. Meng*

**G04. WITHDRAWN**

**G05. Reevaluation of Genomic Test Results for Germline Disorders: A Framework of Critical Considerations on Behalf of CLSI Document Development Committee (DDC) on Nucleic Acid Sequencing (MM09)**

*J. Ji*

**G06. Single Gene Transcript Analysis and 3D Modeling: An Integrated Approach to Variant Assessment**

*F. Vetrini*

**G07. Detection of Allelic Dropout in a Mass Array *HFE* Genotyping Assay**

*A. Campbell*

**G08. Result Interpretation for Clinical Exome and Genome Sequencing: On Behalf of CLSI Document Development Committee (DDC) on Nucleic Acid Sequencing (MM09)**

*J. Buchan*

**G09. Incidental Diagnosis of *NR5A1*-Related 46,XY Disorder of Testicular Development in Neonate with Mosaic Partial Trisomy 2q**

*S. Vallee*

**G10. Optimization and Validation of a Sanger Sequencing Clinical Assay for Germline *BRCA1/2* Gene Mutation Detection at King Hussein Cancer Center**

*W. Naser*

**G11. Mosaicism in Cancer Susceptibility Genes in Unselected Cancer Patients**

*D. Mandelker*

**G12. Presumed Germline Pathogenic Variants in Tumor-Only Sequencing: Frequency and Follow-Up**

*D. Toledo*

**G13. Comparison of Universal versus Traditional Genetic Testing Models for Cancer Patients**

*O. Ceyhan-Birsoy*

**G14. The Prevalence and Distribution of Germ-Line Inherited Cancer-Associated Variants**

*T. Huard*

**G15. Characterization of Reference Materials for Spinal Muscular Atrophy Genetic Testing: A GeT-  
RM Collaborative Project**

*T. Prior*

**G16. A Rare Single Nucleotide Variant Causing a False-Negative *HTT* CAG Repeat Expansion Result in the Evaluation of a Patient for Huntington Disease**

*F. El-Sharkawy*

**G17. Amplification-Free Targeted Enrichment Powered by CRISPR-Cas9 and Long-Read Single Molecule Real-Time Sequencing Can Efficiently and Accurately Sequence Challenging Repeat Expansion Disorders**

*J. Ekholm*

**G18. A Single-Assay Diagnostic Workflow for Genotyping and Phasing SNPs with Repeat Expansions for Allele-Selective Therapy in Huntington Disease**

*S. Statt*

**G19. Review of Analysis Methods for Repeat Expansion Diseases Using Capillary Electrophoresis Data**

*M. Avenarius*

**G20. Test Validation and Characterization of Reference Materials for *ADH5* Genotyping**

*A. Otsubo*

**G21. *CYP2D6* Guided Methadone Dosing in a Multi-Ethnic Population: A Pharmacogenomic Screen to Decrease Withdrawal Morbidity**

*C. Lum*

**G22. Developing *DPYD* Genotyping Method for Personalized 5-fluorouracil Therapy**

*B. Wong*

**G23. High-Throughput Fetal-Fraction Amplification Increases Analytical Performance of Noninvasive Prenatal Screening**

*D. Muzzey*

**G24. A Software Tool That Prevents Incorrect Estimations of Gestational Age and Maternal Age at Estimated Date of Delivery Reported by the College of American Pathologists NIPT Participant Summary**

*Y. Wang*

**G25. Genetic Insights and Incidental Findings from Maternal Cell Contamination Testing**

*N. Kopp*

**G26. The Relationship between Variant Type and Phenotype among Diseases Screened by the Foresight Expanded Carrier Screen**

*K. Karimi*

**G27. Two-Site Evaluation of a Rapid and Simple CFTR PCR/CE Assay and Software Targeting Mutations across Diverse Ethnic Groups**

*S. Filipovic-Sadic*

**G28. SMN1 and SMN2 Copy Number Distribution in 733 Clinical Cases of Carrier Screening for Spinal Muscular Atrophy**

*D. Toledo*

**G29. Proof-of-Concept for Single-Platform Trio Carrier Screening of FMR1, SMN1/2, and CFTR Variants Using PCR and Capillary Electrophoresis with Consolidated Workflows**

*W. Laosinchai-Wolf*

**G30. The Single-Tube SLIMamp NGS Assay for Detection of Mutations Associated with Thalassemia Is both Rapid and Robust**

*X. Wu*

**G31. Exploring Mosaic Mutations in Megalencephaly and Other Growth Disorders by Next-Generation Sequencing**

*N. Madkhali*

---

**HEMATOPATHOLOGY**

**H01. Personalized Medicine in Practice: Comprehensive Genomic Profiling of a Lung Adenocarcinoma Leads to Reclassification of a Concurrent Lymphoma**

*P. Terraf*

**H02. WITHDRAWN**

**H03. Limitation in Confirming Low Allele Frequency Calls from Sensitive Cancer Assays: MSK Experience with the LiquidPlex cfDNA Panel on Hematologic Samples**

*J. Jeon*

**H04. Somatic Mutation Testing for Pediatric Patients with Known or Suspected Inherited Bone Marrow Failure Syndromes**

*K. Fisher*

**H05. A Highly Reproducible Single-Day FISH Assay for Detection of t(11;14) in Multiple Myeloma Patient Samples**

*A. Prokhorova*

**H06. Comparison of Capture-Based Next-Generation Sequencing Designs in a Clinical Myeloid Neoplasm Panel**

*M. Dina*

**H07. Clinical Utility of a Custom-Designed Next-Generation Sequencing (NGS) Panel for Detection of Gene Fusions, Deletions, and Hotspot Mutations in Myeloid and Lymphoid Neoplasms**

*R. Starks*

**H08. Genomic Landscape of Primary Breast Lymphoma Diffuse Large B-Cell Lymphoma (PB-DLBCL)**

*L. Liu*

**H09. Evaluation of the Ion Torrent OncoPrint Myeloid Sequencing Panel**

*B. Houde*

**H10. Proteomics-Based Biomarkers in Squamous Cell Carcinoma: A Pilot Study Correlating Proteomic Profiles and Tumor Differentiation**

*Y. Chen Wongworawat*

**H11. Detection of Low-Frequency Variants for Minimal Residual Disease (MRD) Monitoring of Acute Myeloid Leukemia**

*N. Valencia*

**H12. A Next-Generation DNA Sequencing Assay for Detection of SNVs, Insertions, Deletions, and Copy Number Variants in 25 Lymphoma Genes in Samples**

*S. Roman*

**H13. High Throughput TRG Sequencing in a Clinical Laboratory: Analysis of Equivocal Results**

*V. Smith*

**H14. CloneRetriever: An Automated Algorithm to Identify Clonal Immunoglobulin Gene Rearrangements by Next-Generation Sequencing**

*E. Halper-Stromberg*

**H15. IGH V-Gene Somatic Hypermutation Assessment by Hybrid-Capture**

*E. Mahe*

**H16. Comparison of Next-Generation Sequencing-Based TRG and TRB Assays for the Diagnostic Evaluation of T Cell Lymphoid Malignancies**

*C. Ho*

**H17. Characterization of the Immunoglobulin Heavy- and Light-Chain Repertoires in a Single Reaction**

*G. Lowman*

**H18. Assessment of a High-Throughput Sequencing Assay for Measurable Residual Disease (MRD) Monitoring in Patients with T-Cell Malignancies**

*J. Tung*

**H19. Improved Clonality and Somatic Hypermutation Analysis of CLL with a Highly Multiplex IGHV Assay**

*M. Toro*

**H20. The Development of an NGS Assay of Immunoglobulin Heavy Variable Gene Somatic Hypermutation in CLL**

*G. Shi*

**H21. Validation of MYD88 L265P ddPCR Assay and Application in Assessment of Primary CNS Lymphoproliferative Disorders**

*M. Cantu*

**H22. An Artificial Intelligence System Applied to Recurrent Cytogenetic Aberrations and Derived Genetic Progression Scores Predicts MYC Rearrangements in Diffuse Large B-Cell Lymphoma.**

*R. Garcia*

**H23. Precise Detection of PDL1/PDL2 Copy Number Alterations in Classic Hodgkin Lymphoma Using Combined CD30 Immunophenotyping and FISH Analysis**

*Y. Zhang*

**H24. Clinical and Genetic Risk Factors Associated with Relapse of Hyperdiploid B-ALL: A Single Institution Review 2001-2019**

*J. Schubert*

**H25. Novel Fusion of *PVT1-RCOR1* in B-Cell Prolymphocytic Leukemia (BCPCLL) Producing False FISH Fusion of *MYC-IGH* with an Atypical Pattern**

*P. Koduru*

**H26. Identification of Clinical Molecular Targets for Childhood Burkitt Lymphoma**

*N. Zeng*

**H27. Characterization of *TP53* Mutations in Myeloid Neoplasms for Targeted Therapy**

*A. Mendiola Romero*

**H28. Chromosome Arm Gain or Loss by Next Generation Sequencing**

*M. Dabrowski*

**H29. Clinical Significance of *CEBPA* Double Mutants: Challenges in Variant Classification and Subtyping of Acute Myeloid Leukemia**

*J. Yoon*

**H30. Cytogenetic and Molecular Landscape in Hispanic Acute Myeloid Leukemia Patients from Puerto Rico**

*P. Deb*

**H31. Evaluation and Follow-up of *JAK2* V617F Positive Patients with Low Allele Burden: A Single-Center Experience**

*K. Reddy*

**H32. Number of Variants and Pathogenic Variants in *ASXL1*, *STAG2*, and *RUNX1* Correlate with High Ogata Score by Flow Cytometry in Myelodysplastic Syndromes: A National Reference Laboratory Experience**

*M. Williams*

**H33. Clinical Implementation of a Custom Myeloid NGS Assay and Overview of *NPM1* and *IDH1/IDH2* Mutation Status in a Clinical Cohort**

*M. Kluk*

**H34. Development of *FIP1L1-PDGFR* Real-time RT-PCR Assay**

*M. Mai*

**H35. *FLT3*-ITD Mutant Allelic Ratio: Impact of Using Non-standardized Published Calculations and Potential Correction Based on Marrow Blast Percentage**

*J. Reinartz*

**H36. Atypical CBFB FISH Signal Patterns Warrant Further Investigation for a True CBFB Rearrangement: An Analysis of 2,425 CBFB FISH Tests**

*R. Yang*

**H37. Curation of *FLT3* Variants in Acute Myeloid Leukemia by Clinical Genome Resource Somatic Hematologic Cancer Taskforce (ClinGen HCT)**

*X. Xu*

**H38. Persistent *IDH* Mutations in AML Patients in Remission on IDH Inhibitors**

*J. Xu*



H39. **Diagnostic Value of Molecular Markers in the Work-up of Myelodysplastic Syndromes**  
*R. He*

H40. **Clinical Validation of Mutant *IDH1* and *IDH2* Detection by Multiplex Digital Droplet PCR**  
*J. Racchumi*

H41. **Comparison of Targeted Myeloproliferative Subpanel versus Comprehensive Myeloid Panel in the Evaluation of Suspected *BCR-ABL1*-Negative Myeloproliferative Neoplasms**  
*D. Morlote*

H42. **Haplotype Phase of *CEBPA* Mutations in Acute Myeloid Leukemia**  
*S. Harley*

H43. **Identifying Non-canonical Mutations in Myeloproliferative Neoplasms: Our Experience with *JAK2* Sequencing**  
*L. Baugh*

H44. **Comparison of Whole Genome Sequencing (WGS) with Conventional Cytogenetics in Profiling Genome-Wide Large-Scale Copy Number and Structural Variations in Pediatric and Adolescent AML**  
*L. Wang*

H45. **Workflow Comparison between Two NCCN Guideline Recommended Myeloproliferative Neoplasms Screening Workup: A Single Institution's Experience**  
*N. Tabish*

---

## INFECTIOUS DISEASES

ID01. **Multisite Evaluation of the ARIES MRSA Assay for the Detection of Methicillin-Resistant *Staphylococcus aureus* (MRSA) from Nasal Swabs**  
*B. Buchan*

ID02. **Comparison of a Cartridge-Based Host Gene Expression Test to a Manual Method for Use in the Diagnosis of Sepsis**  
*S. Cermelli*

ID03. **Comparison of Two Multiplex Real-Time PCR Assays for Detection of Tick-Borne Pathogens**  
*T. Uphoff*

ID04. **Development and Performance of a Multiplex Polymerase Chain Reaction (PCR)-Based Assay for Detection of Bacteria in Sterile Body Fluids**  
*C. Johnson*

ID05. **Automated Multiplex Real-Time PCR Detection of *Anaplasma phagocytophilum* and *Ehrlichia chaffeensis* Using the Panther Fusion Open Access System**  
*K. Stellrecht*

ID06. **Automated Real-Time PCR Detection of *Babesia microti* Using the Panther Fusion Open Access System**  
*K. Stellrecht*

ID07. **Evaluation of an Automated rRNA Quantitation System for Rapid AST in Clinical Lab Diagnostics**  
*D. Liu*

**ID08. Prospective Evaluation of a Multiplex HDPCR Tick-Borne Pathogen Panel**

*T. Uphoff*

**ID09. Development of a 29-mRNA Loop Mediated Isothermal Amplification Assay for the Rapid Diagnosis of Acute Infection and Sepsis**

*M. Remmel*

**ID10. *In silico* Performance of a Rapid Sepsis Test in Patients with Candidemia**

*D. Sampson*

**ID11. Development of ViroKey SARS-CoV-2 RT-PCR Test v2.0 for the Sensitive and Accurate Automated Detection of the SARS-CoV-2 Virus**

*I. Ng*

**ID12. Comparison of Four Commercial Molecular Diagnostic Kits for Detection of SARS-CoV-2: A Pilot Study**

*P. Chheda*

**ID13. Evaluation of Ion AmpliSeq SARS-CoV-2 NGS Research Panel**

*W. Liu*

**ID14. Rapid Detection of SARS-CoV-2 Virus via Novel Direct Amplification Methods**

*C. Knox*

**ID15. SARS-CoV-2 Cycle Number as a Metric for Population Trends in New Hampshire**

*E. Bradley*

**ID16. Verification of the Centers for Disease Control and Prevention Real-Time SARS-CoV-2 Assay for Emergency Use Authorization**

*K. Lancor*

**ID17. Analytical Validation of a SARS-CoV-2 Whole Genome Sequencing Method by Amplicon-Based NGS**

*S. Rosenthal*

**ID18. Developing Multiplex of Real-Time PCR Assays for Simultaneous Detection and Differentiation of COVID-19 Plus Flu A and Flu B in a Single Tube Format**

*C. Wang*

**ID19. Comparison of Test Performance of Two Rapid SARS-CoV-2 Viral Assays**

*R. Abdulbaki*

**ID20. Multi-Institutional Evaluation of the Performance of a Rapid Nucleic Acid Amplification Technology for Detecting SARS-CoV-2 on Nasal and Nasopharyngeal Swabs**

*S. Glogowski*

**ID21. Detecting Signatures of SARS-CoV-2 Using Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)**

*R. Barney*

**ID22. A Practical Comparison of Seven Molecular SARS-CoV-2 Methods**

*C. Gentile*

**ID23. Performance of SARS-CoV-2 Assay in Extraction-Free Method Compared to That of Conventional RNA Extraction Using Automated Instrument**

*S. Kim*

**ID24. The Combination Assay for SARS-CoV-2 and Other Respiratory Viruses in Symptomatic Patients and the Statistical Outcome Visualizing Metrics and Trends**  
*S. Lee*

**ID25. Temporal Spatial Heterogeneity of Immune Response to SARS-CoV-2 Lung Infection**  
*N. Desai*

**ID26. Clinical Performance of Six SARS-CoV-2 Nucleic Acid Amplification Assays in Symptomatic and Asymptomatic Pediatric and Maternal Patient Populations**  
*A. Rahman*

**ID27. Evaluating the Clinical Utility of Next-Generation Sequencing of Nasopharyngeal Specimens for SARS-CoV-2 in the COVID-19 Pandemic**  
*P. Velu*

**ID28. Validation of Saliva Testing for SARS-CoV-2 on Abbott m2000**  
*S. Amin*

**ID29. Validation of an Emergency Use Authorization RT-PCR Test for Detecting SARS-CoV-2 in Upper and Lower Respiratory Tract Specimens**  
*L. Cong*

**ID30. Development of a Multiplexed External Control for Monitoring Performance of a Qualitative Laboratory Nucleic Acid Testing Panel Used for Identification of Respiratory Infections, Including SARS-CoV-2**  
*M. Steffen*

**ID31. Development of a Synthetic External Control for Rapid Detection of SARS-CoV-2 for Use on Xpert Xpress SARS-CoV-2**  
*M. Amadei*

**ID32. Development of a Multiplex Respiratory Panel and a Singleplex SARS-CoV-2 External Control for Use in a Rapid Nucleic Acid Amplification Detection System**  
*J. Salem*

**ID33. Comparison of Two High-Throughput qPCR Assays for SARS-CoV-2**  
*S. Turner*

**ID34. Development of a Multiplexed Synthetic Control for Rapid Detection of SARS-CoV-2 and Other Respiratory Pathogens Using a Nucleic Acid Syndromic Testing Panel**  
*T. Schleicher*

**ID35. Comparison of Nasopharyngeal Swabs and Saliva Samples for the Detection of SARS-Cov-2 RNA**  
*T. McMillen*

**ID36. Strategy for Analysis of Human ACE2 Putative Variants Linked to Protein Structure and Stability: Implications for ACE2 Receptor Binding to SARS-CoV-2**  
*E. Hughes*

**ID37. Comparison of Oral Rinses and Nasopharyngeal Swabs for the Detection of SARS-CoV-2 RNA**  
*T. McMillen*

**ID38. Lung Injury Due to COVID-19 Relative to Influenza and Non-viral ARDS and Normal Controls**  
*A. Borczuk*

**ID39. Evaluation of Sample Pooling for the Detection of SARS-CoV-2 RNA Using the Cobas SARS-CoV-2 Test**

*T. McMillen*

**ID40. RT-PCR Detection of SARS-CoV-2 Infection in Formalin-Fixed, Paraffin-Embedded Tissue Sections in Autopsy Cases**

*D. Berman*

**ID41. The Evaluation of Oropharyngeal Swabs and Saliva Samples for the Detection of SARS-CoV-2 RNA**

*T. McMillen*

**ID42. Evaluation of a Sample-to-Answer Cartridge-Based SARS-CoV-2 Assay**

*J. Lefferts*

**ID43. Viral Sequencing Suggesting Transmission of SARS-CoV-2 from a Patient with False-Negative Molecular Results to Health Care Providers**

*D. Green*

**ID44. Digital Droplet PCR to Detect Low-Titer SARS-CoV-2 in Nasopharyngeal, Nasal, and Salivary Specimens**

*J. Xu*

**ID45. Leveraging Clinical Metagenomic Testing against SARS-CoV-2**

*B. Briggs*

**ID46. A Systematic Review of the Genomic Diversity of SARS-CoV-2 Virus Detected in Dartmouth-Hitchcock Hospital**

*D. Green*

**ID47. Evaluation of Saliva as an Alternative Sample Type for SARS-CoV-2 Detection Using the Hologic Panther Aptima EUA Assay**

*W. Rehrauer*

**ID48. Automated, High-Throughput Testing Using the RealTime SARS-CoV-2 Assay**

*M. Johnston*

**ID49. The Utility of Repeat Testing for Severe Acute Respiratory Syndrome-Coronavirus-2 by Reverse Transcriptase-Polymerase Chain Reaction in Improving Diagnostic Accuracy**

*S. Fathima*

**ID50. Clinical Performance of GenMark ePlex SARS-CoV-2 Test Compared to a Laboratory Developed Procedure**

*J. Laudadio*

**ID51. Evaluation of the SARS-CoV-2 Chromacode EUA Assay**

*L. Thompson*

**ID52. Design and Optimization of Novel ITS2-28s rRNA Gene Primers for Fungal Species Detection from Formalin-Fixed, Paraffin-Embedded Tissues with a Targeted Next-Generation Sequencing Assay**

*G. Wang*

**ID53. Non-invasive Microbial Cell-Free DNA Sequencing Detects Invasive Mold Infections in Immunocompromised Patients with Pneumonia**

*T. Blauwkamp*

**ID54. A Comparative Study of qPCR to a NGS Metagenomics Assay to Detect and Quantify DNA Viruses in Pediatric Bone Marrow Transplant Patients**

*L. Cooper*

**ID55. Investigating Targeted Next-Generation Sequencing of 16S RNA as a Tool for Detecting Shiga Toxin-Producing *E. coli* and *Salmonella* in Ground Beef**

*J. Au-Young*

**ID56. Subtyping of Human Papillomavirus (HPV) Using Next-Generation Sequencing (NGS) Data in Cervical Cancer: A Feasibility Study with Comparison to Conventional Clinical Assays**

*J. Chen*

**ID57. Analytical Performance Characteristics of Galileo ONE: An End-to-End Metagenomics Assay for the Unbiased Sequencing and Bioinformatics Analysis of Microbial DNA and RNA Directly from EDTA Plasma**

*M. Carpenter*

**ID58. Application of Whole-Genome Sequencing for Bacterial Strain Typing in Investigating Hospital Infections**

*K. Park*

**ID59. Validation of ddPCR-Quantified Standards for Use in Viral Load Measurements by NGS**

*D. Hoerres*

**ID60. Performance Evaluation of Abbott Alinity m System to Detect HBV, HCV, and HIV-1 Infections: Comparison with Hologic Panther Aptima System**

*J. Han*

**ID61. Characterization and Evaluation of AcroMetrix HIV, HBV, and HCV Whole Process Quality Controls for Molecular Diagnostic Tests Using Cobas 6800 System**

*H. Wang*

**ID62. WITHDRAWN**

**ID63. Evaluation of a Novel VZV Molecular Assay for Detection of VZV from CSF and Swabs**

*A. Cruz*

**ID64. A Multi-Lab Collaboration for Quantitative BK Virus Test Development on the Fully Automated Cobas 6800/8800 OMNI Utility Channel**

*K. Lebel*

**ID65. Utilization of Digital PCR Assay for the Detection of HPV-16 in Cell-Free DNA in Patients with Head and Neck Cancer at an Oncology Center**

*T. McMillen*

**ID66. Detection of Adenovirus Serotype 7 in a Cancer Patient Population**

*R. Sumner*

**ID67. Retrospective Review of Seasonality of Human Parainfluenza Virus Subtypes at an Oncology Center**

*T. McMillen*

**ID68. Validation of the RealStar Adenovirus Reagents on Plasma and Stool Samples and Comparison to a Laboratory-Developed Test Using the MultiCode Adenovirus Reagents**

*C. Lee*

---

## INFORMATICS

I01. **Assessment of RAS Dependency for *BRAF* Mutations Using Real-World Evidence Databases**  
*G. Zheng*

I02. **CarrierSeq, an Expanded Carrier Screening Product Using Next-Generation Sequencing Technology**  
*T. Fahland*

I03. **Evaluation of Roche NAVIFY Mutation Profiler for NGS Variant Annotation and Reporting**  
*P. Ward*

I04. **Optimizing the Detection of Insertions and Deletions Using Next-Generation Sequencing in the Clinical Laboratory**  
*K. Craven*

I05. **Optimizing Reference Mixture Samples for Bioinformatics Pipeline Assessment on Variant Calling Detection for Cancer Diagnostics and Treatment**  
*C. Laing*

I06. **Use and Feasibility of Multi-Algorithmic Consensus-Based Bioinformatics Pipelines in the Detection of Fusions in FFPE Treated Samples**  
*V. Williamson*

I07. **Highly Scalable and Automated Approach to Gut Microbiome Profiling and Quantification Using a New Ion Torrent Next-Generation Sequencing Assay**  
*S. Sarda*

I08. **Microhaplotype Locus-Based Workflow for Sample Contamination Detection in Multiplexed Next-Generation Sequencing (NGS) Assays**  
*J. Balan*

I09. **Prediction of DDR and Other Mutation Signatures Using Panel-Based Sequencing**  
*A. Chellappan*

I10. **Accurate Detection and Quantification of *FLT3* Internal Tandem Duplications in Clinical Hybrid Capture Next-Generation Sequencing Data**  
*J. Tung*

I11. **Identification of Large Deletions Affecting *CTNNB1* Exon 3 in Solid Tumors**  
*Z. Zhang*

I12. **Development of a Clinical Bioinformatics Pipeline for the Comprehensive Genomic Profiling of Patient-Derived Xenograft Tumors**  
*S. Turner*

I13. **Comprehensive Single-Nucleotide, Indel, Structural, and Copy-Number Variant Detection in Human Genomes with PacBio HiFi Reads**  
*W. Rowell*

I14. **Look before You Leap: A Toolkit for Moving Clinical Panels to GRCh38**  
*A. Skol*

**I15. A Novel Machine Learning Approach to Characterize Cancer Signatures for Improved Clinical Reporting**

*S. Shams*

**I16. Pindel as a Back-up INDEL Caller to a GATK4 Mutect2-Based in-House Developed Somatic Secondary Analysis Bioinformatics Pipeline for a Custom Clinical Cancer NGS Panel**

*S. Harada*

**I17. Classification Methods for Germline and Somatic Single Nucleotide Variant (SNV) in Circulating Tumor DNA (ctDNA) of Small Cell (SCLC) and Non-small Cell Lung Cancer (NSCLC)**

*C. Wöstmann*

**I18. Evaluating Machine Learning Methods for Accurate Variant Calling Detection on Acute Myeloid Mutation Analysis**

*C. Laing*

**I19. Noise Reduction Using a Positional Variant-Dependent Error Model for the Detection of Low Frequency Variants in a Pan-Cancer Next-Generation Sequencing Panel**

*C. Laing*

**I20. Clinical Cancer Genomics: Artificial Intelligence Assisted Data Re-analysis to Improve Detection of Potentially Actionable Mutations**

*C. Fischer*

**I21. Capturing and Visualizing Cancer Genomic Data with Category Variants in the JAX Clinical Knowledgebase (JAX-CKB)**

*T. Yin*

**I22. MPath STAR-QC: Automated Quality Control Application for Contamination and Sample Swap Detection Using Short Tandem Repeat Testing**

*S. Lachhander*

**I23. Many NGS-Based Assays, One Platform: Ensuring a High-Quality Case Review and Sign-out Process with NGS Reporter (NGSR)**

*A. Sboner*

**I24. Database for Managing Results of High-Throughput Sequencing Clonality Assays in Clinical Laboratories**

*C. Ho*

**I25. MPath Lab QC: A Centralized Assay Agnostic Approach to Store, Review, and Finalize Laboratory QC for NGS-Based Genomic Clinical Tests**

*A. Agarunov*

**I26. MPath Results PCR: An Integrated Approach to Programmatically Load, Curate and Report Non-NGS Germline Results**

*R. Murray*

**I27. mrLab: Leveraging Mixed Reality in a Precision Medicine Laboratory to Increase Safety and Productivity of Healthcare Workers during the COVID-19 Pandemic**

*A. Sigaras*

**I28. Building a Comprehensive Teaching Repository of Whole Slide Images**

*E. Iriabho*

---

## **OTHER (e.g., Education)**

**OTH01. Effect of Implementation of a Medium-Sized NGS Panel and Organ-Specific Subpanels on Send-out Testing: Experiences of a Small, Hospital-Based Molecular Diagnostics Lab**

*R. Kumar*

**OTH02. Establishment of a Multidisciplinary Precision Medicine Lymphoma Tumor Board Incorporating Results of Massively Parallel Sequencing**

*N. Gupta*

**OTH03. Educating in a Pandemic: Rapid Changes to Molecular Genetic Pathology Graduate Medical Education Training during COVID-19**

*F. El-Sharkawy Navarro*

**OTH04. Economic, Operational, and Clinical Considerations in Deploying Rapid NGS for Lung Cancer**

*C. Sande*

**OTH05. Study of the Critical Role Denials, Appeals, and Patient Engagement Play in the Financial Health of Pathology Practices and Molecular Laboratories**

*D. Richard*

---

## **SOLID TUMORS**

**ST01. Clinical Application of oncoMonitor: A Simple ctDNA Assay for Liquid Biopsy Monitoring of Treatment and Assessment of Therapy in Colorectal and Lung Cancers**

*M. Minarik*

**ST02. Validation and Performance of Fusion Gene Panel for MiT Family Translocation Renal Cell Carcinomas: Quality of RNA Is Important for Fusion Detection**

*S. Harada*

**ST03. Testing for *CDKN2A* Loss in Infiltrating Gliomas Using Targeted Amplicon-Based Sequencing**

*E. Hissong*

**ST04. Long Mononucleotide Repeat Markers Improve Detection of Microsatellite Instability in Non-colorectal Cancers**

*J. Lin*

**ST05. Comprehensive Coverage of Lung Cancer Somatic Mutations by IntelliPlex Lung Cancer Panel**

*L. Felicioni*

**ST06. Assessment of Microsatellite Instability on a Multi-Racial Cohort of High Grade Prostate Cancer Using Idylla MSI Test**

*M. Rodriguez Pena*

**ST07. CANTRK: A Canadian Multi-Centre *NTRK* Gene Fusion Testing Validation in Solid Tumors Project**

*S. Martins-Filho*

**ST08. De-stained Cytology Smears Can Be Used for Detection of *KRAS* Mutations Using the Biocartis Idylla PCR-Based Molecular Diagnostic Assay**

*Q. Wei*



**ST09. A Next-Generation Sequencing Assay for Comprehensive Genomic Profiling and Identification of Microbial Signatures in Tumor Samples**

*M. Yee*

**ST10. Assessment of PD-L1 Expression in Gastric Tumor Samples**

*P. Scorer*

**ST11. Targeted Mutational Analysis of Predictive and Prognostic Biomarkers in Colorectal Carcinoma**

*G. Huang*

**ST12. Simultaneous Detection of Genetic and Copy-Number Variations in *BRCA1/2* Genes**

*L. Georgieva*

**ST13. Analytical Performance Evaluation of TruSight Oncology 500 (TSO500) ctDNA Kit: A Commercial Next-Generation Sequencing Liquid Biopsy Platform**

*S. Verma*

**ST14. Genomic Test Utilization for Neuroblastoma Risk Classification: A Quality Improvement Project**

*H. Jung*

**ST15. Validation of a Comprehensive, Targeted Next-Generation Sequencing Panel for Solid Tumors**

*E. Barrie*

**ST16. MammaPrint and Blueprint Next-Generation Sequencing (NGS) Results Are Robust and Accurate for Patients with Early Stage Breast Cancer**

*D. Kingma*

**ST17. Evaluation of Three RNA Quantification Methods for Next-Generation Sequencing of Formalin-Fixed, Paraffin-Embedded Tumor Samples**

*D. Chan*

**ST18. An Exome- and Transcriptome-Based NeXT Dx Test Enables Therapy Selection for Cancer Patients and Offers Insight into Emerging Composite Biomarkers for Immunotherapy**

*J. Saldivar*

**ST19. A Comprehensive Approach for Detection of Known and Novel Gene Fusions with RNA Sequencing**

*A. Marcovitz*

**ST20. Cancer-Testis Antigen Detection by Targeted RNA Sequencing**

*J. Conroy*

**ST21. WITHDRAWN**

**ST22. *FGFR* Gene Mutation Analysis in Urothelial Cancer Using the theascreen *FGFR* RGQ Assay in FFPE Specimen Type**

*L. Cai*

**ST23. Development and Validation of the OncoScreen RNA Panel for the Detection of Gene Fusions and Splice Variants in Tumors**

*B. Li*

**ST24. Benefits of Rapid Genotyping of *KRAS* Mutations versus NGS in Pancreatic Cyst Fluids**  
*A. Farahani*

**ST25. *PIK3CA* Gene Mutation Analysis in Breast Cancer Using the theascreen *PIK3CA* RGQ Assay in FFPE Specimen Type**  
*L.Cai*

**ST26. Detection of Microsatellite Instability Using Anchored Multiplex PCR and Next-Generation Sequencing**  
*R. Rogge*

**ST27. Clinical and Analytical Validation of the ONCO/Reveal Dx Lung and Colon Cancer Assay (O/RDx-LCCA)**  
*N. Lodato*

**ST28. Noninvasive Genomic Profiling of 113 Patients with Advanced Renal Cell Carcinoma**  
*E. Gedvilaitė*

**ST29. Utilization of a Targeted Next-Generation Sequencing Assay for Assessment of Tumor Cellularity, and Genome-Wide and Gene-Specific Loss of Heterozygosity (LOH)**  
*M. Gupta*

**ST30. Highly Sensitive and Specific Analysis of *PIK3CA* Mutations in Formalin-Fixed, Paraffin-Embedded (FFPE) Samples Using MALDI-TOF Mass Spectrometry**  
*A. Sartori*

**ST31. Internal Validation and Performance Characteristics Using the Oncomine Precision Assay to Detect Multiple Variant Types from Solid and Liquid Biopsy Samples**  
*J. Schageman*

**ST32. Somatic Variant Analysis Using a Pan-Solid Tumor Expanded Gene Panel**  
*S. Deharvengt*

**ST33. Evaluation of a Mass Spectrometry-Based *PIK3CA* Mutation Assay for Predictive Breast Cancer Therapeutic Decision Making**  
*A. Box*

**ST34. Single-Cell RNA Sequencing of Childhood Medulloblastoma**  
*N. Willard*

**ST35. Identifying Prognostic and Predictive Gene Alterations in Metastatic Prostate Cancer**  
*E. Goyette*

**ST36. Validation of an NGS Panel for Pancreatic Cyst Fluid Analysis**  
*J. Huang*

**ST37. Clinical Validation of an Automated 170 Gene Panel Workflow in a CAP/CLIA Laboratory for Solid Tumors**  
*S. Deharvengt*

**ST38. An RNA Sequencing Panel for Detection of Fusions and Splice Site Variants in Solid Tumors**  
*D. Green*

**ST39. Uncovering Subsets of Non-small Cell Lung Cancer (NSCLC) Enriched in Mutations in Cytoskeletal Dynamics and DNA Repair Genes: Additive Value of Large Gene Panels for Clinical Tumor Profiling**

*H. Tu*

**ST40. Rapid qPCR Testing in the NGS Era Enables Same-Day Resulting of *EGFR* Mutant NSCLC**

*N. Z. Georgantas*

**ST41. Rapid Assessment of Microsatellite Instability across a Spectrum of Tumor Types Using the Idylla System**

*A. Momeni-Boroujeni*

**ST42. DNA Methylation Profiling of DNA Extracted from Archived Stained Tissue Slides for Central Nervous System Tumor Diagnostics**

*Z. Abdullaev*

**ST43. WITHDRAWN**

**ST44. *IDH1* and *IDH2* Mutations in Colorectal Cancers**

*M. Lin*

**ST45. Detection of Renal Cell Carcinoma with *TFEB* Amplification Using Archer FusionPlex RNASeq Gene Expression Data**

*S. Harada*

**ST46. Identification of Novel Genomic Alterations in Pineal Parenchymal Tumors**

*R. Ondrasik*

**ST47. Assessment of *NTRK* Alterations and TRK Inhibitor Therapy: A Single Center Experience**

*A. Reddy*

**ST48. Tumor Microbiome in Colorectal Carcinoma: Bacterial Enrichment Is Associated with Oncogenic Variants within Specific Signaling Pathways**

*C. Beech*

**ST49. *NKX2-1* Gene Variants in Solid Tumors: The Spectrum and Potential Impact in Surgical Pathology Diagnosis**

*F. El-Sharkawy Navarro*

**ST50. Comprehensive Genomic Profiling of Different Subsets of Merkel Cell Carcinoma: Insights on Pathogenetic Pathways**

*R. DeCoste*

**ST51. Correlation between MMR IHC and MSI Testing for Detection of MSI-High Solid Tumors**

*M. Shirazi*

**ST52. Circulating Tumor DNA Genomic and Methylation Profiling in Advanced Non-small Cell Lung Cancer Patients**

*J. Qin*

**ST53. Systemic Review of the Clinical Utility of Fluorescence *in situ* Hybridization (FISH) Testing**

*Y. Lo*

**ST54. Commercial Tissue-Based Genomic Profiling on Breast Cancer and Its Impact on Clinical Decision Making: A Single Institution Experience**

*J. Chen*

**ST55. Comprehensive Genomic Profiling in Patients with Advanced Cancer in a Large US Healthcare System**

*B. Piening*

**ST56. Development of Quality Control Reference Materials for Microsatellite Instability (MSI) Testing**

*C. Huang*

**ST57. Mutated Allele Frequency and *NRAS* Mutational Status Are Significantly Associated with High-Risk Prognosis by 31-Gene Expression Profile**

*F. Monzon*

**ST58. Genomic Profiling Uncovers Mutation Signatures That Differentiate Pediatric Rhabdomyosarcoma (RMS) Subgroups and Predict Clinical Outcomes**

*F. Lin*

**ST59. Detection of Actionable Alterations in Breast and Ovarian Tumor Tissues by Testing with a 50-gene NGS Panel**

*C. Ma*

**ST60. Microsatellite Instability Testing for Lynch Syndrome Screening in Colorectal Adenomas**

*A. Javanbakht*

**ST61. Detection and Interpretation of Canonical and Cryptic Splice Sites in Solid Tumors and Their Relevance to FDA Approved Therapies and Clinical Trials**

*E. Bogdanova*

**ST62. Co-occurrence of *PTEN* and *TERT* Mutations Predicts Poor Prognosis in Glioblastomas**

*H. Chen*

**ST63. Gene Expression Profile of Sex Cord Stromal Cell Tumors and Their Relevance to Prognosis**

*P. Bhattacharyya*

**ST64. Expression Profiling Reveals Novel Molecular Signature in Pleomorphic Lobular Carcinoma *in situ***

*E. Makhoul*

**ST65. Aberrant *PAX3* (*Paired Box Gene 3*) RNA Splicing Is a Potential Marker for Diagnosis of Melanoma**

*I. Kasago*

**ST66. Biomarker Testing for Patients with Advanced/Metastatic Non-small Cell Lung Cancer (NSCLC) in Academic and Community-Based Practices in the United States (US)**

*L. Hess*

**ST67. Initial Tertiary Reporting Results from Personalize My Treatment (PMT): A Pan-Canadian Initiative Integrating Precision Oncology across Canada: PMT-001 Pilot Project**

*M. Marques*

**ST68. Neurotrophic Tyrosine Receptor Kinase (*NTRK*) Gene Fusion Testing in Clinical Trials of Larotrectinib**

*E. Rudzinski*

**ST69. Biomarker Testing and Overall Survival among Patients Diagnosed with Advanced or Metastatic Non-small Cell Lung Cancer**  
*L. Hess*

**ST70. A Predictive Model of the Diagnostic Value of Next-Generation Sequencing-Based Genomics Testing in Patients with Advanced or Metastatic Non-small Cell Lung Cancer in the United States**  
*P. Quon*

**ST71. Clinical Characteristics of *RET*- and *NTRK*-Rearranged Tumors in a Single Tertiary Cancer Center**  
*T. Vougiouklakis*

**ST72. Incidence of T790M Mutation by ddPCR in Patients Progressing on First- and Second-Generation TKIs and Clinical Outcomes on Osimertinib**  
*S. Nathany*

**ST73. Frequency of *EGFR* Mutations and ALK Expression in NSCLC in the North of México**  
*B. Montaña Miyagui*

**ST74. Tissue Requirements of a Novel 27-Gene Immuno-Oncology Algorithm Measuring Tumor Microenvironment to Predict Response to Immunotherapies**  
*T. Nielsen*

**ST75. Pan-Cancer Liquid Biopsy Assay for Mutation Profiling in 61 Genes by Low-Depth Sequencing**  
*P. Hao*

**ST76. WITHDRAWN**

**ST77. Spatially Resolved Gene Expression Profiles in Human Glioblastoma**  
*A. Hartnett*

**ST78. Spatially Resolved Molecular Interrogation of Triple Negative Breast Cancer**  
*S. Williams*

**ST79. Quantitative Assessment of Functional Activity of Multiple Signaling Pathways in Recurrent Breast Cancer with Low to Intermediate 21 Gene Recurrence Score**  
*L. Lin*

**ST80. Prospective Study Using Virtual Enrollment to Assess an RNA-FIT Assay for Non-invasive Detection of Colorectal Cancer, Advanced Adenomas, and Other Precancerous Adenomas**  
*E. Barnell*

**ST81. *NAB2-STAT6* Gene Fusions to Identify Primary/Metastasis Hemangiopericytoma/Solitary Fibrous Tumors**  
*N. Singh*

**ST82. Development and Performance of Formalin Compromised FFPE Reference Materials**  
*O. Clement*

**ST83. CNV Detection from a Multi-Cancer NGS Panel: A Single-Tube, Multiplex-PCR Based NGS with 309 Tiled Amplicons**  
*A. LaBonte*

**ST84. Rapid Isolation of High-Quality Ultra-High Molecular Weight Genomic DNA from Blood, Bone Marrow Aspirates, and Fresh Frozen Human Tumors**

*H. Sadowski*

**ST85. Novel Amplicon-Based NGS Library Preparation Protocols Compared and Evaluated across Two Sequencing Technologies**

*E. Petrilli*

**ST86. Chromosomal Microarray Analysis of Benign Mesenchymal Tumors with *RB1* Deletion**

*A. Dusenbery*

**ST87. A Novel Nanoparticle-Based Approach to Improve Extraction of Circulating Tumor DNA (ctDNA)**

*E. Williams*

---

## **TECHNICAL TOPICS**

**TT01. Dimensionality Reduction for Noise Filtering of Big Data Sets**

*E. Mahe*

**TT02. Molecular Profiling in Challenging Oncology Research Samples Using a Novel Library Preparation Chemistry**

*H. Huang*

**TT03. Droplet Digital-PCR (ddPCR) as Confirmatory Method for Low Allelic Frequency Variants Detected by Manual Review of Data in Clinical NGS Testing**

*W. Song*

**TT04. Performance Validation of Magnis BR: A Full-Automatic Capture-Based Library Preparation Platform for Next-Generation Sequencing (NGS)**

*X. Wang*

**TT05. From Plasma to Variants: A Fully Automated Workflow Solution for Low-Frequency Variant Detection in Cell-Free DNA**

*T. Barnes*

**TT06. Concordance of Variant Detection between the MoCha ctDNA Assay and Matched Tissue Biopsy in Non-small Cell Lung Cancer**

*C. Karlovich*

**TT07. Reproducibility of Allelic Fractions of Genomic Variants from Colorectal and Lung Cancer Tissue Downstream of DNA Extraction**

*M. Javey*

**TT08. Flexible and Complete Exome Next-Generation Sequencing (NGS) Solution for Variants Detection with Improved Human Exome Panel**

*M. Hong*

**TT09. DNA Samples with Low Concentration Can Benefit from Speed Vacuum Concentration in NGS Testing**

*W. Song*

**TT10. Comparative Study of Three Assays: Target Capture Sequencing, MassARRAY and Real-Time qPCR for Testing Somatic Mutations in Plasma Cell-Free Circulation Tumour DNA of Non-small Cell Lung Cancer**

*L. Zhang*

**TT11. Workflow Evaluation: Impact of Specimen Storage and Transport on ccfRNA Multiplex Analysis in Dedicated Blood Collection Tubes**

*T. Voss*

**TT12. Reference Materials for Measurable Residual Disease (MRD) Monitoring in Circulating Cell-Free DNA (ccfDNA)**

*Y. Konigshofer*

**TT13. Automation of Fluorescence *in situ* Hybridization Processing and Digital Analysis**

*M. Azim*

**TT14. A Modified Vendor Extraction Protocol Better Preserves the Structural Integrity of Genomic DNA Extracted from FFPE Tissue**

*C. Artymiuk*

**TT15. WITHDRAWN**

**TT16. Detection of the Mutational Status in Colorectal Cancer from Formalin-Fixed, Paraffin-Embedded (FFPE) Tissue**

*E. Haenssler*

**TT17. Centrifugation and RBC Lysis-Free Preparation of Blood Samples in less than 30 Minutes**

*C. Barr*

**TT18. A Complete Yet Flexible Workflow for Library Preparation and Analysis with Enhanced Error Correction for Low Input FFPE Tissue Biopsy and Circulating Tumor DNA Samples**

*S. Lee*

**TT19. Next-Day Analysis from Specimen to Variant Calling with the Genexus System**

*J. Gioia*

**TT20. Pushing the Limits of Cancer Research: An Integrated and Automatic Workflow on Ion Torrent Genexus System from Nucleic Acid Extraction to Next-Generation Sequencing**

*R. Cao*

**TT21. Analytical Performance Testing of the MoCha Circulating Tumor DNA Assay**

*R. Harrington*

**TT22. Digital PCR Paired with High-Speed AFM for Quantitation and Length Analysis of DNA Length Polymorphisms**

*S. Koebley*

**TT23. Focused-Ultrasonication Driven High-Quality DNA and RNA Extraction and Purification from FFPE Samples**

*K. Amirault*

**TT24. Evaluating Effects of PCR Instruments and Temperature Ramp Rates to Base-Composition Bias in TruSight Oncology 500 (TSO500) Panel**

*W. Song*

**TT25. Evaluation of the Biocartis Idylla ctEGFR Mutation Assay on Samples with DNA Concentrations Insufficient for Next-Generation Sequencing (NGS)**

*W. Keegan*

**TT26. Analysis of Simple and Complex Variants and Biomarkers for Comprehensive Genomic Profiling (CGP) of Solid Tumors and Hematologic Malignancies Using a Single NGS Workflow from FFPE and cfDNA Samples**

*R. Samara*

**TT27. Matrix and DNA Source of Reference Material Significantly Affect Extraction Recovery, Drift in qPCR Quantitation, Assay Precision, and Limit of Detection (LOD) in Validation of ctDNA Assay**

*Y. Lu*

**TT28. Archival FFPE and DNA Quality: Optimal Storage Time and Predictive Metrics for Next-Generation Sequencing**

*V. Parimi (Parini)*

**TT29. Confirmation of Fusions Detected with Sequencing**

*D. Jones*

**TT30. Development of a Universal Probe System for Droplet Digital PCR**

*D. Jones*

**TT31. Targeting Clinically Significant “Dark” Regions of the Human Genome with High-Accuracy Long-Read Sequencing**

*C. Heiner*

**TT32. Performance of GeoMx CTA and WTA, High-Plex, Spatial Gene Expression Profiling Tools**

*K. Sorg*

**TT33. Standardizing Plasma ctDNA Measurements Using SNAQ-SEQ ONCO1LB Internal Controls**

*S. Deharvengt*

**TT34. Optical Mapping Enables High-Throughput Analysis of Pathogenic Repeats**

*E. Lam*



## Index of Authors

Abdel-Razeq, Hikmat - G10  
Abdulkaki, Rami - ID19  
Abdullaev, Zied - ST42  
Abedtash, Hamed - ST69  
Abu Jamous, Lama - G10  
Acab, Allan - ST59  
Accola, Molly A - ID47  
Ackermann, Sarah - I27  
Adams, Emily N - ST36  
Adams, Hans-Peter - TT07  
Adhali, Omkar - I26  
Afkhani, Michelle - ST62  
Agarunov, Aaron - I22, I25, I26  
Ahluwalia, Anupamjit - ID07  
Ahmed, Asim A - ID53  
Aizin, Arina - ID11  
Akther, Farhana - ST51  
Al Juhaishi, Taha - TT22  
Aldape, Kenneth - ST42  
Al-Diffalha, Sameer - ST81  
Ale-ali, Amine - ST70  
Al-Ghamdi, Yahya - H33, H40  
Alikhan, Mir B - H31  
Al-Kateb, Hussam - ST61  
Allen, Chris - H12  
Allen, Samantha F - ID15, ID16, ID48, ST32  
Allen, Zoe - G19  
Al-Turkmani, Rabie - ST37  
Alves, Derron A - ID52  
Amadei, Mackenzie - ID30, ID31, ID32, ID34  
Amani, Vladimir - ST34  
Ambinder, Richard - H14  
Amin, Sejal - ID28  
Amirault, Kristopher - TT23  
Amparo, Gilbert - TT18  
Amsberry, Crystal - H28  
An, Paul - I15  
Anagnostou, Valsamo - I20  
Anderson, Ben - ID17  
Anderson, Jennifer L - ID03  
Anderson, Peter G - I2  
Andreas, Jon - ST20  
Andruss, Bernard - G18  
Anekella, Bharathi - ST56, ST82, TT12  
Ang, Shi Hui - ST09  
Ansari, Shajia R - H04  
Antonarakis, Emmanuel S - ST04  
Aoun, Patricia A - ST62  
Aplenc, Richard - H24  
Arana Rosainz, Manuel - ST64  
Arcila, Maria E. - H03, I22, I25, ST41, ST48  
Arezi, Bahram - TT18  
Arias-Stella, Javier - ST62  
Ariyaratne, Pramila - ST09  
Aro, Lori - TT31  
Artymiuk, Cody J - H06, I08, TT14  
Arumugam, Sivakumaran Theru - G05  
Arvanitis, Leonidas D - ST62  
Aryeequaye, Ruth - H23  
Ashton, Jacob - G27  
Askar, Medhat - ID20, ID49  
Aslam, Anoshe - ID35, ID37, ID41  
Asuncion, Lawreen - ST29  
Au, Kaylene - G21  
Austermiller, Bradley - TT33  
Au-Young, Janice - I07, ID55, ST29  
Avenarius, Matthew - G19, ST39  
Ayash, Erin - ST18  
Aye, Min Ko ko - ID11, ST09  
Aypar, Umot - G13, H23  
Azim, Mohammad - TT13  
Azzato, Elizabeth - H44  
Babady, Esther - ID35, ID37, ID39, ID41, ID65, ID66, ID67, ID68  
Bacher, Rowena - ID57  
Badie, Behnam - ST62  
Bae, Ju-Hee - ID23  
Baek, Inji - ST03, TT03, TT09, TT24  
Bagatell, Rochelle - ST14, ST58  
Bagg, Adam - OTH02  
Bagli, Lori K - ID55  
Bailey, Michael - ID38  
Baisre-de leon, Ada - H30  
Balakrishnan, Anoop - I25, I26  
Balan, Jagadheshwar - H06, I08  
Ball, David - ST55  
Bandla, Santhoshi - ST29  
Bao, Jing - TT13  
Bapat, Bela - ST55  
Baptiste, Mishauna - ID07  
Barbee, Jada - ST41  
Barboza, Oralia - ST73  
Bardakjian, Tanya - G16  
Barker, Craig - ST10  
Barnell, Andrew R - ST80  
Barnell, Erica K - ST80  
Barnes, Timothy - TT02, TT05  
Barney, Rachael E - ID21, ID51  
Barr, Christine - TT17  
Barrick, Brian - I06, ST15  
Barrie, Elizabeth - I06, ST15  
Bask, Michael - I03  
Basu, Malay K - I16  
Basu, Shubham - H06, I08  
Batist, Gerald - ST67  
Batra, Ullas - ST72  
Baugh, Laura - H43  
Bayrak-Toydemir, Pinar - G05, G08, G15  
Bee, Gary G - ST19  
Beech, Cameron - ST48  
Beechem, Joseph - ID38, TT32  
Behling, Kathryn C - OTH01  
Bell, Drew A - ID54  
Belsanova, Barbora - ST01  
Benavides, Raul - ID20, ID49  
Benayed, Ryma - H03, I25, ST28  
Benesova, Lucie - ST01  
Benoit, Jeanne - ST26  
Bent, Zachary - ST77, ST78  
Berg, Susan Z - G12  
Berger, Michael F - ST28  
Berman, David - ST07  
Berman, Diana - ID40  
Bertuch, Alison A - H04  
Bettegowda, Chetan - H14  
Beyrer, Julie K - ST69  
Bhandari, Ambica - G01  
Bhandari, Naleen R - ST70  
Bhattacharyya, Pritish K - ST63  
Bi, Tengeng - I11  
Bickford, Michelle A - TT13  
Biegel, Jaclyn A - G02  
Biery, Nancy - ST55  
Bifulco, Carlo - ST55  
Bigras, Gilbert - ST07  
Birsoy, Ozge - I26  
Blüher, Anja - TT07  
Black, Margaret - ST79

Blair, Amanda - ID36  
 Blair, Lily - ID53  
 Blake, Drew - H10  
 Blauwkamp, Timothy A - ID53  
 Blombery, Piers - H37  
 Bockelman, Daniel - I27  
 Boeckh, Michael - ID53  
 Boese, Krystal - ID03  
 Bogdanova, Ekaterina - ST61  
 Bootwalla, Moiz S - G02  
 Borczuk, Alain - ID38, ID40  
 Borrelli, Nicla - ST05  
 Borsu, Laetitia - H03, I25  
 Bossler, Aaron D - H07  
 Bowman, Anita - ST48  
 Box, Adrian - ST07, ST33  
 Boyanapalli, Ramakrishna - G18  
 Boyd, David C - I12  
 Boyle, Theresa - ST65  
 Bradley, Eliza - ID15, ST60, TT25  
 Bram, Yarom - ID38  
 Bramlett, Kelli S - ST31, TT20  
 Brecklin, Dana - ID14  
 Briggs, Benjamin - ID45  
 Broadfoot, Brannon - ID50  
 Brodeur, Garrett - ST58  
 Bryson, Alexandra L - ID33  
 Buchan, Blake W - ID01  
 Buchan, Jillian G - G05, G08  
 Bullard, Brian - I06, ST15  
 Burgher, Blake - ST20  
 Burke, Jennifer - ID55  
 Burnham, Carey-Ann - ID01  
 Butler, Joseph - ID10  
 Butler, Mathew G - ST56, TT12  
 Buttitta, Fiamma - ST05  
 Cadoo, Karen - G13  
 Cai, Gracie - H03  
 Cai, Li - ST22, ST25  
 Calderwood, Michael S - ID43  
 Calio, Anna - ST02, ST45  
 Campan, Mihaela - I03  
 Campbell, Andrew - G07, H45  
 Campbell, Mary - ST55  
 Cantu, Erin - TT06  
 Cantu, Miguel D - H21  
 Cao, Kajia - H24, ST58  
 Cao, Ru - ST31, TT19, TT20  
 Caradonna, Ippolito - ID57  
 Carbone, David - ST39  
 Carlo, Maria - G13  
 Carpenter, Meredith L - ID57  
 Carpenter, Stephanie - ST12  
 Carter, Michael D - ST50  
 Carter, Theodore - ID57  
 Caruthers, Sean - ST39  
 Castaño Gonzalez, Luis Antonio - I07  
 Castro, Allan J - ID05, ID06  
 Casuga, Iris - TT19  
 Catalano, Jeffrey - I23, I27, TT03, TT09  
 Catanese, Joseph - ID17  
 Cermelli, Silvia - ID02  
 Ceyhan-Birsoy, Ozge - G11, G13  
 Chadburn, Amy - H21  
 Chakravarty, Debyani - ST48  
 Chan, Bob - ST16  
 Chan, Danny - ST17  
 Chan, Emily - TT27  
 Chan, Roger - H03, ST41  
 Chang, Chung-Che - H28  
 Chang, Jayde - H17, H19  
 Chang, Ting-Chia - TT06, TT21  
 Chatterjee, Sharmila - ST77, ST78  
 Chaudhuri, Aadel A - ST80  
 Cheang, Gloria - ST03, TT03, TT09, TT24  
 Chebib, Ivan D - ID25  
 Chellappan, Ajithavalli - I09  
 Chen, Alice P - TT21  
 Chen, Chin-Tung - ST48  
 Chen, Derrick J - ID47  
 Chen, Dong - H39  
 Chen, Gloria - ST27  
 Chen, Hsiao-Wei - ST62  
 Chen, Jade - ID07  
 Chen, Jie-Fu - ID56, ST54  
 Chen, Jonathan H - ID25  
 Chen, Keith - TT18  
 Chen, Lei - TT04  
 Chen, Li - TT06, TT21  
 Chen, Liam - ST44  
 Chen, Miaomiao - ST52  
 Chen, Mingyi - H38  
 Chen, Richard - ST18  
 Chen, Rong - ST61  
 Chen, Suping - ST04  
 Chen, Tzu-Chun - TT02, TT05  
 Chen, Weina - H22, H25, H38  
 Chen Wongworawat, Yan - H10  
 Chen, Xiang - H44  
 Cheng, Angie - TT19, TT20  
 Chenn, Anjen - ST22, ST25  
 Cherabuddi, Kartik - ID45  
 Chesney, Alden - TT22  
 Cheung, Carol - ST07  
 Chevarie-Davis, Myriam - ST07  
 Chew, Jennifer - ST77, ST78  
 Chheda, Pratiksha - ID12  
 Chinnappa, Manju - ST18  
 Chiou, Allie - H39  
 Chiou, Jonathan - H39  
 Cho, Hee Won - ID58  
 Choi, Leno - TT28  
 Chu, Clement - G23  
 Chu, Quincy - TT10  
 Church, Melissa - G18  
 Cintrón, Melvili - ID68  
 Clark, Michael J - ST18  
 Clay, Mike - H44  
 Clement, Omoshile - ST56, ST82, TT12  
 Clyde, Karen - ID55  
 Codoy, Maria - ID19  
 Coffin, John - TT10  
 Collingwood, Robin - ST81  
 Columbus, Cristie - ID49  
 Cong, Lin - ID27, ID29, ID40  
 Conley, Kelsey - TT21  
 Conner, Kayla L - ST29  
 Conroy, Jeffrey - ST20  
 Cook, Leanne J - ID16, ID48  
 Cook, Robert - ST57  
 Cooper, Lauren A - ID54  
 Copeland, Sarah - G19  
 Cotter, Philip - G01, ST13  
 Cotzia, Paolo - ST71, ST79  
 Couetoux du Tertre, Mathilde - ST67  
 Covington, Kyle - ST57  
 Coyle, Sabrina - ID09  
 Craney, Arryn - ID27, ID29  
 Craven, Kelly E - I04  
 Cremona, Maria Laura - G05, G08

Cruz, Amorina - ID63  
 Curry, Choladda V - H04  
 Cushing, Melissa - ID27, ID29  
 Cutz, Jean-Claude - ST07  
 Cyanam, Dinesh - ST29  
 Da Silva, Edaise - G11  
 D'Apuzzo, Massimo - ST62  
 Dabrowski, Mia Donna - H28  
 Dadmanesh, Farnaz - ST64  
 Dai, Qunsheng - ID59  
 Dai, Peng - ST75  
 Dalai, Sudeb C - ID53  
 Dale, Elizabeth - ID64  
 Dama, Tavisha - ID12  
 Damerla, Rama - ID65  
 Danaher, Patrick - ID25, ID38  
 Daniel, Sugganth - ST59  
 Danos, Arpad - H37  
 Darvishian, Farbod - ST79  
 Das, Biswajit - TT06, TT21  
 Das Chakravarty, Ushati - TT02, TT05  
 Dasch, Nicole - ID30, ID31, ID32, ID34  
 Datto, Michael - H13  
 Davick, Jonathan J - ST86  
 Davis, Adam - OTH02, OTH03  
 Davies, Gwynivere - H15  
 Davis, Jackson - I27  
 Davis, Thomas - ID54  
 Daviso, Eugenio - TT23  
 De Angelis, Carlo - G22  
 de Jong, Susan - TT17  
 Deardorff, Matthew - G02  
 Deb, Pratik Q - H30  
 DebRoy, Chitrita - ID55  
 DeCoste, Ryan - ST50  
 DeCoteau, John - ST07  
 Deeb, Kristin - H37  
 DeFrank, Gina - H41, ST02, ST08, ST45  
 Deharvengt, Sophie - H09, H27, ID43, ID46, ST11, ST32, ST37, ST38, ST46, ST63  
 Deharvengt, Sophie - TT33  
 Deignan, Joshua L - G25  
 Delahaye, Leonie - ST16  
 Delaney, Nigel - ST78  
 Delgado, Mauricio - ID67  
 Demetrick, Douglas - ST33  
 Den Biezen, Eveline - ST79  
 Desai, Niyati - ID25  
 Desai, Sejal - ST18  
 Deshpande, Vikram - ID25  
 Desmeules, Patrice - ST07  
 Devitskiy, Sergey - ST35  
 Dhaliwal, Parneet - ID49  
 Dhanuka, Sujata - ID12  
 Dharmadhikari, Sumedha - ID57  
 Dickens, Jessica L - TT12  
 Dien Bard, Jennifer - ID01  
 Dina, Michelle A - H06, I08, TT14  
 Ding, Bo - ST31  
 Ding, Yi - G07, H45  
 Dinulos, Mary Beth P - G09  
 Dipaola, James - ID11  
 Dirks, Dawn - ST87  
 Dittmann, David - TT29  
 Doern, Chris - ID33  
 Dogan, Ahmet - H23  
 Dogan, Snjezana - ST48  
 Dokus, Betty - ID48, TT13  
 Donson, Andrew M - ST34  
 Doroshov, James H - TT06, TT21  
 Dorsaint, Princesca - I23  
 Dowdell, Alexa K - ST55  
 Drain, Alicia - ID01  
 Drews, Birgit - I07  
 Drilon, Alexander - ST68  
 Du, Gracie - TT07  
 Du, James - I26  
 Duan, Xiaoping - ST19  
 Dube, Mindy T - ID43  
 Dubeau, Louis - I03  
 Dudley, Edward G - ID55  
 Dunigan, Marisa R - ST28  
 Dunn, James - ID04, ID26  
 Durkin, Daniel - I21  
 Dusenbery, Anna C - ST86  
 Dysert, Peter - ID20  
 Earp, Meredith - TT20  
 Eaves, Allen C - TT17  
 Eberhard, David A - ST55  
 Edmonston, Tina B - ID28, OTH01  
 Eich, Marie-Lisa - ST81  
 Ekholm, Jenny - G17  
 El-Difrawy, Sameh - ST29  
 Elemento, Olivier - I23, I27  
 Elenitoba-Johnson, Kojo - H29, OTH02, OTH04  
 Elghetany, Tarek - H04  
 Elkan, Michael - ID22  
 Ellison, David - H44  
 Elmore, Sandra - ID59  
 El-Sharkawy Navarro, Farah - G16, OTH03, ST49  
 Eltoun, Isam-Eldin A - ST08  
 Eng, Kenneth W - I23  
 Eno, Celeste - ST64  
 Epeldegui, Marta - H14  
 Eshleman, James - H14, I04, I20, ST04, ST36, ST44, TT28  
 Ewalt, Mark - H43  
 Ewen, Elizabeth - ID36  
 Ewing, Aren - ST29  
 Fahit, Margil - ID01  
 Fahland, Tom - I02  
 Fan, Jinbo - ST87  
 Fan, Zhiqian - ST58  
 Farahani, Alexander A - ST24, ST53  
 Farfan, Fernando - H12  
 Farhang, Janet - ID01  
 Faridi, Rehan - H15  
 Faron, Matthew L - ID01, ID63  
 Fathima, Samreen - ID49  
 Fei, Fei - H41  
 Feilolter, Harriet - ST07  
 Felicioni, Lara - ST05  
 Feng, Xue - ST52  
 Ferguson, Donna - ST41  
 Fernadez, James P - TT24, I23, TT03  
 Ferreira-Gonzalez, Andrea - I06, I12, ID33, ST15  
 Figueroa, Israel - ID18  
 Filipovic-Sadic, Stela - G27, G29  
 Fink, Jeffrey - ID22  
 Fink, Marc - ST61  
 Fischer, Catherine - I04, I20  
 Fischer, Christina - TT16  
 Fischer, Jason - ID11, ST09  
 Fisher, Cynthia E - ID53  
 Fisher, Kevin E - H04  
 Fiske, Jared - ST80  
 Flannery, Adrian - I16  
 Flockhart, Ian - ST27  
 Flores, Irvin I - ID01  
 Flores, Juan P - ST73  
 Foreman, Nicholas K - ST34

Formenti, Kim - TT10  
Forst, Jannine - ID57  
Foster, Ashley A - ST28  
Foster, Jacinda - ST70  
Foxy, Jonathan - ID38  
Foy, Scott - H44  
Fratamico, Pina - ID55  
Freedkin, Mark - G24  
Fropf, Robin - TT32  
Fu, Jinpeng - I05, I18, I19  
Fu, Lei - G22  
Fuda, Franklin - H38  
Fung, Eula - I24  
Funke, Birgit - G05, G08  
Furtado, Larissa - H44  
Gagan, Jeffrey - H25, ID44  
Gai, Xiaowu - G02  
Galderisi, Chad - ID13  
Gambaro, Karen - ST67  
Gandhi, Harneet - G01  
Ganesh, Veena - ST15  
Gao, Shuang - ST20  
Garancher, Alexandra - ST34  
Garces-Narvaez, Sofia - H29, OTH02, OTH03  
Garcia, Andrea - ST31, TT20  
Garcia, Rolando - H22, H25  
Garlick, Russell K - TT12  
Garza, Raquel - ST73  
Gaston, Dan - ST50  
Gattam, Sandeep - TT07  
Gau, Vincent - ID07  
Gautam, Anurag - ST31  
Gayhart, Matthew - ST64  
Gebhart, Catherine - ID64  
Gedvilaite, Erika - ST28  
Gentile, Caren - G16, ID22  
Georgantas, Nicholas Z - ST24, ST40  
Georgieva, Lyudmila - ST12  
Gerasimova, Anna - ID17  
Gerlach, Jay - TT11  
Gershon, Timothy - ST34  
Gerstbrein, Derek - ID63  
Ghosh, Jayati - TT18  
Giamo, Vincent - ST20  
Gioia, Jason - TT19  
Giuliano, Armando - ST64  
Glantz, Michael - H14  
Glas, Annuska - ST16  
Glaser, Laurel - ID22  
Glenn, Sean T - ST20  
Glogowski, Sarah - ID20  
Gocke, Christopher - H14, I20, ST36, ST44, TT28  
Godwin, Kelley N - H09, ST60  
Gokul, Shobha - G27  
Goldberg, James D - G23  
Goncharuk, Tamara - ST03, TT03, TT09  
Gong, Jingjing W - ID25, TT32  
Gonzalez, Irene M - I06, ST15  
Gonzalez-Alegre, Pedro - G16  
Gordon, Joan - ID30, ID31, ID32, ID34  
Gottimukkala, Rajesh - I07, ID55, ST19  
Gourguechon, Stephane - ID57  
Gournapaleoudis, Elli - ST63  
Goyal, Jaya - G18  
Goyette, Evan - ST35  
Granfield, Caitlin - G20  
Green, Donald C - H09, H27, ID42, ID43, ID46, ST11, ST32, ST37, ST38, ST46, ST60, ST63, TT25, TT33  
Greenbaum, Benjamin D - ID25  
Greer, Wenda - ST07  
Gregersen, Vivi R - TT26  
Griesinger, Andrea M - ST34  
Griffith, Malachi - ST80  
Griffith, Obi L - ST80  
Griswold, Maddy - TT32  
Gruber, Tanja - H44  
Grupe, Andrew - ST59  
Grutkoski, Patricia S - H35  
Gu, Dongqing - ST62  
Gu, Jian - ST31  
Gu, Yunzhao - TT04  
Guedes, Liana B - ST04  
Gulley, Margaret - ID59  
Gunawan, Joseph - G24  
Gunn, Shelly - G01, ST13  
Guo, Ping - I11  
Guo, Shouying - TT04  
Gupta, Gaorav P - ID59  
Gupta, Mohit - ST29  
Gupta, Neha - OTH02  
Guseva, Natalya V - H07  
Gwon, Sanghun - ID23  
Haas, Kevin R - G23  
Hacohen, Nir - ID25  
Haenssler, Eva - TT16  
Hahn, Elan - G02  
Haley, Lisa M - H14, ST36, TT28  
Halie-Mariam, Tenagne - ID19  
Halkova, Tereza - ST01  
Hall, Bradley - G27, G29  
Hallmark, Elliot - G27  
Halper-Stromberg, Eitan - H14  
Hameed, Meera - H23  
Han, Brady - ID11  
Han, Jin-Yeong - ID60  
Han, Yimei - ST66  
Handler, Michael H - ST34  
Hanif, Khalid - ST31  
Hankinson, Todd C - ST34  
Hanson, Jeff - ST42  
Hantash, Feras - ST61  
Hao, Pengying - ST75  
Haque, Mohammad - I25, I26  
Harada, Shuko - H41, I16, ST02, ST06, ST08, ST45, ST81  
Harbi, Djamel - H41, I16, ST02, ST45  
Harley, Susan - H42  
Harragan-Jokisch, Debra - ID07  
Harrell, J. Chuck - I12  
Harrington, Robin - TT06, TT21  
Harris, Adam - I02  
Harris, Jason - ST18  
Harris, Mack - ST70  
Harris, Rebecca M - ID22  
Harrison, Thomas - ST26  
Harting, John - TT31  
Hartnett, Andrej D - ST77  
Hastie, Alex R - ST84, TT34  
Hauser, Jocelyn - ID65, ID67  
Hayashibara, Kathleen - ID18  
Hayes, Malcom - ST64  
He, Rong - H06, H34, H37, H39, I08, TT14  
Heath, Kim - ID02  
Hebding, Casey - I27  
Hechtman, Jaclyn - ST41, ST48  
Heckel, Aysel - ST12  
Hedges, Dale - H44  
Heilek, Gabrielle - TT07  
Hein, Raymond - ID64  
Heiner, Cheryl - TT31  
Henck, Steven - TT02, TT05

Herlihy, Sarah E - ID22  
Herrmann, E. Clifford - H10  
Herth, Felix - I17  
Hess, Lisa M - ST66, ST69, ST70  
Hesselberth, Jay R - ST34  
Hether, Tyler - ID38  
Heubner, Thomas A - ST80  
Heussel, Claus Peter - I17  
Heyer, Joerg - ST61  
Hickey, Luke A - I13  
Higginson, Daniel - ID65  
Hill, Aaron - ID33  
Hill, Joshua A - ID53  
Hillmer, Lukas - ST83  
Hinzmann, Bernd - I17, TT07  
Hissong, Erika M - ID29, ID40, ST03  
Ho, Carine - ID53  
Ho, Chandler C - H16, H18, I24  
Ho, Hui T - ST03, TT03, TT09  
Hoang, Margaret - TT32  
Hoerres, Derek - ID59  
Hogarty, Michael D - ST14, ST58  
Holdhoff, Matthias - H14  
Hollemon, Desiree - ID53  
Hollmann, Travis - H23  
Holmes, Faith L - ST80  
Hon, Ting - G17  
Hong, David K - ID53  
Hong, David S. - ST68  
Hood, Scott - ST22, ST25  
Hook, Brad - ID14  
Horvath, Kyle - ST13  
Houde, Brianna - H09, H27, ID51  
Hoz De La Rastrollo, Ana Belen - I07  
Hsue, Bilan - TT18  
Hu, Fangqi - ID18  
Hu, JuiYu - ST05  
Hu, Ran - ID61  
Hu, ShianPin - ST05  
Hu, Shimin - H36  
Hu, Yue - TT04  
Hua, Michael - ID17  
Huan, Alan - TT11  
Huang, Catherine - ST56, ST82  
Huang, Chen - H08  
Huang, ChinShiou - ST05  
Huang, Guohong J - ST11, ST32, ST46  
Huang, Hsiao-Yun - TT02, TT05  
Huang, Jialing - ST36, ST44, TT28  
Huang, Mingjie - TT04  
Huang, Weei-Yuarn - ST07, ST17  
Huard, Thomas K - G14  
Huberman, Kety H - ST28  
Hughes, Edward G - G28, ID36, ID48, ST37, ST46  
Hunger, Stephen - H24  
Hunt, Jeffery - ID49  
Hunt, Jennifer - ID50  
Hunt, Matthew - ST39  
Hussain, Annas - H22  
Hutchins, Rebecca - G05, G08  
Hwang, David - G22, ST17  
Hwee, Jason - I25  
Hyland, Fiona C - H12, I07, I09, ST19, ST29  
Hyrca, Martin - ST07  
Ianos-Irimie, Monica - ID28  
Iovine, Nicole - ID45  
Iriabho, Egiebade E - I16, I28  
Irwin, Darryl - ST30, ST33  
Isaacson, Nancy - ID19  
Ishu, Christine - ST17  
Izevbaye, Iyare - ST07, TT10  
Jaicks, Christopher - ID25  
Jain, Parveen - ST72  
Jairam, Sowmya - G11, G13  
James, Keither - ID07  
Jani, Krupa - ID35, ID37, ID39, ID41, ID66, ID67  
Janovsky, Justin - G18  
Janowski, Karen C - H41, ST02, ST45  
Jaso, Jesse M - H38  
Javanbakht, Ayda - ST60  
Javey, Mana - TT07  
Jayakumaran, Gowtham - G13  
Jayaweera, Thilanka - TT20  
Jean, Sophie - ID01  
Jefferson, Keri - G29  
Jennings, Lawrence - TT29, TT30  
Jeon, Diana - G23  
Jeon, Jeong Ok - H03  
Jeong, In-Hwa - ID60  
Ji, Hong - ID18  
Ji, Jianling - G02, G05, G08  
Jiang, Jie-gen - H30  
Jiang, John - I17  
Jiang, LiQun - I04, I20  
Jiang, Qiong - TT26  
Jiang, Tingting - TT06, TT21  
Jiang, Weiyun - H26  
Jiang, Yan - ST52  
Jiao, Ye - ST85  
Jin, So Dam - ID23  
Jiwani, Shahanawaz - TT06  
Johnson, Coreen - ID04  
Johnson, Douglas - G21  
Johnson, Eric - TT11  
Johnson, Ian - ST28  
Johnson, Kory - G21  
Johnson, Sarah - H11, I18  
Johnson, Verity - ST26  
Johnston, Michael A - G28, ID16, ID48  
Jones, Dan - ST39  
Jones, Derek - TT29, TT30  
Jour, George - ST71, ST79  
Ju, Christine - I17, TT07  
Jung, Hou-Sung - ST14  
Jung, Sungmi - ST07  
Jung-Hynes, Brittany - ID47  
Juric, Dejan - ID25  
Kadri, Fauzi - ID11  
Kadri, Sabah - I14  
Kalman, Lisa V - G15  
Kamboj, Mini - ID35, ID37, ID41  
Kam-Morgan, Lauren - ST22, ST25  
Kanagal-Shamana, Rashmi - H37  
Kanap, Rushikesh - I09  
Kane, Troy - I27  
Kaneko, Maki - G02  
Kang, Yiming - ST80  
Karimi, Kambiz - G26  
Karlovlch, Chris A - TT06, TT21  
Kasago, Israel - ST65  
Katz, Sigrid - TT06, TT21  
Kavatkar, Mihir - I26  
Kaznadzey, Denis - ST29  
Ke, Yue - G30, ST27, ST83, ST85  
Keane-Candib, Jake - ID53  
Keegan, William - ID15, ST60, TT25  
Kegan, Ron M. - ID17  
Keiser, John - ID19  
Kemel, Yelena - G13  
Kempainen, Jon - G18

Kermes, Sean - ID57  
 Kersey, Rossio K - ID52  
 Kershner, Julie - G07  
 Keshavan, Raja - I15  
 Keshewani, Varun - ID64  
 Keshinro, Ajaratu - ST48  
 Keuleers, Inge - ID02  
 Khan, Adnan R - ST80  
 Khan, Faisal - H15  
 Khan, Wahab A - G09, ID21, ID36, ID46, ST32, TT13  
 Khodaverdian, Varandt - ST75  
 Houry, Joseph D. - H36  
 Kiecka, Iwona - H03  
 Kilzer, Jennifer M - ST19, ST29  
 Kim, Jin - ST48  
 Kim, Nam G - ID24  
 Kim, Seong-Youl - ID23, ID24  
 Kim, Yoona - TT17  
 Kim, Youngmi - ID38  
 Kim, Yun-Jee - ID23  
 Kingma, Douglas - ST16  
 Kip, Nefize Sertac - ST61  
 Kippbut, Brigitte - ID36  
 Kjolby, Rachel - G23  
 Klassen-Fischer, Mary K - ID52  
 Klco, Jeffery M - H44  
 Kluk, Michael J - H21, H33, H40, I23, TT24  
 Knight, Jay - H44  
 Knock, Becky - G07  
 Knox, Curtis - ID14  
 Knox, Gina - ID02  
 Ko, Yoo-Joung - G22  
 Kochar, Olga - ID19  
 Koduru, Prasad - H22, H25  
 Koebley, Sean - TT22  
 Kok, Yik Lim - ST09  
 Kokaji, Andy - TT17  
 Komissarova, Elena V - ID19  
 Konadu, Eric - ID07  
 Konigshofer, Yves - ST56, TT12  
 Kontor, Akuah - G30, ST83  
 Kopp, Nathan D - G25  
 Korenstein, Deborah - ID35, ID37, ID41  
 Kotecha, Ritesh R - ST28  
 Kraltcheva, Anelia - ST29  
 Kriegsmann, Mark - I17  
 Krock, Bryan L - G05, G08  
 Kruse, Kimberly R - ST80  
 Krysiak, Killannin - H37  
 Kshatriya, Priyanka - ST31  
 Ku, Jeffrey - TT18  
 Kuang, Ting - I11, TT04  
 Kudlingar, Vidya - ST31  
 Kulkarni, Anupriya S - ID25  
 Kulkarni, Priya - H10  
 Kulkarni, Shashikant - H37  
 Kumar, Rahul - OTH01  
 Kumar, Sunil - ID59  
 Kuper, Mark - H05  
 Kurmis, Alexis - H11  
 Kwak, Min Sun - ID60  
 Kwong, Raymond - ID57  
 Kyaw, Aung Win - ST09  
 LaBauve, Annette - ID57  
 LaBonte, Adam - ST83, ST85  
 Lacbawan, Felicitas - ID17, ST59  
 Lacey, Wendy - H05  
 Lachhander, Sean K - I22  
 Ladanyi, Marc - G13, H03, ST28, ST41, ST48  
 Lader, Eric - TT26  
 LaDouceur, Elise E - ID52  
 Laetsch, Theodore W. - ST68  
 Lagana, Stephen - ST51  
 Lagier, Erin - TT19  
 Lai, Jill C - ST84  
 Lai, Kevin - TT02, TT05  
 Laing, Christian - H11, I05, I18, I19  
 Lam, Ernest - TT34  
 Lancor, Kayla - ID16  
 Laosinchai-Wolf, Walairat - G29  
 Lara, Adrian - G18  
 Larson, Jessica - G18  
 Latham, Gary J - G16, G18, G29  
 Laudadio, Jennifer - ID50  
 Laugharn, James - TT23  
 Lea, Kristi - ST31  
 Leach, Patrick - G27  
 Lebel, Kimberly - ID64  
 Ledebor, Nathan A - ID63  
 Leduc, Charles - ST07  
 Lee, Albert K - G23  
 Lee, Charlie - ID11, ST09  
 Lee, Cindy - ID68  
 Lee, Sangwon - TT18  
 Lee, Sirin - ST09  
 Lee, Sungnam - ID24  
 Lee, Taylor - TT17  
 Lee, Wing - I07  
 Lee, Yi-Shan - ID56  
 Lee, Yun Kyung - TT16  
 Lefferts, Joel A - G09, G12, G28, ID15, ID16, ID42, ID43, ID46, ID48, ID51, ST32  
 LeGallo, Robin D - ST86  
 Lehman, Joshua H - TT22  
 Lehmann, Shelisa N - ID20  
 Lennerz, Jochen K - ST24, ST40, ST53  
 Lenzo, Felicia L - ST20  
 Lepine, Guylaine - ST07  
 Leslie, Kevin - TT22  
 Leung, Marco - G05, G08  
 Lewis, Lynette - TT02, TT05  
 Li, Bing - I11  
 Li, Bingsi - ST23  
 Li, Hui - ST61  
 Li, Jiawen - H05  
 Li, Jin - ID13  
 Li, Jisheng - ID18  
 Li, Kelly - ID18  
 Li, Marilyn M - H24, ST14, ST58  
 Li, Peng - H32, H37  
 Li, Qiongjie - TT04  
 Li, Weimin - ST10  
 Li, Yirong - G13  
 Li, Yuewei - H33  
 Li, Yuwen - H37  
 Liang, WenKai - ST05  
 Liang, Yan - TT32  
 Licon, Abel - ST26  
 Lieb, David J - ID25  
 Liechty, Benjamin - ST03  
 Liesenfeld, Oliver - ID09  
 Lim, Lony - G01  
 Lim, Megan S - OTH02  
 Lim, Seok-Hong - ST27  
 Lima, Amorice - ID01  
 Lin, Chieh-Yu - ST54  
 Lin, Fumin - H24, ST58  
 Lin, Jing - H08, I11, ST52  
 Lin, John H - ST04  
 Lin, Lawrence H - ST79

Lin, Ming-Tseh - H14, I20, ST36, ST44, TT28  
Lin, Yingxin - H13  
Lisowe, Abigail J - ID03, ID08  
Liu, Bin - ST52  
Liu, Bing Fang - H33  
Liu, Chenglin - I11, TT04  
Liu, Dakai - ID07  
Liu, Guangxin - ST52  
Liu, Hao - ST23  
Liu, Jing - ST23  
Liu, Jingjing - H08  
Liu, Lihong - H08  
Liu, Liu - ST61  
Liu, Sandra - TT19  
Liu, WeiHua - ID13  
Liu, Yan - ID17  
Liu, Yuting - TT04  
Liu, Zonghan - G30, ST27, ST83  
Lo, Bryan - ST07  
Lo, Ying-Chun - ST53  
Lockwood, Christina M. - ST68  
LoCoco, Jennifer S - TT06, TT21  
Loda, Massimo - I23, I27  
Lodato, Nicholas - ST27, ST83  
Lokhandwala, Parvez - ST44  
Long, Susan - ST39  
Loo, Eric Y - H09, H27, ST32, TT13  
Looney, Timothy - H17, H19  
Lopansri, Bert - ID02  
Lopategui, Jean - ST64  
Lopez, Karina E - ST73  
Lopez-Terrada, Dolores H - H04  
Lotan, Tamara L - ST04  
Louie, Carrie - ST62  
Louis, Sharon A - TT17  
Lowman, Geoffrey M - H17, H19  
Lu, Michael - TT27  
Lu, Wanli - TT04  
Lu, Yabin - TT27  
Lum, Christopher - G21  
Luo, Minjie - H24, ST14, ST58  
Luong, Khai - TT07  
Ly, Thai Yen - ST50  
Lye, Weng Kit - ID11  
Lynnes, Ty C - G15, G20  
Ma, Charles - ST59  
Ma, Deqin - H07  
Ma, Jie - H05  
Ma, Yuanyuan - H03  
Maalouf, Joyce - ID53  
Maceira, Vincente P - ID05, ID06  
Macfarland, Suzanne - ST58  
Machowski, Kimberly - ID64  
Mackinnon, Alexander C - H41, I16, ST02, ST06, ST08, ST45  
Macleod, Gwen - ID30, ID31, ID32, ID34  
Madhavan, Subha - H37  
Madkhali, Nawal - G31  
Madrigal, Andres - OTH04  
Magi-Galluzzi, Cristina - ST02, ST45  
Maglinte, Dennis T - G02  
Mahe, Etienne - H15, TT01  
Mai, Ming - H06, H34, I08, TT14  
Maio, Anna - G13  
Makhoul, Elias - ST64  
Malter, James - ID44  
Mandelker, Diana - G11, G13, I26  
Mani, Coumarane - H37  
Manning, Brenden - ID21  
Mannion, Ciaran - ST63  
Mansour, Amal - ST87  
Mansukhani, Mahesh - ST51  
Mao, Rong - G15  
Marble, Hetal D - ST24, ST40, ST53  
Marchetti, Antonio - ST05  
Marcogliese, Andrea - H04  
Marcovitz, Amir - ST19, ST31  
Marfatia, Twinkal - ST18  
Markulin, Theodore J - G16  
Marques, Maud - ST67  
Marquez, Christopher - ID04  
Martignoni, Guido - ST02, ST45  
Martin, M. Laura - I27  
Martins-Filho, Sebastiao N - ST07  
Mason, Emilia - H23  
Mason, Greg - ID35, ID37, ID41  
Mason, Christopher E - ID38  
Mathew, Christo - ID49  
McCall, Chad M - H13, H14  
McCleave, Julie - ID02  
McClory, Rena - ST18  
McConnell-Wells, Wendy - TT22  
McCormick, Stanley R - H35  
McCoy, Matthew - H37  
McDonnell, Terri - ID14  
McGeachy, Anna - I07  
McKee, Kelly - ID08  
McLaughlin, Ian - G17, TT31  
McMahon, Frank - ST74  
McMillen, Tracy - ID35, ID37, ID39, ID41, ID65, ID66, ID67, ID68  
McNamara, Suzan - ST67  
McNulty, Samantha - ID56  
McQueen, Karina - TT17  
Medeiros, L Jeffrey - H36  
Mee, Sammy - ST16  
Mehendale, Neelima - TT18  
Mehta, Anurag - ST72  
Mehta, Arnav - ID25  
Mehta, Nikita - G13  
Meister, Michael - I17  
Meltzer, Andrew - ID19  
Memmer, Marian - ID07  
Memmott, Regan - ST39  
Mendiola, John R - H35  
Mendoza, Salome - ID19  
Meng, Haiying - G03  
Meng, Leijun - H26  
Merola, Joseph - ID36  
Merrill, David - I07  
Merritt, Chris - TT32  
Meschi, Francesca - ST77  
Mesich, Brian W - ID01  
Messier, BoDean - ID48  
Metcalf, James D - G15  
Meydan, Cem - ID38  
Michael, J. Robert - H44  
Midic, Uros - ID09  
Mikheikin, Andrey - TT22  
Milano, Joseph - OTH04  
Milligan, John - G29  
Minami, Evan - G21  
Minarik, Marek - ST01  
Mindiola Romero, Andres E - H27  
Mirzaa, Ghayda - G31  
Misyura, Maksym - G13  
Mittal, Vinay K - ST19, ST29  
Mittempergher, Lorenza - ST16  
Mockus, Susan M - I21  
Moh, Akira - ST68  
Mohamed, Nehad - ST39  
Momeni-Boroujeni, Amir - ST41

Moncur, Joel T - ID52  
Monroe, Robert - ID25  
Montaño Miyagui, Benjur Y - ST73  
Montgomery, Nathan - ID59  
Monzon, Federico - ST57  
Mook, Jennifer - ID14  
Moore, Franklin - ID64  
Moore, Mathew - G01, ST13  
Mores, Christopher - ID19  
Morlote, Diana - H41, I16, ST02, ST45  
Morra, Massimo - ST18  
Morris, Luc - ID65  
Morrison, Thomas - TT33  
Morrissette, Jennifer J - H29, OTH02  
Mosher, Erin - TT06, TT21  
Mosquera, Juan Miguel - I23, I27  
Motzer, Robert J - ST28  
Mowrey, Philip N - G03  
Moyer, Krista - G26  
Mroz, Pawel - H42  
Muley, Thomas - I17  
Muller, Kristen - ST63  
Muralidharan, Kasinathan - G15  
Murray, Rebecca - I26  
Murray, Samuel J - ST28  
Mustafa, Asma - I14  
Muzzey, Dale - G23  
Myrand, Scott P - ST19  
Nadolski, Krista - OTH05  
Naef, Theodore - ST13  
Nafa, Khedoudja - I22, ST41  
Nair, Shilpa - I09  
Nakitandwe, Joy - H44  
Namiki, Steven - G21  
Naser, Walid - G10  
Nasla, Sunita - OTH02  
Nathany, Shrinidhi - ST72  
Neafie, Fides - ID52  
Neafie, Ronald - ID52  
Neary, Jennifer - H44  
Neerken, Sigi - ST79  
Neff, Jadee L - H13  
Nelson, Ann M - ID52  
Nepomuceno-Perez, Mia - H10  
Nerenz, Robert d - ID36  
Netto, George J - ST02, ST06, ST45  
Newburn, Erin - ST18  
Newman, Scott - H44, ST61  
Neyaz, Azfar - ID25  
Ng, David - H32  
Ng, Ivan - ID11  
Nguyen, Karen - TT32  
Nguyen, Lequan - ST56  
Nguyen, Trang - ST09  
Nguyen, Trinh - ID30, ID31, ID32, ID34  
Niccum, Brittany - TT05  
Nichols, Kim E - H44  
Nielsen, Tyler J - ST74  
Nieman, Linda T - ID25  
Nightingale, Mathew - ST50  
Nikolic, Dejan - ID28  
Nogai, Hendrik - ST68  
Norgaard, Zach - TT32  
Novak, Barbara - TT18  
Ntiamoah, Peter - H23  
Nyirenda, Themba - ST63  
Oakley, Joel - I23  
Oethinger, Margret - ID02  
Offit, Kenneth - G11, G13  
Oh, WonJun - ID24  
Oldakowski, Mark - ST84, TT34  
Oliver, Dwight - H20, H38  
Olson, Damon - ID04  
Olson, Gwyneth - G27  
Olson, Thomas - ST15  
O'Neil, Terri - H44  
Ondrasik, Regina - ST46  
Ong, Thaddaeus - ST09  
Ooi, Kara - TT27  
Ostman, Emily - ID44  
O'Sullivan Coyne, Geraldine Helen - TT21  
Olilano, John - TT03, TT09  
Otsubo, Aiko - G15, G20  
Overman, William - ST22, ST25  
Owen, Carolyn - H15  
Owen, Renius - ID17  
Pabla, Sarabjot - ST20  
Pabon, Carlos - TT18  
Pagani, Ioanna - ID18  
Pallavajjala, Aparna - I04, I20, ST36, ST44  
Palma, John - I17  
Palmer, Jill E - ID47  
Palmer, Stuart - ST05  
Pan, Xiaokang - ST39  
Pancholi, Preeti - ID01  
Pang, Andy W - ST84, TT34  
Parakh, Shilpa - TT05  
Pareja, Fresia - G11  
Parimi (Parini), Vamsi - TT28  
Park, Eva - ST03  
Park, Hyeon Jin - I23, TT03, TT09, TT24  
Park, Jeong Su - ID58  
Park, Kyoung Un - ID58  
Park, Paul - ST07  
Parker, Connor - G27  
Pasternak, Sylvia - ST50  
Patel, Darshana - G18, G29  
Patel, Juber - G11  
Patel, Keyur P. - H36  
Patel, Ulsav - ST41  
Patidar, Rajesh - TT21  
Patro, Jagannath - I09  
Patterson, Sara - I21  
Patterson, Taylor - ST26  
Paulraj, Prabakaran - I06, ST15  
Pavenko, Anna - TT32  
Peach, Amanda - TT06, TT21  
Pedroza, Anthony - TT20  
Pencreach, Erwan - ST30  
Pennington, Rod - ID14  
Perizzolo, Marco - H15, ST33  
Pesek, Milos - ST01  
Peters, Carrie - TT17  
Peters Sengers, Hessel - ID10  
Petitt, Matthew - ID45  
Petrilli, Erin - G30, ST83, ST85  
Petruzelka, Lubos - ST01  
Pettersson, Jonas - I03  
Pettus, Jason - ST35  
Pfeifer, John - G05, G08, ID56  
Pham, Ha T - G15  
Pham, Khoa - ST84  
Philkana, Deepika - ST82  
Pickle, Loni - H17, H19  
Piening, Brian D - ST55  
Pillai, Raju K - ST62  
Pilz, Joseph - ID07  
Pindikuri, Shwetha - ST55  
Pinto, Christopher J - ID25  
Pisapia, David J - I23, ST03



Pittz, Zachary R - ST80  
 Platz, Elizabeth - I20  
 Pollner, Reinhold - I9, H11, I05, I18  
 Polvino, Sean - G30, ST27, ST83  
 Poon, Hoifung - ST55  
 Poore, Allison - TT21  
 Portnow, Jana - ST62  
 Power, Robert - ST18  
 Prasad, Nripesh - G18  
 Pratt, Victoria M - G06, G15, G20  
 Prior, Thomas W - G15  
 Priore, Salvatore F - G16, OTH03, ST49  
 Pritchard, Colin C - ST04  
 Process, Vanessa - TT23  
 Prokhorova, Anya - H05  
 Ptackova, Renata - ST01  
 Ptashkin, Ryan - G11, ST28  
 Pullabhatla, Venu - ST12  
 Punia, Jyotinder N - H04  
 Qin, Dahui - ST65  
 Qin, Jianwen - ST52  
 Qiu, Fujun - I11, ST23  
 Quezado, Martha - ST42  
 Quick, Ann - ST57  
 Quindipan, Catherine - G02  
 Quiroz-Zarate, Alejandro - ID57  
 Quon, Peter - ST70  
 Qureshi, Shumaila - G15  
 Raca, Gordana - G02, H37  
 Racchumi, Joelle - H21, H40  
 Racke, Frederick - ST59  
 Radhakrishnan, Srihari - ID57  
 Raghavan, Ravi - H10  
 Rahman, Aliza - ID26  
 Raimondi, Susana - H44  
 Raj, Ritika - I09  
 Rajadinakaran, Gopinath - I21  
 Rajoria, Gunkeshi - TT03, TT09  
 Rajoria, Raja - ST03  
 Rand, Kenneth - ID45  
 Rao, Pranesh - G27, G29  
 Rao, Rajesh - ST55  
 Rao, Shruti - H37  
 Raphael, Michael Jonathon - G22  
 Raver, Catherine A - ID49  
 Rawling, David - ID09  
 Rebelatto, Marlon - ST10  
 Rector, Adrienne - ID04  
 Reddy, Ashwin C - ST47  
 Reddy, Kalpana S - H31, ST47  
 Reddy, Vishnu - H41  
 Reed, Jason - TT22  
 Reeves, Jason W - ID38, TT32  
 Reeves, John A. - ST68  
 Rehrauer, William M - ID47  
 Reid, James - ST12  
 Reinartz, John - H35  
 Reis-Filho, Jorge S - G11  
 R Emmel, Melissa - ID09  
 Remotti, Helen - ST51  
 Remy, Daphnee - ID07  
 Ren, Bing - ST60  
 Ren, Rongqin - ST39  
 Rennert, Hanna - I23, ID27, ID29, ID40  
 Requesens, Deborah - G15  
 Reuther, Jacquelyn - H04  
 Reynolds, Sheila M - ST55  
 Rheingold, Susan - H24  
 Rhodes, Michael D - TT32  
 Riaz, Nadeem - G11  
 Riccitelli, Nathan - I19, H11, I05, I18  
 Richard, Diana - OTH05  
 Richard-Greenblatt, Melissa - ID22  
 Richman, Geoffrey - G30, ST27, ST83, ST85  
 Riemony, Kent A - ST34  
 Rigali, Lisa - ID01  
 Rijo, Ivelise - I22  
 Ringel, Lando - G18  
 Riordan, Daniel - ST78  
 Rivera, Miguel N - ID25  
 Rivera, Gloryvee - TT06  
 Roberts, Catherine H - TT22  
 Roberts, Helen C - ID23, ID24  
 Robilotti, Elizabeth - ID35, ID37, ID41  
 Robinson, Alyncia - ST81  
 Robson, Mark - G11, G13  
 Rodgers, William - ID07  
 Rodrigo, Mikel Gallego - I07  
 Rodriguez, Erika - ST44  
 Rodriguez Pena, Maria D - ST02, ST06, ST45  
 Rogers, Brenda - TT18  
 Rogge, Ryan A - ST26  
 Rolle, Dre'shon - G01  
 Roman, Steven J - H12, ST19  
 Rootellis, Melanie - ID03  
 Rosado, Flavia - H38  
 Roseman, Nicole - TT05  
 Rosenbaum, Jason N - H29, OTH04, ST49  
 Rosenthal, Sun Hee - ID17, ST59  
 Roshal, Sophia - I27  
 Ross, Jeremy - H05  
 Rossi, Michael R - ST61  
 Roth, Jacquelyn J - OTH03, OTH04  
 Rotundo, Luca - ID55  
 Rowell, William - I13  
 Roy, Angshumoy - H04  
 Roytman, Megan - I15  
 Rubnitz, Jeffrey - H44  
 Rudolph, Marion - ST68  
 Rudzinski, Erin R - ST68  
 Ruetschilling, Teah - G27  
 Ruggiero, Phyllis - ID27, ID29, ID40  
 Ruminski Lowe, Dana - ST82  
 Rumrill, Kimberly A - ID16, ID48  
 Rusch, Michael - H44  
 Russell, Ryan - I21  
 Ryska, Miroslav - ST01  
 Ryulov, Alex - G02  
 Sábato, M. Fernada - I12, ID33, I06, ST15  
 Sadis, Seth - H12, ST19, ST29  
 Sadis, Seth - ST19  
 Sadowska, Justyna - H03, I25  
 Sadowski, Henry B - ST84, TT34  
 Saeed, Iamees - ST65  
 Saeed, Maria - TT06, TT21  
 Saeed-Vafa, Daryoush - ST65  
 Salazar, Paulo - H03, I22  
 Saldívar, Juan-Sebastian - ST18  
 Saleh, Lina Nur - ST09  
 Salem, Joseph - ID30, ID31, ID32, ID34  
 Saliba, Jason - H37  
 Salimi, PhD, Arsalan - G14  
 Salo-Mullen, Erin - G13  
 Salvatore, Steven - ID38, ID40  
 Samara, Raed - TT26  
 Sampson, Dayle - ID10  
 Sandberg, Lawrence - H10  
 Sande, Christopher - OTH04  
 Sands, Zachary - ID19  
 Sanford, Bridget - ST34

Santani, Avni B - G05, G08  
Sarda, Shruti - I07  
Sartori, Alexander - ST30  
Saunders, Hannah - TT20  
Sboner, Andrea - I23, I27, ST03  
Scafe, Charles - H12  
Schadt, Eric E - ST61  
Schageman, Jeoffrey - ST31  
Schauser, Leif - TT26  
Schlaberg, Robert - ID45  
Schleicher, Tyler - ID30, ID31, ID32, ID34  
Schmidt, Ryan J - G02  
Schneider, Marc - I17  
Schonberg, Steven A - G03  
Schrauth, John B - H35  
Schroeder, Brock E - ST55  
Schubert, Jeffrey - H24, ST58  
Schwartz, Roland - ID28  
Schwartz, Robert E - ID38  
Schweitzer, Brock - ST74  
Scicchitano, Lisa - G07, H45  
Scicchitano, Millie - G07  
Scorer, Paul - ST10  
Scott, Karissa - TT02  
Scott, Marietta - ST10  
Scully, Olivia - ST09  
Sebastian, Siby - H13  
Sedova, Marina - ID55  
See, Samuel - ID49  
Seitz, Robert S - ST74  
Selenica, Pier - G11  
Sene, Mohamadou - ID33  
Sepulveda, Antonia R - ID19, ST51  
Sepulveda, Jorge L - ID19  
Sermiyagina, Ekaterina - G14  
Serrette, Rene - H23  
Seth, Arun - ST17  
Shabani-Rad, Meer-Taher - H15  
Shaffer, Jonathan - TT26  
Shafik-Seddik, Hoda - ID07  
Shah, Monika - ID35, ID37, ID41  
Shah, Ronak H - ST28  
Shams, Soheil - I15  
Shao, Lin - TT04  
Sharma, Anurag - ST72  
Sharma, Ashima - G18  
Sharma, Mansi - ST72  
Shaw, Joe - G19  
Sheehan, Margaret - G13  
Sheffield, Brandon - ST07  
Shen, Junqing - G15  
Shen, Shanxiang - H28  
Sherman, Westley - I15  
Sheth, Siddharth - ID59  
Sheu, Jessica - TT02, TT05  
Shi, Dongsheng - ST52  
Shi, Guanglu - H20, H22, H25  
Shi, Qinqin - TT04  
Shi, Zonggao - H37  
Shi, Yong - ST61  
Shia, Jinru - ST48  
Shih, Angela - ID25  
Shiller, Michelle - ID20, ID49  
Shin, Dong H - ID24  
Shin, Heesun - I07  
Shirazi, Maryam - ST51  
Shirts, Brian - G31  
Shivaprakash, Shashikala - ID12  
Sholl, Lynette M - ID25  
Shuang, Lan Shuan - ST61  
Shurtleff, Sheila - H44  
Siddiqui, Osman - ST61  
Siemann, Sandra - TT07  
Sigaras, Alexandros - I23, I27  
Sigouros, Michael - I27  
Silbert, Suzane - ID01  
Silkov, Antonina - H44  
Sill, Martin - ST34  
Sillekens, Peter - ID02  
Simi, Manuele - I23  
Simon, Jayne - TT23  
Sims, David J - TT06, TT21  
Sinclair, Will - ID02  
Singh, Ila - ID26  
Singh, Nirupama - ST81  
Singh, Vishnu - ID07  
Siple, John - ID29  
Skarshaug, Shannon - ST42  
Skol, Andrew - I14  
Smith, Debra - ID01  
Smith, Vanessa L - H13  
Snuderl, Matija - ST71, ST79  
Snyder, Pamela - G19, ST39  
Snyder-Leiby, Teresa - G19  
Soens, Zachry - ST61  
Sokoli, Desiree - ID35, ID37, ID41  
Solomon, James - I23, ST03, TT03, TT09, TT24  
Solovyov, Alexander D - ID25  
Somar, Joshua - I26  
Sompallae, Krishnaveni D - H07  
Sompallae, Ramakrishna R - H07  
Song, Gang - ST27  
Song, Jianbo - ST64  
Song, Wei - I23, I27, ST03, TT03, TT09, TT24  
Song, Xueying - TT04  
Soni, Satyajit - ST72  
SoRelle, Jeffrey - ID44  
Sorg, Kristina - TT32  
Spatz, Alan - ST07  
Speight, Graham - ST12  
Spennhauer, Tania - ID30, ID31, ID32, ID34  
Spiewack, Maurice - I23  
Spittle, Cindy - ID13  
Spotts, David - G18  
Sprenger-Haussels, Markus - TT16  
Spriggs, Elizabeth - ST07  
Staboleski, Allyssa - ID64  
Stadler, Zsofia - G11, G13, ST48  
Starks, Rachel D - H07  
Statt, Sarah J - G16, G18  
Statz, Cara - I21  
Steffen, Michael - ID30, ID31, ID32, ID34  
Stehr, Henning - I10, I24  
Stein, Alisha - ST55  
Steinmetz, Heather B - ID15, ID16, ID48, ST32  
Stellrecht, Kathleen A - ID05, ID06  
Sternberg, Cora N - I27  
Stevens, James - ID48, TT13  
Stevens-Ayers, Terry - ID53  
Stewart, Douglas - H15  
Stockley, Tracy - ST07  
Stone, James R - ID25  
Streitova, Eliska - ST01  
Suarez, Carlos - I10  
Suh, EunRan - G16  
Suhardi, Harry - ID11, ST09  
Sui, Amy - TT03, TT09  
Sultana, Shahida - ID07  
Sumner, Rawlica - ID66  
Surrey, Lea F - H24, ST14, ST58

Suzuki, Matthew R - H35  
 Svoboda, Jakub - OTH02  
 Sweeney, Timothy E - ID09  
 Syed, Ajjazuddin - I25, I26  
 Szabolcs, Annamaria - ID25  
 Tabish, Nabil - H45  
 Tafe, Laura J - G12, ST11, ST32, ST35, ST37, ST38, ST60,  
 TT13, TT25  
 Takebe, Naoko - TT21  
 Tam, Erica - ID04  
 Tam, Wayne - H33, I23, TT24  
 Tan, Aik Choon - ST65  
 Tandon, Preteek - ST18  
 Tang, Claire - ST09  
 Tang, Guillin - H36  
 Tang, Jeffrey M - I23  
 Tang, Shican - ST23  
 Tang, Zhenya - H36  
 Tanner, Michael - ID18  
 Tao, Jessica - I20  
 Tart, Anna - ID50  
 Tashchuk, Maksym - I21  
 Tasian, Sarah - H24  
 Tay, Darwin - ST09  
 Tbakhi, Abdelghani - G10  
 Tebbs, Robert - ID55  
 Teer, Jamie - ST65  
 Telatar, Milhan - ST62  
 Terraf, Panieh - H37  
 Thapar, Vishal - ID25  
 Theilmann, Mark R - G23  
 Theparee, Talent - I24  
 Therrien, Matthew - G18  
 Theru Arumugam, Sivakumaran - G08  
 Thibert, Julie R - G16, G18  
 Thirumurthi, Umadevi - ST61  
 Thomas, Michael - I17  
 Thompson, Ella - H37  
 Thompson, Lucy - ID51  
 Thompson, Stephen - ID02  
 Thorstensen, Erin - ST27  
 Tian, Long - ST61  
 Tillson, Holly - H28  
 Ting, David - ID25  
 Toepfer, Armin - I13  
 Toledo, Diana M - G12, G28  
 Tom, Warren - ST29  
 Tomasek, Michael - ID07  
 Ton, Trang - ID04  
 Toor, Amir - TT22  
 Torlakovic, Emina - ST07  
 Toro, Michelle - H17, H19  
 Toruner, Gokce A. - H36  
 Tran, Hung V - I23, ST03, TT03, TT09  
 Tran-Thanh, Danh - ST07  
 Treece, Amy - H43  
 Tritsch, Sarah - ID19  
 Trull, Austyn - H44  
 Tsai, Yu-Chih - G17, TT31  
 Tsao, Ming-Sound - ST07  
 Tseng, Li-Hui - ST44  
 Tseng, Yu-Ting - H12, ST19, ST29  
 Tsongalis, Gregory J - G09, G12, G28, H09, H27, ID15, ID16,  
 ID21, ID36, ID42ID43, ID46, ID48, ID51, ST11, ST32,  
 ST37, ST38, ST60, ST63, TT13, TT25, TT33  
 Tsui, Dana W.Y. - ST28  
 Tu, Huolin - ST39  
 Tung, Jack K - H16, H18, I10, I24  
 Turner, Jonathan - G18  
 Turner, Scott A - I06, I12, ID33, ST15  
 Ullius, Andrea - TT11  
 Uphoff, Timothy S - ID03, ID08  
 Urbin, Mark - ST27  
 Uygun, Sahra - ST16  
 Uyingco, Cedric R - ST77, ST78  
 Uzilov, Andrew - ST61  
 Vahdatinia, Masha - G11  
 Vail, Eric - ST64  
 Valencia, Nancy - I9, H11  
 Vallee, Stephanie - G09  
 Van De Wiel, Paul - ST79  
 Van Deerlin, Vivianna - G16, ID22  
 Van Hook, Emma C - ST66  
 Van Loy, Cristina - ST29  
 Van Ness, Michael - ST59  
 Van Roey, Erik - ST20  
 Van Strijp, Dianne - ST79  
 Vanderbilt, Chad - ST48  
 Vanhoey, Thierry Vanhoey - ID02  
 Varambally, Sooryanarayana - ST81  
 Vargas, Daniel - ST57  
 Varma, Kamini - ID18  
 Veitch, James - ST29  
 Velu, Priya - I23, ID27, ID29, ID40  
 Venkataraman, Sujatha - ST34  
 Verma, Shalini - I15  
 Verma, Suman - G01, ST13  
 Vetrini, Francesco - G06, G15  
 Viale, Agnes - ID35, ID37, ID41, ST28  
 Vibhakar, Rajeev - ST34  
 Vilches, Natalia - ST73  
 Villy, Carolin - ID11  
 Viswanatha, David S - H06, H34, H37, H39, I08, TT14  
 Viswanathan, Surya - TT11  
 Vogt, Samantha - H14  
 Vora, Chintan - I09  
 Voss, Martin H - ST28  
 Voss, Thorsten - TT11  
 Vougiouklakis, Theodore - ST71  
 Wostmann, Corinna - I17  
 Wagner, Alex - H37  
 Wahl, Justin - I9, H11, I05, I18  
 Walker, Jill - ST10  
 Wall, Gavin R - ID57  
 Wallace, Meghan - ID01  
 Walsh, Michael - G13  
 Walsh, Noreen M - ST50  
 Walters, Ryan - H28  
 Wan, Helen Y - G23  
 Wang, Chunling - ID18  
 Wang, Dan - ST22, ST25  
 Wang, Guanghua - ID52  
 Wang, Hao - G30, ST85  
 Wang, Hongming - I11  
 Wang, Hui - ID61  
 Wang, Jian - TT34  
 Wang, Lei - ST52  
 Wang, Lianjing - H08  
 Wang, Lu - H44  
 Wang, Peng - TT06  
 Wang, Tom - TT34  
 Wang, Wei - H36  
 Wang, Xiaodong - ID13  
 Wang, Xiaotian - TT04  
 Wang, Yian C - G24  
 Wang, Zhaohui - G30, H20, ST27, ST83, ST85  
 Waqiee Ahmed, Kashif - ID49  
 Ward, Pamela - I03  
 Ward, Tabitha - ID04  
 Ward, Thomas - ST55

Warren, Sarah E - ID38, TT32  
Wasnikar, Viren - I15  
Watson, Thomas - ID57  
Watt, Christopher D - ID22  
Watts, Alain - ID57  
Way, Hannah - ST84  
Webb, C. Renee - ID26  
Wechsler-Reya, Robert - ST34  
Wee, Eugene - ID11, ST09  
Weerasinghe, Roshanthi - ST55  
Wehnl, Birgit - I17  
Wei, Congchong - I11  
Wei, Han - TT05  
Wei, Qing - ST08  
Weinstein, Harel - I27  
Weisenfeld, Neil - ST77, ST78  
Weiser, Martin - ST48  
Welker, Noah - G23  
Wenger, Aaron - I13  
Werner, Martina - TT23  
Wertheim, Gerald - H24  
Westblade, Lars - ID27, ID29  
White, Andrew - ID38  
Wick, Ivan - I15  
Wiebrands, Kay - ST12  
Wilber-Mader, Kimberly - H05  
Wilkes, David C - I27  
Wilkinson, Jeff - ST57  
Wilkinson, Mark R - H44  
Willard, Nicholas - H43, ST34  
Williams, Eli S - ST86, ST87  
Williams, Heather - H37  
Williams, Margaret C - H32  
Williams, P Mickey - TT06, TT21  
Williams, Paul D - ST19, ST29  
Williams, Stephen - ST77, ST78  
Williamson, Vernell S - I06, I12, ST15  
Wilson, Lisa I - ID05, ID06  
Wilt, Geoff - TT26  
Winkfein, Robert - ST33  
Winnick, Kimberly N - ID46, ST11, ST32, ST38, ST46  
Witteveen, Anke - ST16  
Wong, Betty Y. L. - G22  
Wong, Nau Nau - ST17  
Wong-Ho, Elaine - ST19, ST29  
Woo, Kwang-Sook - ID60  
Worthey, Elizabeth - I16  
Wright, Tayler - TT23  
Wu, David - H37  
Wu, Huimin - ID07  
Wu, Jinhua - H24, ST58  
Wu, Xianglin - H06, I08, TT14  
Wu, Xiaoxi - G30, ST83  
Wurtzler, Elizabeth M - ST80  
Xi, Liqiang - ST42  
Xian, Rena - H14, I20, ST36, ST44, TT28  
Xu, Feng - ST23  
Xu, Jing - H38, ID44  
Xu, Xinjie - H37  
Xu, Yan - ID44  
Yagi, Yukako - H23  
Yang, Chenchen - H12, H17, ST19, ST29  
Yang, ChiaChi - ST05  
Yang, Ciyu - G13  
Yang, David T - ID47  
Yang, Hainan - G30  
Yang, Richard K. - H36  
Yao, Huiyu - ID44  
Yaung, Stephanie - I17  
Ye, Junyi - I11  
Ye, Weicheng - ST70  
Yee, Mei Qi - ST09  
Yemelyanova, Anna - I16  
Yew, Hooi - ST62  
Yin, C. Cameron - H36  
Yin, Taoferi - I21  
Yin, Yan - ST52  
Yin, Yifeng - ST77, ST78  
Yoon, Ju-Yoon - H29, OTH03, ST49  
Yu, Hanzhong - I01  
Yu, Xiaofei - I06, I12, ST15  
Yu, Yingnan - ST09  
Yun, Anita - I22  
Zanazzi, George J - ST46  
Zanette, Camila - ST16  
Zehir, Ahmet - G13, I22, I25, I26, ST28, ST41, ST48  
Zehnder, James - H16, H18, I10, I24  
Zelley, Kristin - ST58  
Zeng, Naiyan - H26  
Zgonc, Valerie - ST42  
Zhai, Liang - ST52  
Zhang, Bing M - H16, H18, I24  
Zhang, David - ST75  
Zhang, Dong - TT34  
Zhang, Fengli - H37  
Zhang, Guangliang - I11, ST23  
Zhang, Hong - H26  
Zhang, Jing - H26  
Zhang, Jinghui - H44  
Zhang, Lei - TT10  
Zhang, Leisheng - TT04  
Zhang, Liying - G13  
Zhang, Qiang - I11  
Zhang, Sa - ST23  
Zhang, Shengle - ST20  
Zhang, Tong - ST09  
Zhang, Wenjuan - ST64  
Zhang, Wentao - ID09  
Zhang, Wenwen - H11, I18  
Zhang, Xia - TT18  
Zhang, Xiaojie - TT22  
Zhao, Xiaonan - H24  
Zhang, Yanming - H23  
Zhang, Yang - ST84  
Zhang, Yu - I12  
Zhang, Zhihong - ST23, TT04  
Zhang, Zhou - I11, TT04  
Zhao, Chen - TT06  
Zhao, Weiqiang - ST39  
Zhao, Yiqing - I01  
Zhaolin, Xu - ST07  
Zheng, Gang - I01  
Zheng, Hui - ID44  
Zheng, Ruifang - H30  
Zhong, Yiming - H24, H37, ST14, ST58  
Zhou, Cancan - TT04  
Zhou, Jiannan - H08  
Zhou, Kelsey - ST71  
Zhou, Zoey - TT32  
Zhu, Gord Guo - OTH01  
Zhu, Huiping - G18, G29  
Zhu, Pengfei - ST23  
Zhu, Yajun E - ST66  
Zhu, Yun - H12  
Ziegler, Janet - G17, TT31  
Ziegler, John - I22  
Zillmann, Martin - ST27  
Zimmer, Andriene - ST22, ST25  
Zirald, Solongo - ST77, ST78  
Zisimopoulos, Pantelis - I23

Zmuda, Erik - G26  
Zou, Denise - ST70  
Zuo, Zhuang - H36

## Explore The Virtual Expo Hall

### Expo Hall

Be sure not to miss the Virtual Expo Hall - whether you're searching for the latest products and services, are just browsing, or want to connect with one of your current vendors, the AMP Expo Hall has it all! Once in the Virtual Platform, please enter the "Expo Hall" You'll be able to search the "exhibitor index" or scroll through to see booths from AMP Corporate Partners and exhibiting companies.

DON'T MISS THESE EXCITING FEATURES OF THE VIRTUAL EXPO HALL:

- Reserve your "Chat Slot" with Premium Exhibitors during the designated Expo Hall hours.
- Save exhibitor documents to your "Virtual Meeting Bag" and email them to yourself later.
- Participate in the "Scavenger Hunt" in the Expo Hall and the "AMP Leaderboard" throughout the virtual platform! We have some really cool prizes - check them out on the "Leaderboard" menu tab in the Lobby!

### Meet the AMP 2020 Exhibitors

Explore the virtual AMP Expo Hall and meet over 80 exhibiting companies!

Take a few moments to peruse the [list of exhibitors](#) found in the online listing. You can also read about this year's exhibitors in the meeting program. You are encouraged to also engage and interact with exhibitors during the interactive Expo Hall hours:

#### Interactive Expo Hall Hours

##### **Monday, November 16, 2020**

10:30am - 11:15am

2:00pm - 3:00pm - includes demos & drawings

##### **Tuesday, November 17, 2020**

11:00am - 11:45am

2:00pm - 3:00pm - includes demos & drawings

##### **Wednesday, November 18, 2020**

11:00am - 11:45am

2:30pm - 3:30pm - includes demos & drawings

##### **Thursday, November 19, 2020**

11:00am - 11:45am

2:00pm - 3:00pm - includes demos & drawings

##### **Friday, November 20, 2020**

11:00am - 11:45am

2:30pm - 3:30pm - includes demos & drawings

## AMP 2020 Annual Meeting & Expo Exhibitors

10x Genomics  
AccuGenomics, Inc  
**Adaptive Biotechnologies Corp.\***  
Agena Bioscience  
Agendia  
Agilent Technologies  
Amoy Diagnostics Co., Ltd.  
Applied BioCode, Inc.  
Arc Bio LLC  
**ArcherDx\***  
**AstraZeneca\***  
**Asuragen\***  
ATCC  
Bangs Laboratories  
**Bayer Healthcare\***  
Biocartis  
Bionano Genomics  
Bio-Rad Laboratories, Inc.  
Burning Rock Dx  
Caris Life Sciences  
Cepheid  
ChromaCode  
CLINICAL LAB PRODUCTS  
Clinical Omics  
COMBINATI  
Canexia Health  
Covaris, Inc.  
DiaSorin Molecular  
**Eli and Lilly Company\***  
Fabric Genomics  
Fidelis Research  
Foundation Medicine, Inc.  
Genentech  
GenMark Diagnostics  
GenomeWeb  
GlaxoSmithKline  
Hamilton Company  
**Hologic\***  
IDbyDNA  
**Illumina\***  
Integrated DNA Technologies  
Invivoscribe  
LGC, Biosearch Technologies  
LGC SeraCare  
Life Magnetix  
Luminex

Maine Molecular Quality Controls, Inc.  
Menarini Silicon Biosystems  
**Merck\***  
Meridian BioScience Inc.  
MetaSystems Group, Inc.  
MilliporeSigma  
Mission Bio  
NanoString Technologies  
NeoGenomics Laboratories  
New England Biolabs  
Novartis Oncology  
Omega Bio-Tek, Inc.  
Ovation.io  
Oxford Gene Technology  
Paragon Genomics, Inc.  
PCR Biosystems  
PerkinElmer  
Personal Genome Diagnostics  
Personalis  
PierianDx  
Pillar Biosciences Inc.  
PlexBio Co., Ltd  
Promega Corporation  
Purigen Biosystems, Inc.  
QIAGEN  
Quantabio  
Rheonix, Inc.  
Roche\*  
SoftGenetics, LLC  
Sophia Genetics  
STEMCELL Technologies, Inc.  
Streck  
**Takeda\***  
Tempus  
The Jackson Laboratory  
The Pathologist  
**Thermo Fisher Scientific\***  
Twist Bioscience  
Vela Diagnostics  
Zymo Research Corp.

**\*Corporate Partners**

## 10x Genomics

Website: <http://www.10xgenomics.com>

Email: [theresa.craw@10xgenomics.com](mailto:theresa.craw@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.

## AccuGenomics, Inc.

<http://www.accugenomics.com>

[nlazaridis@accugenomics.com](mailto:nlazaridis@accugenomics.com)

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

## CORPORATE PARTNER

### Adaptive Biotechnologies Corp.

<https://www.adaptivebiotech.com/>

[clinicalservices@adaptivebiotech.com](mailto:clinicalservices@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.

## Agena Bioscience

<http://agenabio.com>

[mickie.henshall@agenabio.com](mailto:mickie.henshall@agenabio.com)

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..

## Agendia

22 Morgan

<https://www.agendia.com/>

[dina.scaglione@agendia.com](mailto:dina.scaglione@agendia.com)

Agendia is a precision oncology company headquartered in Irvine, California, committed to bringing early-stage breast cancer patients and their physicians the information they need to make the most effective treatment decisions. The company currently offers two commercially-available genomic profiling tests, supported by clinical and real-world evidence.

MammaPrint®, the 70-gene breast cancer recurrence assay, and Blueprint®, the 80-gene molecular subtyping assay, provide a comprehensive genomic profile and the data physicians need to make more informed decisions in the pre- and post-operative treatment settings. By

developing evidence-based novel genomic tests and conducting groundbreaking research while building an arsenal of data that will help treat cancer, Agendia aims to improve patient outcomes and support the evolving clinical needs of breast cancer patients and their physicians every step of the way, from initial diagnosis

## Agilent Technologies

<http://www.agilent.com>

[inquiries@agilent.com](mailto:inquiries@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.

## Amoy Diagnostics Co., Ltd.

[http://AmoyDiagnostics, Co., Ltd.](http://AmoyDiagnostics,Co.,Ltd.)

[tracykuang@amoydx.com](mailto:tracykuang@amoydx.com)

Amoy Diagnostics Co., Ltd. (AmoyDx) is an R&D based manufacturer of genetic testing products and diagnostic service provider for precision oncology. Our mission is to provide our customers with superior and innovative products and services to improve healthcare and patients' lives.

## Applied BioCode, Inc.

<http://www.apbiocode.com/>

[biz-development@apbiocode.com](mailto:biz-development@apbiocode.com)

Applied BioCode is an IVD manufacturer that designs, develops, and commercializes multiplex testing products. The company has combined "digital barcodes" with immuno- and molecular chemistry to create a new, bio-inspired Barcoded Magnetic Beads (BMB) technology. The micro BMBs, about the diameter of a human hair, are tagged with immunochemistry or molecular probes, allowing the digital barcodes to be easily scanned and accurately identified up to 4,096 barcodes with no ambiguity for biological targets. The company is FDA-510K cleared for their Respiratory 17-plex Pathogen Panel and Gastrointestinal 17-plex Pathogen Panel based on their BioCode® MDx-3000 automated system. Applied BioCode also partners with a variety of diagnostic companies with applications that include the infectious disease, autoimmune disease, allergy, gut microbiome, and veterinary markets.

## Arc Bio LLC

<http://www.arcbio.com>

[info@arcbio.com](mailto:info@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.



## **CORPORATE PARTNER**

### **ArcherDx**

<https://archerdx.com/>

[pbalsley@archerdx.com](mailto:pbalsley@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.

## **CORPORATE PARTNER**

### **AstraZeneca**

<https://www.astrazeneca.com>

[alyssa.u@astrazeneca.com](mailto:alyssa.u@astrazeneca.com)

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.

## **CORPORATE PARTNER**

### **Asuragen**

<https://asuragen.com>

[ecalver@asuragen.com](mailto:ecalver@asuragen.com)

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**

<http://atcc.org>

[adowning@atcc.org](mailto:adowning@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](http://www.atcc.org)

### **Bangs Laboratories**

<http://www.bangslabs.com>

[amy@bangslabs.com](mailto:amy@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.

## **CORPORATE PARTNER**

### **Bayer Healthcare**

<http://www.bayer.us.com>

[bridget.lewis@bayer.com](mailto:bridget.lewis@bayer.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](http://www.bayer.us).

### **Biocartis**

<http://www.biocartis.com/us>

[customerserviceUS@biocartis.com](mailto:customerserviceUS@biocartis.com)

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](http://www.biocartis.com/us)

### **Bionano Genomics**

<http://bionanogenomics.com>

[wobannon@bionanogenomics.com](mailto:wobannon@bionanogenomics.com)

Bionano Genomics, Inc. is a life sciences company in the genome analysis space. Bionano develops and markets the Saphyr® system, a digital cytogenetics platform for genome-wide detection of all structural variant types in cancer and germline/constitutional samples that enables researchers to accelerate the search for new diagnostics and therapeutic targets. To learn more, please visit: [www.BionanoGenomics.com](http://www.BionanoGenomics.com).

### **Bio-Rad Laboratories, Inc.**

<https://www.bio-rad.com>

[sonya\\_sano@bio-rad.com](mailto:sonya_sano@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. Bio-Rad is committed to bringing innovative molecular diagnostic tools to the market with our Droplet Digital PCR, Real-Time PCR, and Molecular Control solutions.

### **Burning Rock Dx**

<https://brbiotech.com/>

[Tom.Li@brbiotech.com](mailto:Tom.Li@brbiotech.com)

Burning Rock Dx specializes in next-generation sequencing diagnostics solutions for precision medicine in oncology. With the unique capability and experience in global trials, we are looking for partnerships to advance the field of companion diagnostics in order to achieve better patient outcomes.

## **Caris Life Sciences**

<https://www.carislifesciences.com/>

[corpcomm@carisls.com](mailto:corpcomm@carisls.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](http://www.CarisLifeSciences.com).

## **Cepheid**

<http://www.cepheid.com>

[arshia.hussain@cepheid.com](mailto:arshia.hussain@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.

## **ChromaCode**

<http://www.chromacode.com>

[spowell@chromacode.com](mailto:spowell@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.

## **CLINICAL LAB PRODUCTS**

<http://www.CLPmag.com>

[timo@medqor.com](mailto:timo@medqor.com)

For more than 50 years, Clinical Lab Products continues to be the preeminent product and technology publication for the clinical laboratory community. The CLP portfolio includes a glossy trade publication that presents feature articles, interviews, product news, and comparative Tech Guides (10x annually), plus a print and online Buyers Guide, webcasts, e-newsletters, white papers, and website—all with a focus on the specialized products and technologies used in clinical laboratories. For a FREE subscription, please reach out to us or visit:

CLINICAL LAB PRODUCTS

## **Clinical Omics**

<http://www.clinicalomics.com>

[smccarthy@liebetpub.com](mailto:smccarthy@liebetpub.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.

## **COMBiNATi**

<http://www.combinati.com>

[adam.langston@combinati.com](mailto:adam.langston@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.

## **Canexia Health (Contextual Genomics)**

<http://www.contextualgenomics.com>

[efarrag@contextualgenomics.com](mailto:efarrag@contextualgenomics.com)

Canexia Health (formerly Contextual Genomics) makes high quality cancer genomic information accessible with our clinically-validated assays, informatics and support. Our suite of genomics-based cancer tests is clinically actionable and cost-effective, designed to improve cancer treatment and monitoring. With our extensive scientific expertise, specialized genomics-based tests, and support from pharmaceutical and diagnostics partners, we are leading the shift towards precision oncology.

## **Covaris, Inc.**

<http://www.covaris.com>

[info@covaris.com](mailto:info@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](http://www.covaris.com) for more information.

## **DiaSorin Molecular**

<http://molecular.diasorin.com>

[marketing-info\\_molecular@diasorin.com](mailto:marketing-info_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.

## **CORPORATE PARTNER**

### **Eli and Lilly Company**

[www.LillyOncology.com](http://www.LillyOncology.com)

For more than 50 years, Lilly has been dedicated to delivering life-changing medicines and support to people living with cancer and those who care for them. Lilly is determined to build on this heritage and continue making life better for all those affected by cancer around the world. To learn more about Lilly's commitment to people with cancer, please visit [www.LillyOncology.com](http://www.LillyOncology.com).

### **Fabric Genomics**

<http://www.fabricgenomics.com>

[info@fabricgenomics.com](mailto:info@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.

### **Fidelis Research**

<https://fidelis-research.com/>

[iliyan.hristov@fidelis-research.com](mailto:iliyan.hristov@fidelis-research.com)

Bespoke biospecimen collections and R&D support services. Fidelis is specialized in human biospecimen collection and processing, as well as customized R&D support services. We are a trusted partner of global pharma, biotech and research organizations. Fidelis works with a wide network of over 60 collection sites in Europe and we are able to conduct projects tailored to your specific needs for fresh or frozen tissue, bone marrow aspirate, PBMCs, BMMCs, plasma, serum or whole blood samples, FFPEs, matched sets and other custom collections. Our inventory comprises banked solid tumor and hematological malignancies samples.

### **Foundation Medicine, Inc.**

<http://www.foundationmedicine.com>

[mmartin@foundationmedicine.com](mailto:mmartin@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](http://www.FoundationMedicine.com).

### **Genentech**

<http://www.gene.com>

[mojaddam@gene.com](mailto:mojaddam@gene.com)

Founded more than 40 years ago as the first biotechnology company, Genentech is dedicated to the rigorous pursuit of science and the development and delivery of life-changing medicines for people facing serious diseases. Headquartered in South San Francisco, California and a proud member of the Roche Group, our community is united by a common purpose and sense of urgency to transform the future of healthcare. Learn more at [gene.com](http://gene.com).

### **GenMark Diagnostics**

<http://www.genmarkdx.com>

[info@genmarkdx.com](mailto:info@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.

### **GenomeWeb**

<http://www.genomeweb.com>

[abaksh@genomeweb.com](mailto:abaksh@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.

### **GlaxoSmithKline**

<http://www.gsk.com>

GSK Oncology

Who we are

A science-led global healthcare company committed to helping those affected by cancer do more, feel better, live longer. Our work in oncology is focused on maximizing patient survival by delivering transformational medicines.

### **Hamilton Company**

<http://hamiltoncompany.com>

[marketingrequest@hamiltoncompany.com](mailto:marketingrequest@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.

### **CORPORATE PARTNER**

#### **Hologic**

<https://www.hologic.com>

[SalesSupport@hologic.com](mailto:SalesSupport@hologic.com)

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.

#### **IDbyDNA**

<http://www.idbydna.com>

[clientservices@idbydna.com](mailto:clientservices@idbydna.com)

IDbyDNA is revolutionizing the use of clinical metagenomics to improve health by decoding the unknown. IDbyDNA's product suite delivers unparalleled data analytics and industry-leading expertise to support medical laboratories with actionable infectious disease testing and pathogen surveillance. By profiling tens of thousands of microorganisms from any specimen with a scalable and intuitive approach, IDbyDNA empowers healthcare providers with greater depth and transparency for better identification of pathogens in order to accelerate triage and treatment and improve public health. For more information, visit <http://www.idbydna.com> or reach out to us on Twitter, Facebook, LinkedIn, Vimeo or YouTube.

## **CORPORATE PARTNER**

### **Illumina**

<http://www.illumina.com>  
[pr@illumina.com](mailto:pr@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.

### **Integrated DNA Technologies**

<https://www.idtdna.com/pages/shows@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.

### **Invivoscribe**

<http://www.invivoscribe.com>  
[marketing@invivoscribe.com](mailto:marketing@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.

### **LGC, Biosearch Technologies**

<http://www.biosearchtech.com>  
[jill.walerius@lgcgroup.com](mailto:jill.walerius@lgcgroup.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.

### **LGC SeraCare**

<http://www.seracare.com>  
[info@seracare.com](mailto:info@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.

### **Life Magnetix**

<https://magnetix.life>  
[info@magnetix.life](mailto:info@magnetix.life)

The next generation of RNA sample preparation is here. Scientists at Life Magnetix have built on the discovery that carbon surfaces have a unique interaction with single stranded nucleic acids like RNA. Life Magnetix company has developed proprietary manufacturing technologies to create carbon surfaces precisely tuned for RNA extraction, with any DNA contamination. Working with leading researchers, we have shown carbon-based surfaces always deliver superior performance as compared to silica-based columns and beads. Talk to us to learn how carbon-based RNA purification can make a difference in your assay.

### **Luminex**

<https://www.luminexcorp.com>  
[info@luminexcorp.com](mailto:info@luminexcorp.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.**

<http://www.mmqci.com>  
[info@mmqci.com](mailto:info@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. INTRON CF Panel I is the first FDA-cleared quality control for genetic testing. Custom orders are welcome at our cGMP facility in Saco, Maine.

### **Menarini Silicon Biosystems**

[bcrumlich@siliconbiosystems.com](mailto:bcrumlich@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.

## **CORPORATE PARTNER**

### **Merck**

Our goal is to translate breakthrough science into innovative oncology medicines to help people with cancer worldwide. At Merck, the potential to bring new hope to people with cancer drives our purpose and supporting accessibility to our cancer medicines is our commitment. As part of our focus on cancer, Merck is committed to exploring the potential of immuno-oncology with one of the largest development programs in the industry across more than 30 tumor types.

**Meridian BioScience Inc.**

<http://www.meridianbioscience.com>

[gina.martin@meridianbioscience.com](mailto:gina.martin@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.**

<http://www.metasystems.org>

[sales@metasystems.org](mailto:sales@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.

**MilliporeSigma**

<http://mandatories.merckgroup.com>

The Life Science business of MilliporeSigma, the U.S. life science business of Merck KGaA, Darmstadt, Germany, has some 21,000 employees and 59 manufacturing sites worldwide, with a portfolio of more than 300,000 products focused on scientific discovery, biomanufacturing and in vitro diagnostics. We specialize in fully-traceable and supply chain-managed manufacturing processes that are driven by diagnostics specialists dedicated to building sustainable relationships with customers through reliability, transparency, and trust.

**Mission Bio**

<http://missionbio.com>

[viernes@missionbio.com](mailto:viernes@missionbio.com)

Mission Bio delivers targeted solutions for high impact applications with the Tapestry Platform. The Tapestry 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.

**NanoString Technologies**

<https://www.nanostring.com>

[info@nanostring.com](mailto:info@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.

**New England Biolabs**

<http://www.neb.com>

[goodwin@neb.com](mailto:goodwin@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.

**Novartis Oncology**

<http://www.novartis oncology.com>

Novartis is reimagining medicine to improve people's lives. We use innovative science and digital technologies to create transformative treatments. Novartis products reach more than 800 million people globally and we are finding innovative ways to expand access to our medicines. About 109,000 people of more than 145 nationalities work at Novartis.

**Omega Bio-Tek, Inc.**

<https://www.omegabiotek.com>

[tradeshows@omegabiotek.com](mailto:tradeshows@omegabiotek.com)

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.

**Ovation.io**

<https://www.ovation.io/>

[dana@ovation.io](mailto:dana@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.

**Oxford Gene Technology**

<http://www.ogt.com>

[michele.elliott@ogt.com](mailto:michele.elliott@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 customized solutions and high-quality Cytocell® FISH probes, SureSeq™ next generation sequencing (NGS) panels, and CytoSure™ array products.

**Paragon Genomics, Inc.**

<http://www.paragongenomics.com>

[cassie@paragongenomics.com](mailto:cassie@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.

**PCR Biosystems**

<https://pcrbio.com>

[info@pcrbio.com](mailto:info@pcrbio.com)

PCR Biosystems is a UK manufacturer of kits and reagents for molecular biology research and diagnostics. This year has seen our expertise in enzyme development and large-scale production be applied to COVID-19 testing solutions for commercial providers and molecular diagnostic companies around the world. We offer a range of standard and custom solutions including bulk supply of reagents, OEM manufacturing and expert technical support to help you achieve the most from our market-leading reagents. To find out more, come and chat with us online!

**PerkinElmer**

<https://perkinelmer-appliedgenomics.com/>

[CustomerCareUS@perkinelmer.com](mailto:CustomerCareUS@perkinelmer.com)

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**

<http://www.pgdx.com>

[info@pgdx.com](mailto:info@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.

**Personalis**

Personalis, Inc. is a leader in population sequencing and cancer genomics, with a focus on data, scale, efficiency and quality. Personalis operates one of the largest sequencing operations globally and is currently the sole sequencing provider to the U.S. Department of Veterans Affairs Million Veteran Program (VA MVP). For more information, please visit [www.personalis.com](http://www.personalis.com) and follow Personalis on Twitter (@PersonalisInc).

**PierianDx**

<http://www.pieriandx.com>

[tsarjantson@pieriandx.com](mailto:tsarjantson@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](http://www.pieriandx.com)

**Pillar Biosciences Inc.**

<https://www.pillar-biosciences.com>

[info@pillar-biosciences.com](mailto:info@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.

**PlexBio Co., Ltd**

<https://www.plexbio.com/>

[marketing@plexbio.com](mailto:marketing@plexbio.com)

PlexBio's commitment to cancer discovery and treatment begins with early detection and the identification of precision treatments. Our proprietary cutting-edge multiplexing platform uses patented Precision Image Code (PiCode) MicroDisc technology to provide rapid, cost-effective, streamline cancer diagnostics.

**Promega Corporation**

<http://www.promega.com>

[cynthia.petty@promega.com](mailto:cynthia.petty@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.

**Purigen Biosystems, Inc.**

<http://www.purigenbio.com>

[paul.moon@purigenbio.com](mailto:paul.moon@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 isotachopheresis (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.

## **QIAGEN**

<https://www.qiagen.com>

[customercare-US@QIAGEN.com](mailto:customercare-US@QIAGEN.com)

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.

## **Quantabio**

<http://www.quantabio.com>

[Ashley.kraus@quantabio.com](mailto:Ashley.kraus@quantabio.com)

Quantabio is a leading provider of advanced DNA and RNA amplification reagents for the most demanding molecular testing applications in the applied, translational and life science research. The Quantabio team leverages decades of experience in developing pioneering amplification technologies to deliver cutting-edge products to researchers focused on critical cloning, PCR, qPCR and Next-Generation Sequencing (NGS) based applications. Based in Beverly, Mass., Quantabio offers a growing portfolio of products through its international sales operations, as well as a global network of distributors and commercial service providers.

## **Rheonix, Inc.**

<http://www.rheonix.com>

[info@rheonix.com](mailto:info@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.

## **CORPORATE PARTNER**

### **Roche**

<http://www.roche.com>

[ellen.byrum@roche.com](mailto:ellen.byrum@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.

## **SoftGenetics, LLC**

<http://www.softgenetics.com>

[info@softgenetics.com](mailto:info@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**

<http://www.sophiagenetics.com>

[events@sophiagenetics.com](mailto:events@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.

## **STEMCELL Technologies, Inc.**

<https://www.stemcell.com/>

[info@stemcell.com](mailto:info@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](http://www.robosep.com)

## **Streck**

<https://www.streck.com/>

[custserv@streck.com](mailto:custserv@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.

## **CORPORATE PARTNER**

### **Takeda**

<https://www.takedaoncology.com/>

Takeda is a patient-focused, innovation-driven global pharmaceutical company that builds on a distinguished 237-year history. Our mission is to strive towards better health and a brighter future for people worldwide through leading innovation in medicine. Learn more at [www.takedaoncology.com](http://www.takedaoncology.com).

## **Tempus**

<http://tempus.com>

[support@tempus.com](mailto:support@tempus.com)

Tempus is a technology company advancing precision medicine through the practical application of artificial intelligence in healthcare. With the of the world's largest libraries of clinical and molecular data, and an operating system to make that data accessible and useful, Tempus enables physicians to make real-time, data-driven decisions to deliver personalized patient care and in parallel facilitate discovery, development and delivery of optimized therapeutic options for patients through distinctive solution sets. The goal is for each patient to benefit from the treatment of others who came before by providing physicians with tools that learn as the company gathers more data.

## **The Jackson Laboratory**

<http://www.jax.org>

[orderquest@jax.org](mailto:orderquest@jax.org)

The Jackson Laboratory 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 Pathologist**

<https://thepathologist.com/>

[kevin.odonnell@texerepublishing.com](mailto:kevin.odonnell@texerepublishing.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.

## **CORPORATE PARTNER**

### **Thermo Fisher Scientific**

<https://www.thermofisher.com>

[lawreen.asuncion@thermofisher.com](mailto:lawreen.asuncion@thermofisher.com)

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.

## **Twist Bioscience**

<http://twistbioscience.com>

[rmabella@twistbioscience.com](mailto:rmabella@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.

## **Vela Diagnostics**

<http://www.veladx.com>

[rachel.yap@veladx.com](mailto:rachel.yap@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.

## **Zymo Research Corp.**

<http://www.zymoresearch.com>

[info@zymoresearch.com](mailto:info@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.



SAVE THE  
NEW DATES



# AMP EUROPE 2021



Clinical Genomics:  
Beyond the Somatic Mutation



In conjunction with the **35th Congress of the Italian Society of Pathology and Translational Medicine (SIPMeT)**

Milan, Italy

**14 – 16 June 2021**

NH Milano Congress Centre

[www.amp-europe-congress.com](http://www.amp-europe-congress.com)



# AMP EUROPE 2021

**Clinical Genomics:  
Beyond the Somatic  
Mutation**



**Milan, Italy  
14 – 16 June 2021**

## **WELCOME TO AMP EUROPE 2020**

The 2nd AMP Europe 2021 Congress on Clinical Genomics: Beyond Somatic Mutation, takes place in Milan, Italy from 14 – 16 June, 2021. The Congress will be held in conjunction with the 35th Congress of the Italian Society of Pathology and Translational Medicine (SIPMeT).

## **SAVE THE NEW DATES**

14 – 16 June 2021

[www.amp-europe-congress.com](http://www.amp-europe-congress.com)

The Congress will bring together a network of molecular professionals and representatives of the diagnostics industry. The aim of the Congress is to educate healthcare practitioners and advance the value of molecular laboratories in providing high quality patient care around the world.

A multi-disciplinary scientific program will showcase molecular technology with clinical applications in oncology (solid tumors, hematopathology), genetics (congenital, heritable), and infectious diseases. Most importantly, there will be an emphasis on modern, user-friendly laboratory analytics supported by informatics tools to facilitate the interpretation of actionable genomic test results.

## **Join us in Milan!**

To gain the latest knowledge in precision medicine and how it directly impacts testing and treatment decisions and engage with other thought leaders in the most talked-about areas of molecular pathology.

