SATURDAY, APRIL 18 AT-A-GLANCE

All sessions eligible for CME credit unless otherwise noted.

8:00 a.m.-10:00 a.m.	Educational Sessions	142-147
8:00 a.m.-10:00 a.m.	Methods Workshops	148-149
9:30 a.m.-4:00 p.m.	Science Ed Professional Advancement Session	150
10:00 a.m.-12:00 p.m.	Educational Session	151
10:15 a.m.-12:15 p.m.	Educational Sessions	152-156
10:15 a.m.-12:15 p.m.	Methods Workshops	157-159
12:00 p.m.-5:00 p.m.	AMC Professional Advancement Session	160
1:00 p.m.-2:30 p.m.	Regulatory Science and Policy Session	161
1:00 p.m.-3:00 p.m.	Educational Sessions	162-167
1:00 p.m.-3:00 p.m.	Methods Workshops	168-170
1:00 p.m.-3:00 p.m.	WICR Professional Advancement Session	171
3:15 p.m.-4:15 p.m.	Meet-the-Expert Session	172
3:15 p.m.-5:15 p.m.	Educational Sessions	173-176
3:15 p.m.-5:15 p.m.	Methods Workshops	177-179
4:30 p.m.-5:30 p.m.	Meet-the-Expert Sessions	180
5:30 p.m.-6:30 p.m.	AACR-Irving Weinstein Lecture	181
5:30 p.m.-6:30 p.m.	Professional Advancement Session	182
5:30 p.m.-6:45 p.m.	AACR-WICR Charlotte Friend Lecture	183
5:30 p.m.-7:30 p.m.	Professional Advancement Session	184
6:30 p.m.-10:30 p.m.	Meet and Greet	185

EDUCATIONAL SESSIONS

Saturday, 8:00 a.m.-10:00 a.m.

Room 113, Pennsylvania Convention Center

From Chemistry to the Clinic: Pathways for Drug Discovery and Development, Part 1: Optimizing Drug Discovery: Insights on an Important Process

Chairperson: Michael J. Luzzio, Biogen Idec, Inc., Cambridge, MA

Drug discovery efforts to identify therapeutics to effectively treat cancer are more intense than ever seen previously. Given the multitude of sciences and work that goes into this process, medicinal chemistry is a key science that drives drug discovery. The drug discovery process is iterative and relies upon data generally collected from the primary discovery functions, i.e., in vitro biology, drug metabolism/pharmacology, toxicology, and in vivo tumor growth inhibition studies. The biological activity of small molecules is optimized towards the desired target in question while at the same time efforts are made to minimize off-target activity and toxicity. In concert with this work, the ADME and in vivo pharmacology are continuously monitored and improved to optimize the drug's exposure towards the target in question while trying to maintain or improve target activity. All the molecule's properties have to dovetail effectively to produce a quality compound for consideration for clinical development. However, not all drug discovery processes are successful without some major hurdle with the molecules that are being optimized that has to be solved by the project team.

In this session, three presentations on three different biochemical targets, two of which are first-time structure disclosures, will be presented in which unique solutions were achieved through chemistry, which provided compounds that allowed the project team to determine a go/no go decision to either drive towards nomination of a molecule for clinical development or stand down from the target. Chemistry optimized molecules are necessary to understanding the biological processes and target validation. Regardless of being a small molecule or an antibody-drug conjugate, all potential chemically modified agents will realize improved anticancer activity, utilizing ADME, toxicology, and pharmacology data as the drivers towards further compound optimization towards finding effective agents with minimal toxicities and significantly improved anticancer activities. Further, data from human clinical studies of current agents in which resistance, mutations in the biochemical target has been observed further impact the design and evaluation of potential small molecule treatments. These talks will present lessons

learned from the process of identifying agents for clinical development where chemistry utilized a unique lead optimization process against a target with minimized off-target activities to drive towards a candidate.

Introduction
Michael J. Luzzio, Biogen Idec, Inc., Cambridge, MA

8:00 a.m. **Discovery of a potent covalent mutant-selective EGFR inhibitor: The journey from high-throughput screening to EGF816**
Gerald Lelais, Genomics Institute of the Novartis Research Institute, San Diego, CA

8:30 a.m. **Discussion**

8:40 a.m. **Lead optimization through modulation of physicochemical properties: A case study in the discovery of novel CDK9 inhibitors**
Yusong Tong, AbbVie Inc., North Chicago, IL

9:10 a.m. **Discussion**

9:20 a.m. **Discovery of pan-notch inhibitors as anticancer agents** *(not eligible for CME credit)*
Ashvinikumar V. Gavai, Bristol-Myers Squibb Co., Princeton, NJ

9:50 a.m. **Discussion**

Terrace Ballroom I (400 Level), Pennsylvania Convention Center

The Fundamentals of Big Data Analysis

Chairperson: Yu Shyr, Vanderbilt-Ingram Cancer Center, Nashville, TN

The last decade has seen a veritable explosion in the amount of raw information generated by biomedical researchers worldwide. Modern technology allows the collection of biomedical information at an unprecedented level of detail and in increasingly vast quantities. To reap real knowledge from the mountains of data produced from biomedical research, however, requires interdisciplinary skills – a background not only in biology but also in bioinformatics tools and techniques. This session will outline the skills and knowledge necessary to meet the challenges of conducting big data research as well as analyzing the data generated from basic science research and clinical trials that include genomic and proteomic

experiments. Common mistakes made when analyzing high-density biomarker data will be discussed. The overall goal of this session is to build the fundamental knowledge for conducting cancer research involving big data.

Introduction
Yu Shyr, Vanderbilt-Ingram Cancer Center, Nashville, TN

8:00 a.m. **Epigenetics for beginners**
Peter W. Laird, Van Andel Research Institute, Grand Rapids, MI

8:25 a.m. **Discussion**

8:30 a.m. **Clinical genomics and medicine: An informatics perspective**
Warren A. Kibbe, National Cancer Institute, Rockville, MD

8:55 a.m. **Discussion**

9:00 a.m. **Big data analysis for the uninitiated**
Yu Shyr, Vanderbilt-Ingram Cancer Center, Nashville, TN

9:25 a.m. **Discussion**

9:30 a.m. **Using genomics to direct patient care**
Sameek Roychowdhury, The Ohio State University Comprehensive Cancer Center, Columbus, OH

9:55 a.m. **Discussion**

include use of optical probes and Raman-based technologies, and intra-vital imaging that will help us better understand tumor-host interplay in cancer progression and metastasis, particularly how this might be modulated for therapeutic benefit.

8:00 a.m. **Introduction: New techniques for imaging cancer in the niche**
Margaret C. Frame, University of Edinburgh, Edinburgh Cancer Research Centre, Edinburgh, United Kingdom

8:15 a.m. **Imaging drug-tolerant microenvironments**
Erik Sahai, Cancer Research UK, London, United Kingdom

8:45 a.m. **Discussion**

8:50 a.m. **Imaging immune-tumor interactions**
Matthew F. Krummel, University of California, San Francisco, CA

9:20 a.m. **Discussion**

9:25 a.m. **Long-term imaging of the perivascular niche in metastasis and therapy responses**
Frank A. Winkler, German Cancer Research Center, Heidelberg, Germany

9:55 a.m. **Discussion**

Room 103, Pennsylvania Convention Center
Imaging the Tumor Niche and Therapeutic Responses

Chairperson: Margaret C. Frame, University of Edinburgh, Edinburgh Cancer Research Centre, Edinburgh, United Kingdom

It is clear that the behavior of tumors cannot be ascribed solely to cancer cell-autonomous traits that are typically monitored by tissue culture experiments. The tumor niche is composed of multiple cell types, only a proportion of which are cancer cells. In this educational session, we will consider the complexity of the cancer niche, using imaging to examine the role of non-tumor cell types - such as cancer associated fibroblasts, immune cells, and pericytes which key determinants of tumor progression and therapeutic responses. Techniques to be discussed will

EDUCATIONAL SESSIONS

Saturday, 8:00 a.m.-10:00 a.m.

Terrace Ballroom II-III (400 Level), Pennsylvania Convention Center
Liquid Biopsy Biomarkers

Chairperson: Caroline Dive, CRUK Manchester Institute, Manchester, United Kingdom

Optimization of cancer patients' treatment management based on a routinely obtained, simple, and economically realist blood test as a "liquid biopsy" is a pivotal goal in cancer research. This session will overview the "state of art" and research horizons relating to biomarker discovery and development, assay validation, and clinical utility of a range of liquid biopsy approaches. The ability to retrieve critical molecular information contained in circulating free nucleic acids and circulating tumor cells that informs on tumor progression and a patient's response to treatment will be discussed as well as the new concepts concerning the ability to isolate and characterize subpopulations of tumor initiating cells from patients' blood samples.

8:00 a.m.	**Circulating cell free DNA and cancer** Alain R. Thierry, INSERM U896, Montpellier, France
8:25 a.m.	**Discussion**
8:30 a.m.	**Circulating miRNAs** Muneesh Tewari, University of Michigan Medical School, Ann Arbor, MI
8:55 a.m.	**Discussion**
9:00 a.m.	**Circulating tumor cell biopsies** Caroline Dive, CRUK Manchester Institute, Manchester, United Kingdom
9:25 a.m.	**Discussion**
9:30 a.m.	**Malignant stem cells in the circulation** Andreas Trumpp, German Cancer Research Center, Heidelberg, Germany
9:55 a.m.	**Discussion**

Room 108, Pennsylvania Convention Center
The Mechanism of Chromothripsis

Chairperson: David Pellman, Dana-Farber Cancer Institute, Boston, MA

Genome sequencing has uncovered a new mutational phenomenon in cancer and human congenital disorders called chromothripsis. Chromothripsis is characterized by extensive chromosome rearrangements and an oscillating pattern of DNA copy number levels that is typically restricted to one or a few chromosomes. Statistical analysis has suggested that chromothripsis is likely to occur through a single catastrophic event. However, the underlying mechanism has not been known. In this session we will discuss very recent progress towards recapitulating chromothripsis in the laboratory. We will discuss mechanisms that may promote chromothripsis, which include chromosome translocations, chromosome bridges, and the generation of micronuclei. Approaches include whole genome sequencing of experimentally derived clonal populations, live cell imaging, and single cell genome sequencing. We will review the criteria for defining chropmothripsis, and in light of new mechanistic insights, discuss the prevalence of these types of mutational events in human cells.

8:00 a.m.	**Patterns and incidence of chromothripsis across cancers** Peter J. Campbell, Wellcome Trust Sanger Institute, Cambridge, United Kingdom
8:25 a.m.	**Discussion**
8:30 a.m.	**Generation of chromothripsis events in a cell-based system** Jan Korbel, European Molecular Biology Laboratory, Heidelberg, Germany
8:55 a.m.	**Discussion**
9:00 a.m.	**Chromosome rearrangements that arise as a consequence of mitotic errors** René H. Medema, Netherlands Cancer Institute, Amsterdam, The Netherlands
9:25 a.m.	**Discussion**
9:30 a.m.	**Chromothripsis from DNA damage in micronuclei** David Pellman, Dana-Farber Cancer Institute, Boston, MA
9:55 a.m.	**Discussion**

Room 119, Pennsylvania Convention Center
Strategies for Measuring Diet Quality in Population Studies of Cancer Outcomes

Chairperson: Terryl J. Hartman, Emory University, Atlanta, GA

Efforts to measure diet quality strive to capture the complexity of diet and to account for the potential for interactions among dietary constituents. Ideally methods will permit comparisons across study populations. Diet quality has been assessed in a variety of ways including

multidimensional a priori indices and novel measures developed to assess adherence with nutrition-related public health guidelines. This session will feature several methods for assessing diet quality, which can be applied in studies of cancer outcomes. Presentations will include varying methodological approaches, challenges encountered during implementation, and put into context of the broader availability of diet and lifestyle indices.

8:00 a.m.   **Diet quality measures based on recommendations for general health and as applied to studies of cancer outcomes**
Terryl J. Hartman, Emory University, Atlanta, GA

8:25 a.m.   **Discussion**

8:30 a.m.   **Measuring the inflammatory potential of diet: The dietary inflammatory index and risk of cancer**
Susan E. Steck, University of South Carolina, Columbia, SC

8:55 a.m.   **Discussion**

9:00 a.m.   **The American Cancer Society Cancer Prevention Guidelines and risk of chronic disease endpoints using an a priori score: Recent findings**
Marjorie L. Mccullough, American Cancer Society, Atlanta, GA

9:25 a.m.   **Discussion**

9:30 a.m.   **Measuring diet quality through scores: Considerations when assessing diet across European populations**
Anne-Claire Vergnaud, Imperial College London, London, United Kingdom

9:55 a.m.   **Discussion**

Room 120, Pennsylvania Convention Center
Targeting Genetic Drivers in Premalignancy

Chairperson: Scott M. Lippman, UCSD Moores Cancer Center, La Jolla, CA

Genetic "drivers" of cancer progression and metastasis can occur in premalignancy or even in benign lesions. *PIK3CA, FGFR, BRAF* and *P53* driver mutations have been reported in epidermal nevi, seborrheic keratoses, and rheumatoid arthritis synovium. *Cyclin D1* amplification was among the first genetic drivers in head and neck premalignant lesions (HNPLs), and drug targeting of *Cyclin D1* produced early

promising prevention results. LOH profiles were recently shown to prospectively stratify cancer risk in patients with HNPLs. The recent EPOC (Erlotinib Prevention of Oral Cancer) phase III multicenter trial validated specific LOH profiles as genetic drivers and identified potential new oncogenic drivers in high-risk HNPLs (e.g., *PIK3CA*). Many of these genomic alterations converge on the aberrant activation of the PI3K/AKT/mTOR pathway in HNPLs. Emerging evidence supports that the over-reliance in this signaling mechanism for tumor progression can expose a cancer vulnerability that can be exploited for cancer prevention and treatment. Studies of a) lung carcinogenesis have identified early genetic drivers of squamous cell carcinoma and adenocarcinoma (e.g., 3q26 amplification) and b) HNPLs in China have identified oncogenic *NOTCH1* driver mutations. We will discuss genetic drivers in HN and lung premalignancy and emerging opportunities to develop molecular prevention strategies.

8:00 a.m.   **Overview of targeting genetic drivers in premalignancy**
Scott M. Lippman, UCSD Moores Cancer Center, La Jolla, CA

8:25 a.m.   **Discussion**

8:30 a.m.   **The precancer genome atlas for squamous cell lung cancer**
Avrum E. Spira, Boston University School of Medicine, Boston, MA

8:55 a.m.   **Discussion**

9:00 a.m.   **Targeting the PI3K-mTOR signaling circuitry with metformin for oral cancer prevention**
J Silvio Gutkind, Oral & Pharyngeal Cancer Branch, NIH, Bethesda, MD

9:25 a.m.   **Discussion**

9:30 a.m.   **The conundrum of "driver" mutations in benign conditions**
Razelle Kurzrock, UCSD Moores Cancer Center, La Jolla, CA

9:55 a.m.   **Discussion**

EDUCATIONAL SESSIONS

Saturday, 8:00 a.m.-10:00 a.m.

Terrace Ballroom IV (400 Level), Pennsylvania Convention Center

Therapeutic Targeting and Monitoring Tumor Microenvironments

Chairperson: Lisa M. Coussens, OHSU Knight Cancer Institute, Portland, OR

All cancers contain a diverse population of cells, including those harboring genetic mutations typically referred to as "tumor" or "cancer" cells, as well as other "normal" cell types that are activated and/or recruited to the local tumor microenvironment (TME), e.g., fibroblasts and other mesenchymal support cells, innate and adaptive immune cells, and cells that line blood and lymphatic vessels. Reciprocal interactions between these responding "normal" cells, their mediators, structural components of extracellular matrix, and genetically altered neoplastic cells regulate all aspects of tumorigenicity. This session will discuss novel approaches to therapeutically target components of the TME, as well as approaches to monitor changes in the TME related to efficacy of therapeutics.

8:00 a.m.	**Introduction to stromal heterogeneity** Lisa M. Coussens, OHSU Knight Cancer Institute, Portland, OR
8:10 a.m.	**Therapeutic targeting and monitoring tumor immunity in melanoma** Jennifer A. Wargo, The University of Texas MD Anderson Cancer Center, Houston, TX
8:30 a.m.	**Discussion**
8:35 a.m.	**Phenotypic and functional assessment of the bone marrow immune microenvironment in acute myeloid leukemia (AML)** Evan Lind, Oregon Health and Science University, Portland, OR
8:55 a.m.	**Discussion**
9:00 a.m.	**Targeting stromal components in pancreas cancer** Sunil R. Hingorani, Fred Hutchinson Cancer Research Center, Seattle, WA
9:20 a.m.	**Discussion**
9:25 a.m.	**In vivo MR imaging of TME-targeted drug responses** Alexander Guimaraes, Oregon Health and Science University, Portland, OR
9:45 a.m.	**Discussion**
9:50 a.m.	**General Discussion**

Grand Ballroom (300 Level), Pennsylvania Convention Center

Tumor Immunology and Immunotherapy for the Non-Immunologist

Chairperson: Julie Y. Djeu, Moffitt Cancer Center and Research Institute, Tampa, FL

The immune system is a powerful deterrent to cancer development and progression, and its evasion is a key hallmark of cancer. Innate immunity serves as the first line of defense which, when breached, allows the establishment of a tumor that can create an environment conducive to suppression of adaptive immunity against cancer. With loss of innate and adaptive immunity, the growth potential of tumors goes unchecked. Ironically, inflammation may positively or negatively impact cancer immunity and tumor growth. Recent work on inflammation and cancer points to the gut microbiome as an important component in balancing immune responses to cancer. Better understanding of the underlying mechanisms of immune modulation in cancer is needed to develop new therapeutic strategies that can effectively recover immunity against cancer and result in a durable clinical outcome and better patient survival. The presentations in this session will touch upon all these areas, beginning with the microbiota, followed by deliberation on the role of various types of innate lymphoid cells and T cells, and bringing to the clinic practical approaches to treat cancer from lessons learned. What antigens T cells must recognize to tame the cancer is also a critical issue and how neoantigens created by mutant genes in the cancer cell can be identified and put to use will also be discussed.

This session is intended to familiarize non-immunologists with fundamental immune responses to cancer and highlight innovative strategies for immunotherapy of cancer. It will also be informative to tumor immunologists as they will learn of the latest research efforts of the speakers. Immediately following the session, the Cancer Immunology Working Group (CIMM) has set up one-on-one roundtable tutorials with experts in the field; this session will be held from 10:00 a.m.-12:00 p.m., in the Liberty Ballroom (Level 3), of the Philadelphia Marriott Downtown for participants who are interested in learning more.

8:00 a.m.	**Microbiome, inflammation and cancer** Giorgio Trinchieri, National Cancer Institute-Frederick, Frederick, MD
8:25 a.m.	**Discussion**

8:30 a.m.	**Innate immunity and cancer** Todd A. Fehniger, Washington University School of Medicine, St. Louis, MO	**9:00 a.m.**	**Proteogenomic analysis of colon tumors and cell lines** Robbert J.C. Slebos, Vanderbilt University, Nashville, TN
8:55 a.m.	**Discussion**	**9:25 a.m.**	**Discussion**
9:00 a.m.	**Neoantigens and immunotherapy of cancer** Ton Schumacher, Netherlands Cancer Institute, Amsterdam, The Netherlands	**9:30 a.m.**	**Dissecting signaling pathways in cancer using proteomics** Akhilesh Pandey, Johns Hopkins University, Baltimore, MD
9:25 a.m.	**Discussion**	**9:55 a.m.**	**Discussion**
9:30 a.m.	**Checkpoint inhibitors and clinical application in melanoma** Jeffrey S. Weber, Moffitt Cancer Center and Research Institute, Tampa, FL		
9:55 a.m.	**Discussion**		

Room 118, Pennsylvania Convention Center

What Can Proteomics Teach Us That Genetics Cannot?

Co-Chairpersons: Daniel C. Liebler, Vanderbilt University, Nashville, TN; Bing Zhang, Vanderbilt University School of Medicine, Nashville, TN

The emerging wave of genomics data for human cancers presents the formidable challenge of connecting genomic alterations to tumor phenotypes. Proteomics technologies provide a critical layer of information to bridge this gap. This session describes applications of proteomics that enable interpretation of genomic data and provide insights beyond the boundaries of genomics. A key theme is the integration of genomic and proteomic data to better understand cancer. Speakers will highlight key technology platforms and advances and bioinformatics tools to integrate genomic and proteomic data. Use of these approaches will be described in applications to proteogenomic analysis of colon cancer and the characterization of cancer signaling networks.

8:00 a.m.	**State of the art in proteomics technologies** Daniel C. Liebler, Vanderbilt University, Nashville, TN
8:25 a.m.	**Discussion**
8:30 a.m.	**Leveraging the synergy between genomics and proteomics through bioinformatics** Bing Zhang, Vanderbilt University School of Medicine, Nashville, TN
8:55 a.m.	**Discussion**

METHODS WORKSHOPS

Saturday, 8:00 a.m.-10:00 a.m.

Room 201, Pennsylvania Convention Center

Design and Method Workshop for Clinical Trials and Population Studies, Part 1: Design and Implementation of Innovative Clinical Trials for Targeted Therapies

Chairperson: J. Jack Lee, The University of Texas MD Anderson Cancer Center, Houston, TX

Rapid advancements in cancer biology, immunology, genomics, and treatment development demand innovative methods to identify better therapies and the most appropriate population for a given therapy in a timely, efficient, accurate, and cost-effective way. This one-day educational workshop has four parts that share the theme of better patient selection, treatment evaluation, discovery and validation of predictive markers, and statistical design and analysis in support of delivering precision medicine to each patient. Part 1 provides investigators with an overview of the design and analysis of clinical trials in light of today's challenges in developing targeted therapies. The session introduces the best practice in molecular diagnostics and its interface with targeted therapy trials. Enhancements to the success of a study through efficient design and flexible trial conduct will be illustrated, including the enrichment and adaptive enrichment of a study population, as well as Bayesian adaptive trial designs. Perspectives on the past, present, and future of targeted therapy development will be given. Drs. J. Jack Lee and Edith A. Perez are the organizers of this session.

8:00 a.m. **Molecular diagnostics: Interface with targeted therapeutics clinical trials**
Russell R. Broaddus, The University of Texas MD Anderson Cancer Center, Houston, TX

8:20 a.m. **Discussion**

8:30 a.m. **Enrichment and adaptive enrichment designs for clinical trials with targeted therapies**
Richard M. Simon, National Cancer Institute, Bethesda, MD

8:50 a.m. **Discussion**

9:00 a.m. **We learn as we go: Bayesian adaptive designs for efficient and flexible clinical trials**
J. Jack Lee, The University of Texas MD Anderson Cancer Center, Houston, TX

9:20 a.m. **Discussion**

9:30 a.m. **Perspectives on trial designs: The past, present, and future of the targeted therapy development**
Sumithra J. Mandrekar, Mayo Clinic, Rochester, MN

9:50 a.m. **Discussion**

Room 115, Pennsylvania Convention Center

Human Biospecimens in Cancer Research: Do You Know Where Your Samples Came From and Where They Have Been? Are You Analyzing Artifact Instead of Biology?

Chairperson: Carolyn C. Compton, Arizona State University, Scottsdale, AZ

This session will educate scientists about the quality requirements for human biospecimens that are destined for genomic or proteomic analysis. The session will review the biospecimen science data that demonstrates the effects of collection, handling, processing, and storage variables (preanalytical variables) on the biomolecular quality and composition of human tissues and blood and how those effects alter scientific analysis data in artifactual ways. The session will further review that steps that a being undertaken by the National Biomarker Development Alliance in partnership with the College of American Pathologists and other professional organizations to control, eliminate (where possible), and record key variables that have the greatest impact on specimen quality and analysis results. Speakers will include stakeholders from the public and private sectors in which the problem of human biopsecimen quality variation has a large detrimental impact on scientific and translational progress.

8:00 a.m. **"Garbage in" and cancer research**
Carolyn C. Compton, Arizona State University, Scottsdale, AZ

8:25 a.m. **Discussion**

8:30 a.m. **What a genomicist needs to know about clinical biospecimens**
Kenneth Bloom, Clarient, Inc., Aliso Viejo, CA

8:55 a.m. **Discussion**

9:00 a.m. **Human biospecimens for in vitro diagnostics: Regulatory considerations**
Yun-Fu Hu, U.S. Food and Drug Administration, Silver Spring, MD

9:25 a.m. **Discussion**

9:30 a.m.   **Sample suitability for studies with cancer proteomics**
Christopher Kinsinger, National Cancer Institute, Bethesda, MD

9:55 a.m.   **Discussion**

Room 204, Pennsylvania Convention Center
Methods for Pharmacogenomics Discovery and Interpretation

Chairperson: Angelique Whitehurst, UT Southwestern Simmons Comprehensive Cancer Center, Dallas, TX

Clinical responses to cancer treatment are frequently incomplete and notoriously unpredictable. The field of pharmacogenomics seeks to leverage genomic information to uncover molecular traits that influence the efficacy and toxicity of anticancer therapies. These studies also reveal new targets for drug discovery efforts. The purpose of this workshop is to provide an overview of the statistical methods used to identify polymorphisms predictive of adverse drug response, the approaches that uncover tumor-specific alterations that specify therapeutic efficacy, and the translation of these findings into patient-tailored treatment regimens.

8:00 a.m.   **Introduction**
Angelique Whitehurst, UT Southwestern Simmons Comprehensive Cancer Center, Dallas, TX

8:30 a.m.   **Statistical challenges and opportunities in pharmacogenetics**
Alison Motsinger-Reif, North Carolina State University, Raleigh, NC

8:55 a.m.   **Discussion**

9:00 a.m.   **Identification of genomic predictors of drug response by high-throughput cell line screening**
Cyril Benes, Massachusetts General Hospital Cancer Center, Charlestown, MA

9:25 a.m.   **Discussion**

9:30 a.m.   **Clinical implications of cancer genome sequencing**
Ramaswamy Govindan, Washington University School of Medicine, St. Louis, MO

9:55 a.m.   **Discussion**

Room 121, Pennsylvania Convention Center
Systems Approaches to Cancer

Chairperson: Chris Sander, Memorial Sloan Kettering Cancer Center, New York, NY

Advances in systems biology methods are contributing an increasing level of quantitative experimental-computational sophistication to basic and applied cancer research. This eclectic survey of current developments will illustrate the essential role of medium to large scale molecular profiling of cancer cells as a basis for modeling the response of cells to oncogenic alterations and therapeutic interventions. The discovery of therapeutic vulnerabilities, of mechanisms of drug resistance, of phenotypic diversity, and of effective combination therapies are fertile areas of systems approaches to cancer. Training in data-rich experimental technology and in mathematically sophisticated modeling is an excellent point of departure for a new generation of quantitively oriented cancer researchers.

8:00 a.m.   **Perturbation biology in cancer: Data-driven network models for the discovery of combination therapy**
Chris Sander, Memorial Sloan Kettering Cancer Center, New York, NY

8:25 a.m.   **Discussion**

8:30 a.m.   **Systematic elucidation of non-oncogene dependencies in human malignancies**
Andrea Califano, Columbia University, New York, NY

8:55 a.m.   **Discussion**

9:00 a.m.   **Statistical tools for the study of network adaptation: Implications in drug resistance and the design of combination therapies**
Michael J. Lee, University of Massachusetts Medical School, Worcester, MA

9:25 a.m.   **Discussion**

9:30 a.m.   **Single-cell proteomics to analyze cell-to-cell variability in tumors**
Grégoire Altan-Bonnet, Memorial Sloan Kettering Cancer Center, New York, NY

9:55 a.m.   **Discussion**

PROFESSIONAL ADVANCEMENT SESSION *(not eligible for CME credit)*

Saturday, 9:30 a.m.-4:00 p.m.

Grand Ballroom Salons G-L (Level 5), Philadelphia Marriott Downtown
Tenth Annual Undergraduate Student Caucus and Poster Competition
Organized by the Science Education Committee

Chairperson: Kathleen W. Scotto, Rutgers, The State University of New Jersey, New Brunswick, NJ

The Undergraduate Student Caucus and Poster Competition provides an opportunity for undergraduates to learn more about the exciting research being conducted in the cancer field, hear from investigators about educational pathways and career development, explore various career options in the cancer field, and compete for prizes while presenting their research. Poster competition winners will be awarded the AACR-Gary J. Miller Undergraduate Student Prizes for Cancer and Biomedical Research. First prize consists of $1,500 in funding to support the cost of participation in the AACR Annual Meeting 2015 in Philadelphia, PA. Second and third place will also receive monetary prizes. AACR members serve as judges for this competition, and we thank them for supporting the next generation of cancer researchers. Preregistration was encouraged; limited onsite registration may be available.

9:30 a.m.   **Registration**

10:00 a.m.   **Welcome**
Kathleen W. Scotto, Rutgers, The State University of New Jersey

10:10 a.m.   **Understanding Cancer**
Donald S. Coffey, Johns Hopkins University School of Medicine, Baltimore, MD

10:30 a.m.   **Message from a Cancer Advocate**
Cynthia Ryan, University of Alabama at Birmingham, Birmingham, AL

10:45 a.m.   **Special Remarks: Navigating the Annual Meeting**
Lewis C. Cantley, Sandra and Edward Meyer Cancer Center at Weill Cornell Medical College, New York, NY

11:00 a.m.   **Remarks from Lead Judge and Introduction of Judges**
Beverly Lyn-Cook, FDA-National Center for Toxicological Research, Jefferson, AR

11:15 a.m.   **Poster Session and Exhibits**

1:00 p.m.   **Break and Lunch Served**

1:30 p.m.   **Professional Development Panel and Q&A**
José G. Treviño, University of Florida, Gainesville, FL

Panelists:
Samuel Antwi, University of South Carolina, West Columbia, SC
Amanda Brinker, University of Kansas Medical Center, Kansas City, KS

3:00 p.m.   **Remarks from 2014 First Place Miller Prize Winner**
Malori A. Lankenau, The Ohio State University, Columbus, OH

3:10 p.m.   **Prize Distribution**

3:45 p.m.   **Closing Remarks and Evaluation**

EDUCATIONAL SESSION

Saturday, 10:00 a.m.-12:00 p.m.

Liberty Ballroom (Level 3), Philadelphia Marriott Downtown

Cancer Immunology for the Non-Immunologist - Tutorial

Chairperson: Dmitry I. Gabrilovich, The Wistar Institute, Philadelphia, PA

The Cancer Immunology Working Group (CIMM) will offer roundtable tutorials for attendees seeking information or advice on immunological topics and approaches related to their work. CIMM members will be at preassigned tables ready to promote dialogue and respond to questions from interested investigators. This session immediately follows the Tumor Immunology for Non-Immunologists Educational Session that will be held in the Grand Ballroom (300 Level), in the Pennsylvania Convention Center. The participants in that session as well as all other meeting attendees with immunology-based questions are encouraged to attend.

Immuno-gene therapy of cancer
Steven M. Albelda, Abramson Cancer Center of the University of Pennsylvania, Philadelphia, PA

Myeloid-derived suppressor cells
Vincenzo Bronte, University of Verona, Verona, Italy

Immunity to papillomavirus and cancer
Neil D. Christensen, Penn State University College of Medicine, Hershey, PA

The immune properties of extracellular matrix in tumor microenvironment
Mario P. Colombo, Fondazione IRCCS Institute Nazionale Tumori, Milan, Italy

Regulatory dendritic cells in the tumor microenvironment
Jose R. Conejo-Garcia, The Wistar Institute, Philadelphia, PA

Natural killer cells and cancer
Julie Y. Djeu, Moffitt Cancer Center and Research Institute, Tampa, FL

Chemokines and cancer therapy
Steven M. Dubinett, David Geffen School of Medicine at UCLA, Los Angeles, CA

Natural killer cells
Todd A. Fehniger, Washington University School of Medicine, St. Louis, MO

Vaccines for cancer prevention
Olivera J. Finn, University of Pittsburgh School of Medicine, Pittsburgh, PA

Immune suppressive microenvironment
Dmitry I. Gabrilovich, The Wistar Institute, Philadelphia, PA

Regulation of tumor microenvironment
Tim F. Greten, National Cancer Institute, Bethesda, MD

Inflammation and cancer: How the immune system can promote tumor development and progression
Sergei I. Grivennikov, Fox Chase Cancer Center, Philadelphia, PA

Immunotherapy of pancreatic cancer
Elizabeth M. Jaffee, Johns Hopkins University, Baltimore, MD

Therapeutic cancer vaccines
Samir N. Khleif, Georgia Regents University Cancer Center, Augusta, GA

Metabolism of myeloid cells
Augusto C. Ochoa, Louisiana State University Health Sciences Center, New Orleans, LA

Tumor-infiltrating lymphocytes in treatment of melanoma
Shari A. Pilon-Thomas, Moffitt Cancer Center and Research Institute, Tampa, FL

Indoleamine 2,3-dioxygenase (IDO) in cancer therapy
George C. Prendergast, Lankenau Institute for Medical Research, Wynnewood, PA

Fibroblast targeting in therapy of cancer
Ellen Puré, University of Pennsylvania School of Veterinary Medicine, Philadelphia, PA

Neoantigens on tumor cells
Ton Schumacher, Netherlands Cancer Institute, Amsterdam, The Netherlands

Dendritic cells
Michael R. Shurin, University of Pittsburgh Medical Center, Pittsburgh, PA

Microbiota and cancer
Giorgio Trinchieri, National Cancer Institute-Frederick, Frederick, MD

Novel therapeutic strategies not involving checkpoint inhibitors
Robert H. Vonderheide, Abramson Cancer Center of the University of Pennsylvania, Philadelphia, PA

Checkpoint proteins and their therapeutic biomarkers
Jeffrey S. Weber, Moffitt Cancer Center and Research Institute, Tampa, FL

Chemotherapy and immune response
Laurence Zitvogel, Institute Gustave-Roussy, Villejuif, France

EDUCATIONAL SESSIONS

Saturday, 10:15 a.m.-12:15 p.m.

Room 115, Pennsylvania Convention Center

Bench to Bedside and Back Again: Biology and Therapy of ALK and BRAF Cancers

Chairperson: D. Ross Camidge, University of Colorado Denver, Aurora, CO

Oncogenic activation of the ALK and BRAF pathways has been identified as the dominant driver in key subsets of cancer. Pharmacological inhibition of these pathways has produced both clinical successes and failures, with the specific molecular makeup of the tumor seeming to determine whether initial benefit occurs and the natural roles of these signaling molecules potentially determining some of the key side effects seen with drug inhibition. Even after initial benefit occurs, acquired resistance in the clinic occurs and is now being dissected on a molecular level leading to promising new approaches to prolong control of these diseases.

10:15 a.m.	**BRAF biology in health and disease** Richard M. Marais, Cancer Research UK Manchester Institute, Manchester, United Kingdom
10:40 a.m.	**Discussion**
10:45 a.m.	**ALK biology in health and disease** Ruth Palmer, Umeå University, Umeå, Sweden
11:10 a.m.	**Discussion**
11:15 a.m.	**BRAF inhibitors: Clinical activity across different cancers, innate and acquired resistance** Grant A. McArthur, Peter MacCallum Cancer Center, Melbourne, Australia
11:40 a.m.	**Discussion**
11:45 a.m.	**ALK inhibitors: Clinical activity across different cancers, innate and acquired resistance** D. Ross Camidge, University of Colorado Denver, Aurora, CO
12:10 p.m.	**Discussion**

Terrace Ballroom I (400 Level), Pennsylvania Convention Center

Biomarkers for Solid Tumors in a Post-TCGA World

Chairperson: Jorge S. Reis-Filho, Memorial Sloan Kettering Cancer Center, New York, NY

The Cancer Genome Atlas and other large scale massively parallel sequencing endeavors have resulted in the characterization of the repertoire of somatic genetic alterations, epigenetic changes and transcriptomic profiles of human malignancies. These findings are leading to profound changes in the taxonomy of human cancers. Whilst subtypes of cancers from the same anatomical site have now been shown to be driven by distinct genetic alterations, tumors from distinct anatomical sites and seemly unrelated have been found to be underpinned by similar repertoires of mutations and/or copy number alterations. Furthermore, massively parallel sequencing endeavors have provided direct evidence of intra-tumor genetic heterogeneity in solid malignancies, and demonstrated that even some driver genetic alterations may be present only in subclones of a tumor. In this session, we will contextualize the impact of intra- and intertumor genetic heterogeneity and the diversity of mutations in solid tumors on the development and validation of biomarkers, use of gene signatures, and genomic features for prognostication and prediction.

10:15 a.m.	**The impact of intra- and intertumor genetic heterogeneity on the development of biomarkers** Jorge S. Reis-Filho, Memorial Sloan Kettering Cancer Center, New York, NY
10:40 a.m.	**Discussion**
10:45 a.m.	**New diagnostic, prognostic, and predictive biomarkers in sarcomas** Jonathan A. Fletcher, Brigham and Women's Hospital, Boston, MA
11:10 a.m.	**Discussion**
11:15 a.m.	**The role of gene expression profiling in the post-TCGA world** Britta Weigelt, Memorial Sloan Kettering Cancer Center, New York, NY
11:40 a.m.	**Discussion**
11:45 a.m.	**Genomic aberrations as biomarkers in breast cancer** Anne-Lise Børresen-Dale, Norwegian Radium Hospital, Oslo, Norway
12:10 p.m.	**Discussion**

Room 204, Pennsylvania Convention Center
Computational and Functional Modeling of Hot Big Data

Chairperson: Daniel S. Peeper, Netherlands Cancer Institute, Amsterdam, The Netherlands

In recent years, we have experienced a spectacular increase in the power and versatility of both analytical and modeling platforms. This ranges from new technologies to decipher nucleic acid sequences and identify proteins at great depth and decreasing cost, to effective methods to functionally mine the genome in vitro and in animal models. The typical output of such approaches is "big data", which comes with several challenges. The topic that the speakers in this session will cover is the functional annotation of big data. For example, you will get insight into data-driven identification of synthetic lethality networks to identify cancer-specific vulnerabilities on a genome-wide scale. Furthermore, we will discuss high-throughput shRNA and CRISPR-Cas9 genetic perturbation screens in vitro and in vivo, aiming to uncover novel cancer genes as well as targets amenable to therapeutic intervention. Finally, large-scale mouse knockout programs will be presented that allow for identification of tumor modifiers.

10:15 a.m. **Large-scale genetic perturbations to reveal cancer vulnerabilities in vitro and in vivo**
Daniel S. Peeper, Netherlands Cancer Institute, Amsterdam, The Netherlands

10:40 a.m. **Discussion**

10:45 a.m. **Analyzing large genomic, phenotypic, and clinical data identifies novel synthetic lethal cancer drug targets**
Eytan Ruppin, Center for Bioinformatics and Computational Biology (CBCB), College Park, MD

11:10 a.m. **Discussion**

11:15 a.m. **Large-scale genetic screens in mice: Pathways, drivers, and drug resistance**
David J. Adams, Wellcome Trust Sanger Institute, Cambridge, MA

11:40 a.m. **Discussion**

11:45 a.m. **Genome-scale CRISPR/Cas9 screening: Technology and applications**
Neville Sanjana, Broad Institute of MIT and Harvard, Cambridge, MA

12:10 p.m. **Discussion**

Terrace Ballroom IV (400 Level), Pennsylvania Convention Center
Detecting Treatment Response and Investigating the Tumor Microenvironment Using Magnetic Resonance Imaging

Chairperson: Kevin M. Brindle, Cancer Research UK Cambridge Research Institute, Cambridge, United Kingdom

MRI can be used to assess tumor morphology, detecting treatment response through changes in tumor size. MRI can also be used to assess aspects of tumor biology, which can be used to both enhance detection of treatment response and to investigate the tumor microenvironment. This session will examine some of these MRI methods. Chemical exchange saturation transfer (CEST) imaging measurements of amide proton exchange can be used to rapidly monitor treatment response and to separate recurrent brain tumors from treatment necrosis, and sugars can be used as contrast agents for tumor diagnosis. Diffusion-weighted (DW)-MRI can be used to assess treatment-induced loss of tumor cellularity through quantification of changes in tumor water mobility and dynamic contrast agent enhanced (DCE)-MRI can be used as a sensitive pharmacodynamic marker of angiogenesis. The massive gain in sensitivity afforded by hyperpolarization techniques means that metabolic fluxes in tumors can be assessed using hyperpolarized 13C-labeled cell substrates.

10:15 a.m. **Chemical exchange saturation transfer (CEST) imaging for detecting treatment response and more**
Peter C. M. van Zijl, Johns Hopkins University School of Medicine, Baltimore, MD

10:40 a.m. **Discussion**

10:45 a.m. **Application of diffusion-weighted MRI for cancer response assessment**
Brian D. Ross, University of Michigan School of Medicine, Ann Arbor, MI

11:10 a.m. **Discussion**

11:15 a.m. **DCE-MRI as a cancer biomarker**
Peter Choyke, National Cancer Institute, Bethesda, MD

11:40 a.m. **Discussion**

11:45 a.m. **Imaging of tumor metabolism with hyperpolarized 13C-labeled cell metabolites**
Kevin M. Brindle, Cancer Research UK Cambridge Research Institute, Cambridge, United Kingdom

12:10 p.m. **Discussion**

EDUCATIONAL SESSIONS

Saturday, 10:15 a.m.-12:15 p.m.

Room 121, Pennsylvania Convention Center

Epidemiology of Cancer Prognosis and Outcomes

Chairperson: Lawrence H. Kushi, Kaiser Permanente, Oakland, CA

A growing body of research uses epidemiologic observational study designs to investigate factors influencing cancer prognosis and outcomes. Such studies were pioneered by the investigation of late effects of cancer diagnosis and treatment in pediatric cancers. These studies have demonstrated that people with pediatric cancers are at risk of various chronic diseases, partly as a function of therapies received. Prospective studies of cancer etiology have also been used as platforms for studies that follow cancer cases arising in those cohorts. Such studies have provided substantial insight into the role of lifestyle factors such as diet and physical activity in colorectal, breast, and other cancers. More recently, epidemiologic studies have been designed specifically to study outcomes after cancer diagnosis, enrolling patients with cancer and following them through recurrence and death. This session will provide examples and summarize the important contributions that epidemiologic studies are making in understanding cancer outcomes.

10:15 a.m.	**Long-term outcomes in adult survivors of childhood cancer** Leslie L. Robison, St. Jude Children's Research Hospital, Memphis, TN
10:40 a.m.	**Discussion**
10:45 a.m.	**Studies in the role of diet and lifestyle in colorectal cancer survival** Charles S. Fuchs, Dana-Farber Cancer Institute, Boston, MA
11:10 a.m.	**Discussion**
11:15 a.m.	**Mechanisms linking lifestyle to prognosis: From fitness to omics** Cornelia M. Ulrich, Huntsman Cancer Institute, University of Utah, Salt Lake City, UT
11:40 a.m.	**Discussion**
11:45 a.m.	**Epidemiologic studies of cancer prognosis in integrated health care settings** Lawrence H. Kushi, Kaiser Permanente, Oakland, CA
12:10 p.m.	**Discussion**

Room 113, Pennsylvania Convention Center

From Chemistry to the Clinic: Pathways for Drug Discovery and Development, Part 2: Discovery and Development of Potent Drug Conjugates: From Basic Principles to Clinically Approved Drugs

Chairperson: Peter D. Senter, Seattle Genetics, Inc., Bothell, WA

A great deal of interest has surrounded antibody drug conjugates for cancer therapy, with two recently approved drugs and more than 50 in various stages of clinical development. The field has advanced greatly over the past several years due to the identification of novel cytotoxic payloads and conditionally stable linkers for targeted delivery, together with new conjugation technologies that allow for preservation of the pharmacologic and pharmacokinetic properties of the carrier proteins. This session will overview many of the theoretical and experimental parameters that impact drug delivery with carriers that range from constrained small peptides that rapidly extravasate to antibodies that have extended circulation times. Several new targeted drugs will be described, and a summary of advancements in the field will be provided.

10:15 a.m.	**Theoretical and experimental limits in macromolecular-based tumor targeting** Karl Dane Wittrup, Massachusetts Institute of Technology, Cambridge, MA
10:40 a.m.	**Discussion**
10:45 a.m.	**Tumor targeting with engineered peptides and peptide-Fc fusions** Jennifer R. Cochran, Stanford University, Stanford, CA
11:10 a.m.	**Discussion**
11:15 a.m.	**Applying medicinal chemistry core competencies to the discovery of next-generation antibody drug conjugates** Christopher O'Donnell, Pfizer, Inc., Groton, CT
11:40 a.m.	**Discussion**
11:45 a.m.	**Potent antibody drug conjugates for cancer therapy** Peter D. Senter, Seattle Genetics, Inc., Bothell, WA
12:10 p.m.	**Discussion**

Room 103, Pennsylvania Convention Center
Is the Stroma Tumor Suppressive or Tumor Promoting?

Chairperson: Valerie M. Weaver, UCSF Medical Center, San Francisco, CA

Tumor cells exist within a constantly evolving cellular stromal microenvironment composed of stromal cells from the vasculature, immune cells, adipocytes, and cancer-associated fibroblasts. Structures generated by the cellular stroma and soluble factors secreted by these cellular constituents compromise the immune response, stimulate tumor cell growth, enhance survival, and induce migration to promote malignant transformation and potentiate metastasis. Furthermore, malignant transformation is also accompanied by increased deposition and remodeling of the extracellular matrix which contributes to tumor fibrosis and tissue stiffening that physically destroy tissue integrity and facilitate invasion and migration directly or enhance or corrupt the behavior of the cellular stroma to foster tumor progression and aggression. Consistently, in experimental models normalizing the behavior of the cellular stroma or preventing aberrant extracellular matrix remodeling can repress malignancy. Yet, efforts to translate these findings to the clinical have been mixed and in many instances disappointing. To this end, recent experimental data emphasize the complexity of the tumor stroma, including its heterogeneity, rapid evolution, and tissue specificity and the findings emphasize that in some instances the stromal response may actually temper tumor evolution. These data suggest that the desmoplastic response in a tumor is highly context and time dependent and may both enhance and restrict tumor progression. In this symposium the speakers will summarize the current status of stromal-epithelial interactions in cancer and they will discuss the most recent findings regarding the pro- and antitumorigenic properties of the tumor microenvironment emphasizing experimental approaches and clinical relevance.

10:15 a.m.   **Introduction**
Valerie M. Weaver, UCSF Medical Center, San Francisco, CA

10:15 a.m.   **Immune privilege by T cell exclusion in the tumor microenvironment: The definitive T cell checkpoint**
Douglas T. Fearon, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY; Weill Cornell Medical College, New York, NY

10:40 a.m.   **Discussion**

10:45 a.m.   **Complex tumor-stroma interactions in pancreatic cancer**
Ben Z. Stanger, Abramson Cancer Center of the University of Pennsylvania, Philadelphia, PA

11:10 a.m.   **Discussion**

11:15 a.m.   **The functional contribution of stroma and tumor immunity in PDAC**
Valerie Lebleu, The University of Texas MD Anderson Cancer Center, Houston, TX

11:40 a.m.   **Discussion**

11:45 a.m.   **It is the context: Extracellular matrix remodeling promotes or restricts cancer progression depending on tissue and driving oncogenes**
Mikala Egeblad, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

12:10 p.m.   **Discussion**

EDUCATIONAL SESSION

Saturday, 10:15 a.m.-12:15 p.m.

Room 114, Pennsylvania Convention Center

Pediatric Low-Grade Gliomas: Silent But Still Deadly

Chairperson: Samuel C. Blackman, Juno Therapeutics, Seattle, WA

Pediatric low-grade gliomas (LGGs) are the most common pediatric brain tumor. Despite their low-grade nature, LGGs can cause significant morbidity and mortality in children afflicted with them. Current therapeutic approaches have been limited for children with non-resectable disease. Early efforts to identify mutations showed these tumors were mostly "silent," which limited opportunities for application of targeted therapeutics. The lack of genetic lesions contrasts with a unique biology, including tumors that frequently undergo senescence, and the far lower risk of malignant transformation compared to adult LGGs. Recently, next-generation sequencing has revealed genetic lesions that may be actionable. This session will provide an overview of the biology of LGGs (Jones), progress and challenges in the treatment of these tumors, including long-term toxicity (Mueller), attempts at defining new mutations that could serve as therapeutic targets (Stiles), and future treatment opportunities within the developmental therapeutic pipeline (Blackman).

10:15 a.m. **Pediatric low-grade glioma: An overview of biology and molecular diagnostic, prognostic markers**
David T.W. Jones, German Cancer Research Center, Heidelberg, Germany

10:40 a.m. **Discussion**

10:45 a.m. **Past and future challenges for the clinical care of children with low-grade gliomas**
Sabine Mueller, University of California, San Francisco, CA

11:10 a.m. **Discussion**

11:15 a.m. **Targeted therapies for pediatric low-grade astrocytomas**
Charles D. Stiles, Dana-Farber Cancer Institute, Boston, MA

11:40 a.m. **Discussion**

11:45 a.m. **Therapeutic opportunities for pediatric low-grade gliomas: An industry perspective**
Samuel C. Blackman, Juno Therapeutics, Seattle, WA

12:10 p.m. **Discussion**

METHODS WORKSHOPS

Saturday, 10:15 a.m.-12:15 p.m.

Room 201, Pennsylvania Convention Center

Design and Method Workshop for Clinical Trials and Population Studies, Part 2: Design Considerations for Expanding the Success of Immunotherapy Trials

Chairperson: Edith A. Perez. Mayo Clinic, Ponte Vedra Beach, FL

Rapid advancements in cancer biology, immunology, genomics, and treatment development demand innovative methods to identify better therapies and the most appropriate population for a given therapy in a timely, efficient, accurate, and cost-effective way. This one-day educational workshop has four parts that share the theme of better patient selection, treatment evaluation, discovery and validation of predictive markers, and statistical design and analysis in support of delivering precision medicine to each patient. Part 2 provides investigators with an overview of the complexity of the immune system and its implication for designing successful immunotherapy trials. The impact of recently reported immunotherapy trials and the lessons learned will be reviewed. To expand the success of immunotherapy trials, it is critical to choose the right parameters, biomarkers, and endpoints to measure the immuno-response. Special statistical considerations for the design and analysis of cancer immunotherapy trials will be provided. Drs. J. Jack Lee and Edith A. Perez are the organizers of this session.

10:15 a.m.   **Complexity of immune system and its implication on designing successful immunotherapy trials**
Edith A. Perez, Mayo Clinic, Ponte Vedra Beach, FL

10:35 a.m.   **Discussion**

10:45 a.m.   **Impact of recently reported immunotherapy trials: What have we learned?**
Mario Sznol, Yale Cancer Center, New Haven, CT

11:05 a.m.   **Discussion**

11:15 a.m.   **Choosing the right parameters, biomarkers, endpoints in measuring the immuno-response**
Axel Hoos, GlaxoSmithKline, Collegeville, PA

11:35 a.m.   **Discussion**

11:45 a.m.   **Statistical issues on the design and analysis of cancer immunotherapy trials**
Tai-Tsang Chen, Bristol-Myers Squibb, Wallingford, CT

12:05 p.m.   **Discussion**

Room 118, Pennsylvania Convention Center

How and When to Use Chemical Probes

Chairperson: Valeria R. Fantin, Pfizer, Inc., San Diego, CA

The use of well-characterized chemical probes has helped increase our understanding of a wide range of fundamental processes and mechanisms in cancer biology. It is clear that chemical probes are complementary to standard genetic tools used in exploratory biology. In the context of drug discovery, they provide a means to assess whether a potential therapeutic target is druggable, to establish the relationship between target engagement and biological outcome, and to dissect detailed molecular mechanism of action. Chemical probes have also helped to identify parameters related to drug sensitivity and resistance, which supports the preclinical prediction of patient populations most likely to respond to drug treatment. When combined to genotypic data, small molecule probes enable the interrogation of cancer cell line panels and preclinical tumor models for genotype-related vulnerabilities and synthetic lethal interactions. This session will cover new advances in chemical probe development and will provide examples of unique insights derived by the use of chemical probes.

10:15 a.m.   **Chemical probes in exploratory biology**
Valeria R. Fantin, Pfizer, Inc., San Diego, CA

10:40 a.m.   **Discussion**

10:45 a.m.   **Chemical tools for the study of individual protein kinases**
Kevan M. Shokat, University of California and HHMI, San Francisco, CA

11:10 a.m.   **Discussion**

11:15 a.m.   **Chemical probes to investigate epigenetic regulators**
Cheryl Arrowsmith, Princess Margaret Cancer Centre, Toronto, ON, Canada

11:40 a.m.   **Discussion**

11:45 a.m.   **Cancer and chemical biology**
James E. Bradner, Dana-Farber Cancer Institute, Boston, MA

12:10 p.m.   **Discussion**

METHODS WORKSHOPS

Saturday, 10:15 a.m.-12:15 p.m.

Grand Ballroom (300 Level), Pennsylvania Convention Center

Large-Scale Functional Genomic Screens: In Need of Controls?

Chairperson: Roderick L. Beijersbergen, Netherlands Cancer Institute, Amsterdam, The Netherlands

The continuous development and improvement of tools that allow for large-scale perturbation of gene expression have led to a widespread adoption of these technologies for functional genomic screening in mammalian cells. In particular, pooled collections of shRNA or CRISPR reagents have been applied for the identification of novel drug targets, the understanding of resistance, and the discovery of effective combination therapies. With the increased use of these technologies it has become crucial to establish ways to assess and improve the performance of individual screens and to allow comparison of different screens. The implementation of appropriate sets of controls will be crucial for benchmarking different strategies for analysis and hit selection. This workshop will focus on the different technologies to perform and interpret large-scale functional genomic screens including shRNA, CRISPR, and haploid-screens. We will address the development and implementation of controls in large-scale screens to increase their potential to discover novel treatment strategies.

10:15 a.m.   **On the use and selection of controls for pooled shRNA screens**
Roderick L. Beijersbergen, Netherlands Cancer Institute, Amsterdam, The Netherlands

10:45 a.m.   **Discussion**

10:55 a.m.   **Retooling CRISPR to turn genes on and off**
Luke Gilbert, University of California, San Francisco, CA

11:25 a.m.   **Discussion**

11:35 a.m.   **The art and design of haploid genetic screens in human cells**
Thijn Brummelkamp, Netherlands Cancer Institute, Amsterdam, The Netherlands

12:05 p.m.   **Discussion**

Terrace Ballroom II-III (400 Level), Pennsylvania Convention Center

Organoids

Chairperson: Hans Clevers, Hubrecht Institute, Utrecht, The Netherlands

In recent years, rapid strides have been made in the discovery of organ stem cells. This has been followed by the definition of culture conditions that allow the long-term expansion of these stem cells and their progeny from biopsies or surgical specimens. It is now possible to culture healthy and diseased (cancer) tissue from the same individual, allowing functional analyses in vitro such as the determination of drug sensitivity. This technology provides an exciting new platform to study cancer biology and for drug development. Organoids hold the promise to fill the gap between DNA/RNA sequencing and patient trials.

10:15 a.m.   **Modeling of colorectal cancer using CRISPR/Cas9-mediated engineering of human intestinal organoids**
Toshiro Sato, Keio University School of Medicine, Tokyo, Japan

10:40 a.m.   **Discussion**

10:45 a.m.   **Next-generation cell culture for the functional analysis of human tumors**
Richard Schlegel, Georgetown University Medical School, Washington, DC

11:10 a.m.   **Discussion**

11:15 a.m.   **Organoid cultures from benign and malignant prostate epithelium**
Yu Chen, Memorial Sloan Kettering Cancer Center, New York, NY

11:40 a.m.   **Discussion**

11:45 a.m.   **Growing epithelial organoids from internal organs and their cancers**
Hans Clevers, Hubrecht Institute, Utrecht, The Netherlands

12:10 p.m.   **Discussion**

Room 120, Pennsylvania Convention Center

What Can Pathology Teach The Modern Cancer Biologist?

Chairperson: David Huntsman, BC Cancer Agency, Vancouver, BC, Canada

Pathology is the study of disease. In the clinical domain pathologists attempt to derive clinical impactful data from the study of patient derived specimens. Many of the concepts and tools as well as the expertise that underpins modern pathology practice can be informative for basic cancer biologists. Herein we will discuss, with examples, how the consideration of disease taxonomy and the quality of pathological annotation are a major determinant of the success of -omic and other research, how to optimally use immunohistochemistry for the evaluation of proteins in clinical samples, in particular how to technically and clinically validate immunohistochemical biomarkers and, lastly, how cell context specific model systems are essential for functional validation of mutations and other features in cancer.

10:15 a.m. Introduction
David Huntsman, BC Cancer Agency, Vancouver, BC, Canada

10:25 a.m. Immunohistochemistry and how to measure my protein of interest: Technical and clinical validation
Blake Gilks, Vancouver Coastal Health Research Institute, Vancouver, BC, Canada

10:55 a.m. Discussion

11:01 a.m. Pathology driven genomics to genomic driven pathology
David Huntsman, BC Cancer Agency, Vancouver, BC, Canada

11:31 a.m. Discussion

11:37 a.m. Pathology subtype specific model systems: Functional validation in the correct cellular context
Ronny I. Drapkin, University of Pennsylvania, Philadelphia, PA

12:07 p.m. Discussion

PROFESSIONAL ADVANCEMENT SESSION *(not eligible for CME credit)*

Saturday, 12:00 p.m.-5:00 p.m.

Grand Ballroom, Salons H-J, Philadelphia Marriott Downtown
Eighteenth Annual Grant Writing Workshop
Organized by the Associate Member Council (AMC)

Held annually, this year the intensive half-day workshop has been reformatted to allow all attendees to have a new special opportunity to hear directly from a diverse range of funding agencies and a patient advocate. Registrants will learn about funding and how to write a successful grant by listening to a series of presentations and interacting with senior scientists during roundtable discussions. Another new feature this year is roundtables specifically geared toward answering funding and grant writing questions from current physician-scientists, those with a general interest in clinical research, and international researchers' questions from Asia, Europe, and the U.K. This workshop is aimed towards Associate Members and nonmember graduate students, medical students and residents, and clinical and postdoctoral fellows with limited or no experience in preparing grant applications. Lunch will be provided. There is a $45 registration fee for AACR members and a $95 registration fee for nonmembers. This workshop is currently sold out; limited spots may be available onsite on a first-come, first-served basis. **#AACRGWW**

Introduction from a past attendee
Camille C. R. Ragin, Fox Chase Cancer Center, Philadelphia, PA

Getting funded: Where to begin and what to consider
Steven M. Dubinett, David Geffen School of Medicine at UCLA, Los Angeles, CA

An overview of grant writing basics: How to write a successful research proposal
Grant A. McArthur, Peter MacCallum Cancer Centre, East Melbourne, Australia

Preparing for submission and what to expect
Mary "Nora" L. Disis, University of Washington, Seattle, WA

Mini-Lectures
Joe W. Gray, Oregon Health and Science University Knight Cancer Institute, Portland, OR
Jennifer Rubin Grandis, University of California, San Francisco, CA
Mehmet Toner, Massachusetts General Hospital, Charlestown, MA
Susan L. Weiner, Children's Cause for Cancer Advocacy, Washington, DC
Jonathan S. Wiest, National Cancer Institute-CCT, Bethesda, MD

Roundtable Mentors
Mary-Ann Bjornsti, University of Alabama at Birmingham, Birmingham, AL
A. William Blackstock, Jr., Wake Forest University School of Medicine, Winston-Salem, NC
Mario P. Colombo, Fondazione IRCCS Inst. Nazionale Tumor, Milan, Italy
Mary "Nora" L. Disis, University of Washington, Seattle, WA
Steven M. Dubinett, David Geffen School of Medicine at UCLA, Los Angeles, CA
Manel Esteller, Bellvitge Biomedical Research Institute, Barcelona, Spain
Jennifer Rubin Grandis, University of California, San Francisco, CA
Joe W. Gray, Oregon Health and Science University Knight Cancer Institute, Portland, OR
Mien-Chie Hung, The University of Texas MD Anderson Cancer Center, Houston, TX
Stephen D. Hursting, University of North Carolina at Chapel Hill, Chapel Hill, NC
Charles Keller, Children's Cancer Therapy Development Institute, Fort Collins, CO
Murray Korc, Indiana University Simon Cancer Center, Indianapolis, IN
Andrea M. Mastro, Penn State University, University Park, PA
Suresh Mohla, National Cancer Institute-DCB, Bethesda, MD
Julia A. Newtown Bishop, University of Leeds, Leeds, United Kingdom
Selvarangan Ponnazhagan, University of Alabama at Birmingham, Birmingham, AL
Camille C. R. Ragin, Fox Chase Cancer Center, Philadelphia, PA
Paul S. Rennie, Vancouver Prostate Centre, Vancouver, BC, Canada
Andrea L. Richardson, Brigham & Women's Hospital, Boston, MA
Jeffrey M. Rosen, Baylor College of Medicine, Houston, TX
Victoria L. Seewaldt, Duke University Medical Center, Durham, NC
Makoto Mark Taketo, Kyoto University Graduate School of Medicine, Kyoto, Japan
Danny R. Welch, University of Kansas Cancer Center, Kansas City, KS
Jonathan S. Wiest, National Cancer Intitute-CCT, Bethesda, MD
Christopher S. Williams, Vanderbilt University School of Medicine, Nashville, TN

REGULATORY SCIENCE AND POLICY SESSION

Saturday, 1:00 p.m.-2:30 p.m.

Room 105, Pennsylvania Convention Center

The Past, Present, and Future of FDA Regulation of Next-Generation Sequencing (NGS)

Chairperson: David Litwack, U.S. Food and Drug Administration, Silver Spring, MD

In vitro diagnostic tests that utilize NGS to identify cancer-causing mutations in patients are rapidly integrating into both research and clinical practice in the field of oncology. To ensure that these tests are safe and effective, scientists, physicians, and clinical lab directors should understand the regulations that govern their development and use, whether for research or as part of clinical care. In this session, I will discuss FDA regulations governing the use of NGS tests in clinical investigations and clinical practice, lessons learned from review of previous NGS tests by FDA, and future policy directions. I will also present outcomes from an FDA-sponsored workshop intended to consider new concepts in the regulation of NGS tests that will advance precision medicine.

Speaker:

David Litwack, U.S. Food and Drug Administration, Silver Spring, MD

EDUCATIONAL SESSIONS

Saturday, 1:00 p.m.-3:00 p.m.

Room 114, Pennsylvania Convention Center
Aspirin, NSAIDS, and Cancer: New Opportunities

Chairperson: Raymond N. DuBois, Biodesign Institute of Arizona State University, Tempe, AZ

It has been known for over two decades that use of aspirin and NSAIDS leads to a reduction in cancer risk, especially for those at risk for colon cancer. More recently 600 mg of aspirin daily was shown to reduce the overall cancer incidence for patients with Lynch Syndrome (HNPCC). This session will focus on recent developments delineating the pathways involved in NSAID inhibition and the role of inflammatory mediators such as PGE2 in cancer progression. One known concern with use of some NSAIDs is their increased risk for cardiovascular side effects. Development of safer approaches for using these drugs will be discussed as well as utilizing COX-2 as an early target for cancer detection.

1:00 p.m.   **PGE2 promotes cancer progression by modulation of cells in the tumor microenvironment**
Raymond N. DuBois, The Biodesign Institute at Arizona State University, Tempe, AZ

1:25 p.m.   **Discussion**

1:30 p.m.   **15-PGDH: A key regulator in human colon carcinogenesis**
Sanford D. Markowitz, Case Western Reserve University, Cleveland, OH

1:55 p.m.   **Discussion**

2:00 p.m.   **Safer approaches to aspirin and NSAIDs use in cancer prevention**
Chinthalapally V. Rao, University of Oklahoma Health Sciences Center, Oklahoma City, OK

2:25 p.m.   **Discussion**

2:30 p.m.   **COX-2 as a target for early detection of cancer and targeted delivery of chemotherapeutics**
Lawrence J. Marnett, Vanderbilt University School of Medicine, Nashville, TN

2:55 p.m.   **Discussion**

Room 103, Pennsylvania Convention Center
Chemical Biology and Molecular Pharmacology

Chairperson: Olivia W. Rossanese, Vanderbilt University School of Medicine, Nashville, TN

Chemical biology is defined broadly as the use of chemical tools to perturb and study biologic systems. The application of small molecule probes to the study of cancer biology can reveal the specific molecular pharmacology driving target modulation and provides a unique opportunity to conduct sophisticated functional and temporal studies of target biology that are not possible with genetic approaches. These studies often occur within the framework of an ongoing drug discovery program, with the goal of discovering therapeutics to treat cancer. Therefore, small molecule tools are also used to validate the therapeutic importance of the target, confirm inhibition of the relevant function, and inform on potential mechanisms of resistance. This session will provide specific examples of the use of small molecules to provide mechanistic insight into target biology, target validation, compound action, and resistance.

1:00 p.m.   **Exploring ras signaling with small molecule activators of nucleotide exchange**
Olivia W. Rossanese, Vanderbilt University School of Medicine, Nashville, TN

1:25 p.m.   **Discussion**

1:30 p.m.   **Refining our understanding of therapeutic targets through comparative pharmacology**
Igor Vivanco, The Institute of Cancer Research, London, United Kingdom

1:55 p.m.   **Discussion**

2:00 p.m.   **Chemical probes for target (in)validation**
Philip Jones, The University of Texas MD Anderson Cancer Center, Houston, TX

2:25 p.m.   **Discussion**

2:30 p.m.   **Elucidating novel mechanisms of sensitivity and resistance to protein kinase and Hsp90 inhibitors**
Paul Workman, The Institute of Cancer Research, London, United Kingdom

2:55 p.m.   **Discussion**

Room 113, Pennsylvania Convention Center

From Chemistry to the Clinic: Pathways for Drug Discovery and Development, Part 3: New Opportunities in Epigenetic Therapies

Chairperson: Gary G. Chiang, AbbVie, North Chicago, IL

The explosion of research into epigenetics over the past few years has led to a growing appreciation of its roles in both normal biology and pathological processes. Epigenetics refers to heritable alterations in phenotype that do not arise from changes in the underlying DNA sequence, but instead are due to changes in chromatin "state" due to DNA methylation and/or histone post-translational modifications. These reversible chromatin modifications are mediated by three classes of effectors: "writers" (e.g., DNA methyltransferases, histone methyltransferases, and acetyltransferases), "erasers" (e.g., histone demethylases and deacetylases), and "readers" (e.g., bromodomains, WD40 domains). Given their fundamental effects on gene transcription, targeting epigenetic regulators within these classes may have broad therapeutic relevance to multiple diseases, such as cancer, inflammation, metabolic disorders, and neurological disorders. The speakers in this session will provide an overview of ongoing efforts to generate small molecule inhibitors against epigenetic targets in order to deepen our understanding of epigenetic processes and identify novel strategies for therapeutic intervention.

1:00 p.m.   **Introduction**
Gary G. Chiang, AbbVie, North Chicago, IL

1:30 p.m.   **Chemical probes for epigenetic proteins**
Paul Brennan, University of Oxford, Oxford, United Kingdom

1:55 p.m.   **Discussion**

2:00 p.m.   **Discovering chemical probes of histone methyltransferases**
H. Ümit Kaniskan, Icahn School of Medicine at Mt. Sinai, New York, NY

2:25 p.m.   **Discussion**

2:30 p.m.   **Discovery of EPZ015666: A first-in-class PRMT5 inhibitor with potent in vitro and in vivo activity**
Kenneth W. Duncan, Epizyme, Inc., Cambridge, MA

2:55 p.m.   **Discussion**

Room 120, Pennsylvania Convention Center

Intravital Imaging in Animal Models of Cancer

Chairperson: Paul Timpson, Garvan Institute of Medical Research, Darlinghurst, Australia

Cancer progression and metastasis occur in a complex three-dimensional environment, with reciprocal feedback from the surrounding host tissue and stroma governing cell behavior. Intravital (in vivo) imaging is providing new insights into how cells behave in their native microenvironment, thereby improving our understanding of the critical events that lead to progression, dissemination and spread of the primary tumor. Using various model systems, ranging from 3D-matrices, transparent zebrafish, and chicken embryos, to genetically engineered FRET mouse models and CARs imaging, we will highlight how intravital imaging is helping us to uncouple how tumor cell dissociation, invasion, and progression are controlled and how this is linked to the development of metastatic disease. We also explore properties of the three-dimensional tumor microenvironment that contribute to poor drug targeting in order to pinpoint critical barriers that impair efficient tumor targeting.

1:00 p.m.   **Imaging drug delivery, response and turnover in live tumors using intravital biosensor imaging**
Paul Timpson, Garvan Institute of Medical Research, Darlinghurst, Australia

1:20 p.m.   **Discussion**

1:24 p.m.   **Intravital imaging of mice expressing Förster resonance energy transfer (FRET) biosensors**
Michiyuki Matsuda, Kyoto University, Kyoto-shi, Japan

1:44 p.m.   **Discussion**

1:48 p.m.   **Intravital imaging of brain metastasis using transparent zebrafish and chicken models**
Richard L. Klemke, UCSD Moores Cancer Center, La Jolla, CA

2:08 p.m.   **Discussion**

2:12 p.m.   **Imaging cancer phenotypes and protein function in live animals**
Alan Serrels, Edinburgh Cancer Research UK Centre, Edinburgh, United Kingdom

2:32 p.m.   **Discussion**

2:36 p.m.   **Cancer invasion highways revealed by correlative intravital-3D scanning electronmicroscopy**
Peter Friedl, The University of Texas MD Anderson Cancer Center, Houston, TX

2:56 p.m.   **Discussion**

EDUCATIONAL SESSIONS

Saturday, 1:00 p.m.-3:00 p.m.

Room 204, Pennsylvania Convention Center
Mechanisms of Cancer Therapy Resistance

Chairperson: Joan S. Brugge, Harvard Medical School, Boston, MA

Despite dramatic advances in the treatment of cancer, therapy resistance remains the most significant hurdle in improving the outcome of cancer patients. In this session, we will discuss many different aspects of therapy resistance, including a summary of our current understanding of therapy-resistant tumor cell populations as well as analyses of the challenges associated with intratumoral heterogeneity and adaptive responses to targeted therapies.

1:00 p.m.   **Tumor heterogeneity and drug resistance**
Charles Swanton, Cancer Research UK London Research Institute, London, United Kingdom

1:30 p.m.   **Discussion**

1:40 p.m.   **Principles of resistance to targeted therapy**
Levi A. Garraway, Dana-Farber Cancer Institute, Boston, MA

2:10 p.m.   **Discussion**

2:20 p.m.   **Adaptive rewiring of signaling pathways driving drug resistance to targeted therapies**
Taru E. Muranen, Harvard Medical School, Boston, MA

2:50 p.m.   **Discussion**

Terrace Ballroom I (400 Level), Pennsylvania Convention Center
Metabolism Vulnerabilities in Cancer

Chairperson: Matthew G. Vander Heiden, MIT Koch Institute for Integrated Cancer Research, Cambridge, MA

The central pathways involved in cell metabolism are well known, and there is a growing appreciation that the regulation of these pathways is altered in cancer cells. Increasing evidence suggests that cancer cells can use a variety of nutrients in different contexts, but how specific fuels and pathways contribute to the energetic and biosynthetic needs of tumors is an area of active investigation. A better understanding of the metabolic vulnerabilities of cancer cells is critical to exploit altered

metabolism for new therapies, and this session will review our current understanding of different nutrient dependencies, including how glucose, serine, and autophagy are used to support tumor progression. The manner in which environmental context impacts metabolic state will also be discussed, including new insights into how oxygen levels impact metabolic regulation. Current methodologies to study metabolism with a focus on the use of mouse cancer models will be described, with particular consideration given to how emerging knowledge in this field could be translated to benefit patients.

1:00 p.m.   **Serine metabolism and cancer therapy**
Karen H. Vousden, Beatson Institute for Cancer Research, Glasgow, United Kingdom

1:25 p.m.   **Discussion**

1:30 p.m.   **Autophagy, metabolism, and cancer**
Eileen P. White, Rutgers-The Cancer Institute of New Jersey, New Brunswick, NJ

1:55 p.m.   **Discussion**

2:00 p.m.   **Hypoxia and tumor metabolism**
M. Celeste Simon, Abramson Family Cancer Research Institute, Philadelphia, PA

2:25 p.m.   **Discussion**

2:30 p.m.   **The role of glucose metabolism in cancer proliferation**
Matthew G. Vander Heiden, MIT Koch Institute for Integrated Cancer Research, Cambridge, MA

2:55 p.m.   **Discussion**

Room 121, Pennsylvania Convention Center
Network Medicine

Chairperson: Douglas A. Lauffenburger, Massachusetts Institute of Technology, Cambridge, MA

Systems biology has emerged as a conceptual and technical approach to study of biological problems in a manner that integrates a relatively large number of components, interactions, and processes with a goal of improved prediction capability for effects of molecular-level alterations or interventions on physiological operation and treatment of pathology. Key aspects of the approach are emphasis on multivariate and quantitative experimental

measurement across diverse contexts, with hypotheses for explanatory account of system behavior generated by computational "reverse-engineering" modeling and predictions for implications of these hypotheses generated by computational "forward-engineering" modeling. This session will present current ideas and methods in application to cancer-relevant problems, spanning a spectrum of experimental data types and computational analysis frameworks.

1:00 p.m.   **Proteomic analysis of reciprocal tumor-stroma signaling**
Claus Jorgensen, The Institute of Cancer Research, London, United Kingdom

1:25 p.m.   **Discussion**

1:30 p.m.   **Linking signaling pathways to transcriptional programs in tumors**
Christina Leslie, Memorial Sloan Kettering Cancer Center, New York, NY

1:55 p.m.   **Discussion**

2:00 p.m.   **Invasion-associated networks**
Alissa M. Weaver, Vanderbilt University Medical Center, Nashville, TN

2:25 p.m.   **Discussion**

2:30 p.m.   **Feedback and crosstalk in receptor tyrosine kinase networks**
Douglas A. Lauffenburger, Massachusetts Institute of Technology, Cambridge, MA

2:55 p.m.   **Discussion**

Room 119, Pennsylvania Convention Center
The Price of Cure: Long-Term Outcomes in Adult Survivors of Childhood Cancer

Chairperson: Paul C. Nathan, The Hospital for Sick Children, Toronto, ON, Canada

The majority of children diagnosed with cancer will survive their disease. Consequently, there are almost 400,000 survivors of childhood cancer in the U.S., a majority of whom are at risk for therapy-related chronic health conditions (late effects) and even premature mortality. As these children age into adulthood, their risk for cancer relapse fades, but late effects such as second malignant neoplasms and cardiovascular disease can have significant

health impacts. The treatment and patient-related risk factors (including genetic predisposition) for developing late effects are a focus of considerable research. As survivors age, late effects can "interact" with the normal processes of senescence, placing older survivors at significant risk for frailty, and potentially debilitating chronic illness – outcomes that may be addressed by lifestyle modification. Unfortunately, strategies to prevent or mitigate the development of late effects, such as risk-based surveillance, are often hampered by failure to transition survivors to knowledgeable adult health care providers, necessitating the development of novel methods for delivering appropriate heath care to this growing and vulnerable population.

1:00 p.m.   **A new chronic disease? The growing burden of adverse health outcomes in childhood cancer survivors**
Paul C. Nathan, The Hospital for Sick Children, Toronto, ON, Canada

1:25 p.m.   **Discussion**

1:30 p.m.   **Cardiovascular morbidity in childhood cancer survivors: From etiology to risk-reduction strategies**
Saro Armenian, City of Hope, Duarte, CA

1:55 p.m.   **Discussion**

2:00 p.m.   **Physiologic frailty in young adult survivors of childhood cancer**
Kirsten K. Ness, St. Jude Children's Research Hospital, Memphis, TN

2:25 p.m.   **Discussion**

2:30 p.m.   **Challenges in providing life-long risk adapted care to childhood cancer survivors**
Tara O. Henderson, University of Chicago Comer Children's Hospital, Chicago, IL

2:55 p.m.   **Discussion**

EDUCATIONAL SESSIONS

Saturday, 1:00 p.m.-3:00 p.m.

Grand Ballroom (300 Level), Pennsylvania Convention Center

Principles of Immunotherapy: Stepping on the Accelerator

Chairperson: Suzanne L. Topalian, Johns Hopkins Kimmel Comprehensive Cancer Center, Baltimore, MD

The immune response against cancer is modulated by the interplay between stimulatory and inhibitory factors. The net result is often immunosuppression within the tumor microenvironment, supporting tumor progression. Methods for overcoming this immunosuppression include activation of endogenous antitumor immune cells in situ by engaging co-stimulatory factors such as CD137, CD27, and OX40; vaccinating patients with the appropriate tumor antigens and optimal adjuvants to induce or enhance tumor-specific responses; and transferring tumor-specific lymphocytes that have been modified ex vivo to promote enhanced tumor killing potential. Combining these diverse modalities in synergistic treatment regimens based on preclinical data is anticipated to have greater impact than monotherapy approaches and is a focus of current clinical development.

1:00 p.m.	**Co-stimulatory receptors and ligands** Yong-Jun Liu, MedImmune, Bensalem, PA
1:25 p.m.	**Discussion**
1:30 p.m.	**Cancer vaccines** Nina Bhardwaj, Icahn School of Medicine at Mount Sinai, New York, NY
1:55 p.m.	**Discussion**
2:00 p.m.	**Tumor-infiltrating lymphocytes and genetically engineered T cells** James Chung-Yin Yang, National Cancer Institute, Bethesda, MD
2:25 p.m.	**Discussion**
2:30 p.m.	**Combination therapy based on immune modulation** Suzanne L. Topalian, Johns Hopkins Kimmel Comprehensive Cancer Center, Baltimore, MD
2:55 p.m.	**Discussion**

Terrace Ballroom IV (400 Level), Pennsylvania Convention Center

Role of Noncoding RNAs in Cancer

Chairperson: Carlo M. Croce, The Ohio State University Comprehensive Cancer Center, Columbus, OH

This session focuses on the role of microRNAs and other noncoding RNAs in the pathogenesis and progression of human cancer. The first talk concerns the mechanisms of microRNA action in cancer and how microRNAs are downstream targets of pathways involved in cancer causation. The second talk expands on the first and introduces the role of long noncoding RNAs in cancer. The third talk focuses on the role of microRNAs in drug sensitivity and resistance. Finally, the last talk introduces microRNA-based strategies to inhibit cancer growth.

1:00 p.m.	**Causes and consequences of noncoding RNA dysregulation** Carlo M. Croce, The Ohio State University Comprehensive Cancer Center, Columbus, OH
1:25 p.m.	**Discussion**
1:30 p.m.	**About Noam Chomsky DNA patterns: Noncoding RNAs and cancer patients** George A. Calin, The University of Texas MD Anderson Cancer Center, Houston, TX
1:55 p.m.	**Discussion**
2:00 p.m.	**MicroRNAs in lung tumorigenesis and response to chemotherapy** Michela Garofalo, Cancer Research UK Manchester Institute, Manchester, United Kingdom
2:25 p.m.	**Discussion**
2:30 p.m.	**MicroRNA-based strategies to combat cancer** Frank John Slack, BIDMC Cancer Center/Harvard Medical School, Boston, MA
2:55 p.m.	**Discussion**

Terrace Ballroom II-III (400 Level), Pennsylvania
Convention Center
Tumor Heterogeneity and Evolution

Chairperson: Carlo C. Maley, UCSF Helen Diller Family
Comprehensive Cancer Center, San Francisco, CA

One of the major challenges for both the measurement and
management of cancer is its heterogeneity. Recent studies
have revealed both extensive inter- and intratumor
heterogeneity at the genotypic and phenotypic levels.
Leaders in the field will discuss this challenge, its origins,
dynamics and clinical importance. They will also review
how we can best measure and deal with tumor
heterogeneity, particularly intratumor heterogeneity.

1:00 p.m. **Universal biomarkers: How to handle tumor
heterogeneity**
Carlo C. Maley, UCSF Helen Diller Family
Comprehensive Cancer Center,
San Francisco, CA

1:25 p.m. **Discussion**

1:30 p.m. **Heterogeneity of resistance to cancer therapy**
Ivana Bozic, Harvard University, Cambridge, MA

1:55 p.m. **Discussion**

2:00 p.m. **Determinants of phenotypic intratumor
heterogeneity: Integrative approach**
Andriy Marusyk, Dana-Farber Cancer
Institute, Boston, MA

2:25 p.m. **Discussion**

2:30 p.m. **Cancer clonal complexity and evolution at
the macro- and microheterogeneity scale**
Marco Gerlinger, Institute of Cancer
Research, London, United Kingdom

2:55 p.m. **Discussion**

METHODS WORKSHOPS

Saturday, 1:00 p.m.-3:00 p.m.

Room 115, Pennsylvania Convention Center
Advances and Applications of Single Cell Sequencing Technologies in Cancer Research

Chairperson: Nicholas E. Navin, The University of Texas MD Anderson Cancer Center, Houston, TX

In this workshop we will discuss the most recent developments in single cell genome and transcriptome sequencing methods. We will cover various technologies for isolating single cancer cells, whole-genome or transcriptome amplification, and next-generation sequencing analysis. We will discuss computational methods for analyzing large-scale single cell sequencing datasets and mitigating technical errors that confound data analysis. We will also discuss the myriad of biological applications that these tools have for studying complex processes in cancer, including invasion, clonal evolution, metastasis, and chemoresistance. Finally, we will discuss translational applications in the clinic, where single cell sequencing methods are likely to have a major impact on noninvasive monitoring, prognosis, early detection, and improving targeted therapy.

1:00 p.m. **Cancer genomics: One cell at a time**
Nicholas E. Navin, The University of Texas MD Anderson Cancer Center, Houston, TX

1:25 p.m. **Discussion**

1:30 p.m. **Molecular archaeology of cancer**
Peter Van Loo, The Francis Crick Institute, London, United Kingdom

1:55 p.m. **Discussion**

2:00 p.m. **MALBAC whole-genome amplification of single cancer cells**
Chenghang Zong, Baylor College of Medicine, Houston, TX

2:25 p.m. **Discussion**

2:30 p.m. **Single cell RNA sequencing of circulating tumor cells**
David T. Ting, Massachusetts General Hospital Cancer Center, Charlestown, MA

Room 108, Pennsylvania Convention Center
Cell Line Authentication: Improving the Reproducibility and Translatability of Preclinical Cancer Research

Chairperson: Leonard P. Freedman, Global Biological Standards Institute, Washington, DC

Cell line misidentification and contamination from other cells or microbes remain significant problems in preclinical cancer research, wasting resources and slowing the development of new medicines. The Global Biological Standards Institute is leading a multipartner effort to build awareness among cancer researchers of the importance of cell authentication and to actively change laboratory practices to reduce misidentification, mislabeling, and contamination of cancer cell lines, and to produce credible, reproducible, and translatable data and results. As a result of improved training and practices using standards for authentication and best practices for cell culture, 1) knowledge of why and how to perform cell authentication will improve, 2) research reproducibility problems involving cell lines will decrease, 3) millions of dollars in wasted research expenditures will be saved, and 4) translation time from bench to clinic to bedside will be decreased.

1:00 p.m. **Closing the reproducibility gap in cancer research with cell authentication**
Leonard P. Freedman, Global Biological Standards Institute, Washington, DC

1:25 p.m. **Discussion**

1:30 p.m. **Improving research reproducibility through education and training**
Vivian Siegel, Broad Institute of MIT and Harvard, Cambridge, MA

1:55 p.m. **Discussion**

2:00 p.m. **Cell line authentication to improve preclinical cancer research: Methods in cell line authentication, quality control, and annotation** *(not eligible for CME credit)*
Richard M. Neve, Genentech, Inc., South San Francisco, CA

2:25 p.m. **Discussion**

2:30 p.m.   **Consider the source: The importance of minimizing the degrees of separation between the cell line in your lab and its original source in authentication and reproducibility of results**
Stephen P. Ethier, Medical University of South Carolina, Charleston, SC

2:55 p.m.   **Discussion**

Room 201, Pennsylvania Convention Center
Design and Method Workshop for Clinical Trials and Population Studies, Part 3: Challenges of Genomics, Integromics, and Tumor Heterogeneity in Clinical Trial Designs

Chairperson: Kim-Anh Do, The University of Texas MD Anderson Cancer Center, Houston, TX

Rapid advancements in cancer biology, immunology, genomics, and treatment development demand innovative methods to identify better therapies and the most appropriate population for a given therapy in a timely, efficient, accurate, and cost-effective way. This one-day educational workshop has four parts that share the theme of better patient selection, treatment evaluation, discovery and validation of predictive markers, and statistical design and analysis in support of delivering precision medicine to each patient. Part 3 presents genomic research that, through multidisciplinary collaborations, produces methods of general applicability to clinical trials and data analysis. An overview of efficient statistical methodology for data integration in functional genetics, genomics, and proteomics will be given first. Subsequently, topics on novel clinical trial designs will be introduced, including: (i) The use of genomics to identify patient subgroups and imaging to measure response, versus trials that use imaging to infer genomic information for patient stratification, with application to brain tumors; (ii) Clinical trial design that incorporates findings from studies of tumor heterogeneity to improve therapeutic effectiveness and better understand treatment resistance; specifically identifying somatic driver mutations that can be targeted with novel therapies by incorporating next-generation DNA sequencing technology to identify genomic variations within the same tumor; and (iii) Developing a class of response-adaptive Bayesian designs that can define sequential stopping rules with response-adaptive

randomization to quantify potential gains for ongoing cancer sequencing projects. Drs. J. Jack Lee and Edith A. Perez are the organizers of this session.

1:00 p.m.   **Advancing research in precision medicine through integromics: An overview of statistical challenges**
Kim-Anh Do, The University of Texas MD Anderson Cancer Center, Houston, TX

1:20 p.m.   **Discussion**

1:30 p.m.   **Integration of imaging and genomics for patients and target identification in clinical trials**
Benjamin M. Ellingson, University of California, Los Angeles, CA

1:50 p.m.   **Discussion**

2:00 p.m.   **Accounting for tumor heterogeneity in clinical trial design in the genomic era**
Philippe L. Bedard, University of Toronto University Health Network, Toronto, ON, Canada

2:20 p.m.   **Discussion**

2:30 p.m.   **Biomarker-stratified adaptive basket designs for multiple cancers**
Lorenzo Trippa, Dana-Farber Cancer Institute, Boston, MA

2:50 p.m.   **Discussion**

METHODS WORKSHOPS

Saturday, 1:00 p.m.-3:00 p.m.

Room 118, Pennsylvania Convention Center
Novel Platforms for Early Detection of Malignancies

Chairperson: Sam M. Hanash, The University of Texas MD Anderson Cancer Center, Houston, TX

The development of biomarker panels for cancer early detection has represented a substantial challenge. Recent advances in technologies have allowed comprehensive profiling of biological fluids at an unprecedented depth of analysis. These developments have made it possible to discover potential biomarkers directly in the fluid as opposed to the tissue source, thus providing a direct path from discovery to validation in the chosen biospecimen type, notably serum or plasma. This session will explore several innovative strategies for biomarker discovery relevant to early detection. Moreover, effective early detection of cancer is highly dependent on identification of subjects at risk for particular cancers. Methodology for identifying high risk individuals for future screening programs will be presented.

1:00 p.m.   **Advances in proteomics for cancer biomarker discovery**
Sam M. Hanash, The University of Texas MD Anderson Cancer Center, Houston, TX

1:25 p.m.   **Discussion**

1:30 p.m.   **Current metabolomic strategies for the discovery of circulating markers for cancer risk assessment and early detection**
Oliver Fiehn, University of California, Davis, CA

1:55 p.m.   **Discussion**

2:00 p.m.   **High-density antibody arrays to profile circulating biomarkers**
Paul D. Lampe, Fred Hutchinson Cancer Research Center, Seattle, WA

2:25 p.m.   **Discussion**

2:30 p.m.   **Risk prediction models in lung cancer: The methodology for identifying high-risk individuals for future screening programs**
John K. Field, University of Liverpool, Liverpool, United Kingdom

2:55 p.m.   **Discussion**

PROFESSIONAL ADVANCEMENT SESSION *(not eligible for CME credit)*

Saturday, 1:00 p.m.-3:00 p.m.

Regency Ballroom (Second Floor), Loews Philadelphia Hotel

WICR Professional Advancement Session: The Power of Assertiveness
Organized by the Women in Cancer Research (WICR) Council

Co-Chairpersons: Patricia M. LoRusso, Yale Cancer Center, New Haven, CT; S. Percy Ivy, National Cancer Institute-DCTD, Rockville, MD

In this workshop, three different facets of professional assertiveness will be discussed: assertiveness for professional growth, assertiveness as a necessary tool for leadership, and assertiveness for maintaining effective and productive teams. For individuals to contribute fully, and for teams to be effective, individuals need to feel comfortable in asserting their ideas and viewpoints. Individual assertiveness is crucial to harness the power of diverse skill sets to conquer cancer. The significant power of assertiveness in the workplace should be used in the right time and context. To have an impact, to be a voice in the workforce, and to empower oneself for career advancement, women scientists must learn how to assert themselves based on their position, goals and needs. Women in the workplace need to master an assertive skill set to be perceived in a similar fashion to their male counterparts.

For AACR members, all 2015 Professional Advancement Sessions are free with your Annual Meeting registration (except for the Grant Writing Workshop) and are an added benefit of your membership. For nonmembers, there is an additional fee of $50 ($95 for the Grant Writing Workshop) for attendance at each session. If you are not an AACR member, we strongly encourage you to join and take advantage of the many benefits of membership, which include attendance at these sessions. Participation is on a first-come, first-served basis, and space is limited. Nonmembers are required to pay onsite.

1:05 p.m.   **Facilitator Presentation**

Matthew Mirisola, Matt Mirisola Consulting, Provincetown, MA

1:35 p.m.   **Panel Discussion**

Assertiveness for Effective Leadership
Margaret A. Tempero, University of California, San Francisco, CA

Advocating for Yourself While Climbing the Career Ladder
Cheryl L. Willman, University of New Mexico Cancer Research and Treatment Center, Albuquerque, NM

Assertive Skills for Team Leaders
Mary C. Beckerle, University of Utah Huntsman Cancer Institute, Salt Lake City, UT

2:20 p.m.   **Audience engagement (Q&A)**

MEET-THE-EXPERT SESSIONS

Saturday, 3:15 p.m.-4:15 p.m.

Room 115, Pennsylvania Convention Center
The 21st Century Hazards of Smoking and Benefits of Stopping

Richard Peto, University of Oxford, Oxford, United Kingdom

Recent studies of the hazards of people in the U.K., U.S., or Japan who began smoking in adolescence or early adult life show loss of about 10 years of life expectancy if they continue, and avoidance of more than 90% of the excess risk if they stop before age 40 (and preferably well before age 40). Smokers who did not start in early adult life have much smaller hazards in middle and old age than those who did. Hence, when smoking becomes common among a population of young adults, the full eventual effects of tobacco on mortality rates in middle and old age take more than half a century to emerge in that population. For women in many developed countries and men in many other countries, there will be a large increase in tobacco-attributed mortality over the next few decades as a result of increases in smoking that have already happened, unless there is widespread cessation. For U.K. and U.S. women, the full hazards per smoker became apparent only in the present century. Because the increase in the hazard per smoker, particularly among women, has counterbalanced the effects of the decreasing prevalence of smoking, tobacco still accounts for about 30% of all U.S. cancer deaths.

Room 204, Pennsylvania Convention Center
Cancer Moon Shot Initiative: Accelerating Translation and Impact

Ronald A. DePinho, The University of Texas MD Anderson Cancer Center, Houston, TX

Our deepening knowledge of cancer and numerous disruptive technologies prompted MD Anderson to conduct a large multidisciplinary analysis of major translational opportunities across major cancers that, if fully applied, would accelerate declines in cancer mortality in the next 5 to 10 years. Flagship projects spanning prevention, early detection treatment were launched in several major cancers: NSCLC, MDS/AML, CLL, prostate, melanoma, and TNBC/HGSOV. These projects required significant knowledge to be in hand to enable near-term clinical impact. To insure systematic translation of such knowledge, we created nine professional platforms capable of industry-like execution yet fully integrated with academic scholars and disease experts. These large multidisciplinary teams and platforms are being adequately resourced to enable projects to achieve ultimate goals in a milestone-driven and accountable

manner. The presentation will describe the guiding principles of the moon shot program, highlight several platforms, and describe projects and interim progress over the first two years in a number of diseases.

Room 118, Pennsylvania Convention Center
New Insights into BRCA1 Function

David M. Livingston, Dana-Farber Cancer Institute, Boston, MA

BRCA1, an established breast and ovarian cancer suppressor gene, is dedicated to the maintenance of genome integrity. While much circumstantial evidence links this generic function to the suppression of archetypical BRCA1 cancer, how they are connected remains a major mystery. Recently, a series of new observations have significantly expanded the established repertoire of BRCA1 biological and biochemical functions. Among the newly detected functions are replication stress suppression, inhibition of translesional DNA synthesis, support of proper estradiol metabolism, regulation of RNA splicing, participation in the silencing of heterochromatin-associated satellite RNA synthesis, and the suppression of transcription/R loop- associated DNA damage. New insights into the mechanism underlying the BRCA1 control of mammary progenitor cell differentiation have also emerged. This expanded body of evidence has stimulated the discussion of new models of BRCA1 cancer suppression.

Room 103, Pennsylvania Convention Center
Systematic Interrogation of Cancer Dependencies

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

Cancer genome annotation projects have identified the type and frequency of genetic alterations that occur in many primary human cancers. However, the number and diversity of such alterations complicates efforts to identify those genes involved in specific cancer phenotypes. This session will focus on new advances in gene manipulation technologies that allow the systematic interrogation of cancer alleles and co-dependencies. In particular the use of both genome scale RNA interference and Cas9-CRISPR technology for loss of function genetics and high throughput overexpression studies will be discussed. Specific application of these technologies to understand RAS, PI3K and β-catenin signaling will be discussed.

EDUCATIONAL SESSIONS

Saturday, 3:15 p.m.-5:15 p.m.

Room 108, Pennsylvania Convention Center

Cancer Drug Discovery 2015: Challenges and Opportunities for Academia and Industry

Chairperson: Donald Ogilvie, Cancer Research UK Manchester Institute, Manchester, United Kingdom

During the last decade, the pharmaceutical industry has reduced its presence in the early drug discovery space and this has been accompanied by a resurgence of academic drug discovery driven, in part, by scientists with considerable industrial experience. With reduced internal resources, the pharmaceutical industry is increasingly reliant on external innovation to access not only novel targets but also, increasingly, active drug discovery projects. In contrast, academic groups are often closer to breaking science but cannot easily access the capital-intensive resources required to progress drug discovery projects optimally. This has provided opportunities for innovative partnership models between academic and industrial drug discovery groups. In this session, experts from both academia and industry will discuss the challenges and opportunities afforded by this scenario, with particular reference to the early stages of small molecule drug discovery in cancer.

3:15 p.m.	**Introduction** Donald Ogilvie, Cancer Research UK Manchester Institute, Manchester, United Kingdom
3:15 p.m.	**Chemical biology approaches to target validation in cancer** Julian Blagg, Institute of Cancer Research, Sutton, Surrey, United Kingdom
3:40 p.m.	**Discussion**
3:45 p.m.	**Collaborating with industry to find chemical hits versus difficult targets** Allan M. Jordan, Cancer Research UK Manchester Institute, Manchester, United Kingdom
4:10 p.m.	**Discussion**
4:15 p.m.	**Reducing the PAIN in academic drug discovery** Jonathan B. Baell, Monash University, Parkville, Australia
4:40 p.m.	**Discussion**
4:45 p.m.	**Partnering with academia in early drug discovery: An industry perspective** Dashyant Dhanak, Janssen Research Development, LLC, Spring House, PA
5:10 p.m.	**Discussion**

Grand Ballroom (300 Level), Pennsylvania Convention Center

Clinical Interpretation of Cancer Genomes

Chairperson: Nikhil Wagle, Dana-Farber Cancer Institute, Brookline, MA

Remarkable advances in sequencing technology over the past two decades has made it possible to comprehensively profile tumors and identify clinically relevant genomic alterations and incorporate sequencing into clinical trial design. This has advanced our ability to direct the appropriate treatment to the appropriate patient at the appropriate time – a hallmark of "precision cancer medicine." The major challenges will now revolve around on how best to realize the impressive potential benefits of incorporating next-generation sequencing into clinical care of patients.

In this session, we will review approaches to analyzing, interpreting, and communicating clinical sequencing data to clinicians and patients. In the first half of the session, we will focus on the technical and computational issues around analyzing clinical sequencing data, as well as the process of assigning clinical meaning and evidence to potentially actionable genomic alterations. We will then discuss methods of communicating these results to clinicians who will ultimately use the data. Finally, we will review clinical trial models being used to evaluate the utility of clinical sequencing in patient care.

3:15 p.m.	**Approaches to clinical analysis of cancer genomes: Laboratory and computational** Trevor J. Pugh, Princess Margaret Cancer Centre, Toronto, ON, Canada
3:40 p.m.	**Discussion**
3:45 p.m.	**Assigning clinical meaning to cancer genome data** Nikhil Wagle, Dana-Farber Cancer Institute, Brookline, MA
4:10 p.m.	**Discussion**
4:15 p.m.	**Developing tools to communicate clinically actionable genomic alterations to clinicians** Mia A. Levy, Vanderbilt University, Nashville, TN
4:40 p.m.	**Discussion**
4:45 p.m.	**Designing clinical trials to evaluate the clinical utility of cancer genomic data** Fabrice André, Institut Gustave Roussy, Villejuif, France
5:10 p.m.	**Discussion**

EDUCATIONAL SESSIONS

Saturday, 3:15 p.m.-5:15 p.m.

Room 120, Pennsylvania Convention Center
Endogenous Steroid Hormones and Risk of Cancer

Chairperson: Regina G. Ziegler, National Cancer Institute, Bethesda, MD

Endogenous estrogens and androgens are associated with increased breast cancer risk. In pooled analyses of individual participant data from prospective studies, relative risk was 1.8-2.6 across extreme quintiles of circulating steroid hormones for postmenopausal breast cancer and 1.2-1.7 for premenopausal disease. These associations are being explored by breast cancer subtype, as mediating and joint effects, and for underlying mechanisms. Multiple laboratory-based hypotheses exist about the role of specific estrogen metabolites and metabolic profiles in breast cancer etiology. With the advent of robust, comprehensive estrogen metabolism assays, these hypotheses are being tested in epidemiologic studies. Elucidating the endocrine basis of breast cancer has led to therapies and prognostic biomarkers based on response and resistance to estrogen deprivation in breast cancer treatment. New laboratory methods and national standardization programs are improving the accuracy, precision, and sensitivity of testosterone and estradiol assays used in patient care, clinical trials, and epidemiologic and laboratory research.

3:15 p.m.	**Epidemiologic studies of endogenous hormones and breast cancer** Rudolf Kaaks, German Cancer Research Center, Heidelberg, Germany
3:40 p.m.	**Discussion**
3:45 p.m.	**Estrogen metabolism and risk of breast cancer** Regina G. Ziegler, National Cancer Institute, Bethesda, MD
4:10 p.m.	**Discussion**
4:15 p.m.	**Importance of endogenous sex steroids in breast cancer treatment** Mitch Dowsett, The Royal Marsden Hospital, London, United Kingdom
4:40 p.m.	**Discussion**
4:45 p.m.	**Importance of improving testosterone and estradiol assays** Hubert W. Vesper, Centers for Disease Control and Prevention, Atlanta, GA
5:10 p.m.	**Discussion**

Room 113, Pennsylvania Convention Center
From Chemistry to the Clinic: Pathways for Drug Discovery and Development, Part 4: Design of Small Molecules Targeting Tumor Metabolism

Co-Chairpersons: Janeta V. Popovici-Muller, Agios Pharmaceuticals, Cambridge, MA; Rene M. Lemieux, Agios Pharmaceuticals, Cambridge, MA

Malignant cell transformation and tumor progression have been associated with alterations in several metabolic pathways such as glycolysis, mitochondrial metabolism, and control of reactive oxygen species, fatty acid synthesis, and amino acid metabolism. This session will focus on the design of small molecules targeting mitochondrial glutamine metabolism and metabolic alterations in glycolysis, which may have therapeutic implications for a wide range of tumor types. We will discuss two approaches targeting lactate metabolism caused by dysregulated glycolytic flux: inhibition of lactate dehydrogenase A (LDHA) that regulates the conversion of pyruvate to lactate, and inhibition of a key tumor-associated lactate transporter (MCT1) – as an alternative strategy targeting the glycolytic phenotype of tumors. We will also discuss some of the issues and challenges encountered due to target mediated toxicities and unique rescue strategies utilized in research to discover nicotinamide phosphoribosyltransferase (NAMPT) inhibitors with improved safety/efficacy profile.

3:15 p.m.	**Optimization of glutaminase inhibitors for the treatment of cancer** Rene M. Lemieux, Agios Pharmaceuticals, Cambridge, MA
3:40 p.m.	**Discussion**
3:45 p.m.	**Discovery of in vivo inhibitors of lactate dehydrogenase A (LDHA) *(not eligible for CME credit)*** Hans Purkey, Genentech, Inc., South San Francisco, CA
4:10 p.m.	**Discussion**
4:15 p.m.	**Discovery of a potent, selective, NAMPT inhibitor from the pyridyloxyacetyl-dihydro-isoquinoline-sulfonamide series that demonstrated robust efficacy and improved tolerability with nicotinic acid co-administration** Timothy P. Burkholder, Eli Lilly and Company, Indianapolis, IN
4:40 p.m.	**Discussion**
4:45 p.m.	**MCT: The journey from phenotypic screen hit to clinical candidate** Jon Winter, AstraZeneca R&D, Cheshire, United Kingdom
5:10 p.m.	**Discussion**

Room 122, Pennsylvania Convention Center

Improving Cancer Drug Bioavailability by Use of Controlled Delivery and Release

Chairperson: Dennis E. Hallahan, Washington University School of Medicine, St. Louis, MO

Radiation therapy induces the expression of stress proteins in cancer which can be exploited for drug delivery. Likewise, hyperthermia can be used to deliver drugs and control the release of cancer therapeutics. Clinical trials have explored the use of x-rays to control drug delivery for the use of viral vectors and inducible gene therapy. Radiation has also been used to guide drug delivery to cancer by use of nanoparticles and antibodies. Thermal regulated cancer drug release has been achieved by use liposomal drug delivery. We will discuss each of these new technologies that can be used to prove the control of cancer therapeutics.

3:15 p.m.	**Thermal regulation of cancer drug release** Mark W. Dewhirst, Duke University Medical Center, Durham, NC
3:40 p.m.	**Discussion**
3:45 p.m.	**Tumor targeting nanoparticles with radiation-enhanced permeability and retention** Stephen J. Kron, The University of Chicago, Chicago, IL
4:10 p.m.	**Discussion**
4:15 p.m.	**Radiation controlled delivery of cancer drugs** Roberto Diaz, Moffitt Cancer Center and Research Institute, Tampa, FL
4:40 p.m.	**Discussion**
4:45 p.m.	**Therapeutic antibodies targeting radiation inducible antigens on cancer** Dennis E. Hallahan, Washington University School of Medicine, St. Louis, MO
5:10 p.m.	**Discussion**

Room 126, Pennsylvania Convention Center

Population Screening for Inherited Breast and Ovarian Cancers: Are We There Yet?

Chairperson: Olufunmilayo I. Olopade, University of Chicago Medical Center, Chicago, IL

In the era of precision medicine, high-throughput genomic testing is increasingly used in the management of cancer patients. Germline mutations in the BRCA1 and BRCA2 genes are the most predictive indicators of inherited breast and ovarian cancer susceptibility but penetrance of these mutations varies widely. Risk reducing interventions can improve outcomes in at risk individuals but genomic testing usually occurs after a diagnosis of cancer. Following more than two decades of fundamental research on BRCA biology, there is need for a fundamental shift in our approach to population genomic screening for inherited cancers.

3:15 p.m.	**Mutations in context: How is breast cancer risk modified across the African diaspora?** Olufunmilayo I. Olopade, University of Chicago Medical Center, Chicago, IL
3:40 p.m.	**Discussion**
3:45 p.m.	**Prevalence and penetrance considerations in population screening** Kenneth Offit, Memorial Sloan Kettering Cancer Center, New York, NY
4:10 p.m.	**Discussion**
4:15 p.m.	**Population-based strategy for breast cancer screening in Brazil** Patricia Ashton-Prolla, Hospital de Clinicas de Porto Alegre, Porto Alegre RS, Brazil
4:40 p.m.	**Discussion**
4:45 p.m.	**Population screening for inherited BRCA1 and BRCA2 mutations** Ephrat Levy-Lahad, Shaare Zedek Medical Center, Jerusalem, Israel
5:10 p.m.	**Discussion**

EDUCATIONAL SESSIONS

Saturday, 3:15 p.m.-5:15 p.m.

Terrace Ballroom II-III (400 Level), Pennsylvania Convention Center

Therapeutic Targeting the Diverse Immune Inhibitory Pathways in the Tumor Microenvironment

Chairperson: Drew M. Pardoll, Johns Hopkins Kimmel Comprehensive Cancer Center, Baltimore, MD

The revolution in cancer immunotherapy that we are currently experiencing was launched by the application of inhibitors of molecules that dampen antitumor immunity – so called checkpoints. Anti-CTLA-4 and anti-PD-1 are both approved for melanoma immunotherapy and various PD-1 pathway blocking antibodies will be approved in 2015 in renal cancer, lung cancer, Hodgkin's disease, and bladder cancer. We now know that these two checkpoints represent a tiny proportion of the total inhibitory molecules and cells that are therapeutically targetable. Beyond conventional membrane ligand-receptor interactions, a number of metabolic enzymes can inhibit local antitumor immunity and two cell types, regulatory T cells (Treg) and myeloid-derived suppressor cells (MDSC), also participate in tumor immune resistance. This session will explore all of these mechanisms as well as the opportunities they offer for dramatic improvement in immunotherapy potency.

3:15 p.m. **Coordinate induction and combinatorial blockade of checkpoint receptors on killer T cells**
Drew M. Pardoll, Johns Hopkins Kimmel Comprehensive Cancer Center, Baltimore, MD

3:40 p.m. **Discussion**

3:45 p.m. **Targeting the indoleamine 2,3-dioxygenase (IDO) pathway**
David H. Munn, Georgia Regents University, Augusta, GA

4:10 p.m. **Discussion**

4:15 p.m. **Targeting Tregs in tumors**
Dario A. Vignali, University of Pittsburgh School of Medicine, Pittsburgh, PA

4:40 p.m. **Discussion**

4:45 p.m. **Myeloid cells and cancer progression**
Vincenzo Bronte, University of Verona, Verona, Italy

5:10 p.m. **Discussion**

Room 114, Pennsylvania Convention Center

Translating Insights from Mouse Cancer Models to Therapeutic Targeting

Chairperson: Terry A. Van Dyke, Frederick National Laboratory, Frederick, MD

Significant advances have been made in developing targeted cancer treatments. Yet, despite great promise, most cancers have resisted a plethora of treatments. Given the complexity and the range of cancer subtypes, significant improvements in success require implementation of preclinical animal platforms capable of identifying potentially efficacious therapies. Murine cancer models designed to capture human cancer complexity, specifically patient-derived xenografts and genetically engineered mice, currently offer the most advanced opportunities for improved therapeutic and biomarker development. Although preclinical research in these models is increasing, effective application to clinical research directives is an emerging science that currently lacks standard operating procedures. Achieving the accuracy and reproducibility required to improve clinical outcomes is challenging. Yet, early efforts are promising. Experts in this session will highlight recent developments in the field and provide guidance in navigating the challenges of preclinical evaluation in complex murine cancer models, which are critical to enhancing clinical efficacy determination.

3:15 p.m. **Know your models: Considerations for effective preclinical evaluation in murine platforms**
Terry A. Van Dyke, Frederick National Laboratory, Frederick, MD

3:40 p.m. **Discussion**

3:45 p.m. **Insights from pre- and postclinical trials in pancreatic ductal adenocarcinoma**
Kenneth P. Olive, Columbia University Irving Comprehensive Cancer Center, New York, NY

4:10 p.m. **Discussion**

4:15 p.m. **Patient derived xenograft (PDX) platforms for clinical trials**
Neal Goodwin, Champions Oncology, Inc., Hackensack, NJ

4:40 p.m. **Discussion**

4:45 p.m. **The role of mouse tumor models in drug development and identification of resistance mechanisms**
Meghna Das Thakur, Genentech, Inc., San Francisco, CA

5:10 p.m. **Discussion**

METHODS WORKSHOPS

Saturday, 3:15 p.m.-5:15 p.m.

Room 201, Pennsylvania Convention Center

Design and Method Workshop for Clinical Trials and Population Studies, Part 4: Leveraging Population Data and Electronic Medical Record Databases for Hypothesis Generation, Validation, and Decision Support

Chairperson: Tianxi Cai, Harvard T. H. Chan School of Public Health, Boston, MA

Rapid advancements in cancer biology, immunology, genomics, and treatment development demand innovative methods to identify better therapies and the most appropriate population for a given therapy in a timely, efficient, accurate, and cost-effective way. This one-day educational workshop has four parts that share the theme of better patient selection, treatment evaluation, discovery and validation of predictive markers, and statistical design and analysis in support of delivering precision medicine to each patient. Part 4 will discuss how to leverage the available population data and electronic medical record databases for hypothesis generation and validation, and to support clinical decisions of the best treatment for each patient. This part will also introduce the use of propensity score analysis to analyze observational data and provide information comparable to that obtained from randomized trials. Also discussed will be the challenge, process, effort, and reward of assessing and using large population databases and electronic medical records in an integrated decision support system to select the best treatment for each patient. Drs. J. Jack Lee and Edith A. Perez are the organizers of this session.

3:15 p.m. **The potential of electronic medical records data for personalized medicine research**
Tianxi Cai, Harvard T. H. Chan School of Public Health, Boston, MA

3:35 p.m. **Discussion**

3:45 p.m. **Phenomics, genomics, and pharmacogenomics in the electronic health record: A platform to advance precision medicine**
Joshua C. Denny, Vanderbilt University School of Medicine, Nashville, TN

4:05 p.m. **Discussion**

4:15 p.m. **Comparing apples and oranges: Analyzing observational data like a randomized trial via the propensity score analysis**
Liang Li, The University of Texas MD Anderson Cancer Center, Houston, TX

4:35 p.m. **Discussion**

4:45 p.m. **ORIEN: A consortium to build cancer precision medicine**
Michael A. Caligiuri, James Cancer Hospital and Solove Research Institute, Columbus, OH

5:05 p.m. **Discussion**

Room 121, Pennsylvania Convention Center

Developing Technologies to Investigate Single Cells and Tumor Heterogeneity

Chairperson: Crispin Miller, Cancer Research UK Manchester Institute, Manchester, United Kingdom

There is widespread heterogeneity in gene expression between cells within a population. Considerable genetic heterogeneity between tumor cells is also apparent, and consequences are numerous: from distinct gene expression patterns at different sites within a tumor, to increasing evidence that identification of specific low-frequency sub-clones at diagnosis is necessary to correctly forecast outcome. Until recently, genome-wide approaches to analyze single cells have been thwarted by the small amounts of starting material available from an individual cell. However, rapid advances in technology have made genomic profiling of single cells a reality. This workshop will survey the current state of the art in single cell genomics and the computational analyses required to exploit these techniques.

3:15 p.m. **Methods for rapid profiling of single cells to assess heterogeneity in solid tumors and circulating cells**
James B. Hicks, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

3:45 p.m. **Discussion**

3:55 p.m. **Approaches for global single cell profiling of DNA and RNA and their application to circulating tumor cells**
Crispin Miller, Cancer Research UK Manchester Institute, Manchester, United Kingdom

4:25 p.m. **Discussion**

4:35 p.m. **The biological and clinical implications of intratumor heterogeneity**
Zoltan Szallasi, Boston Children's Hospital, Boston, MA

5:05 p.m. **Discussion**

METHODS WORKSHOPS

Saturday, 3:15 p.m.-5:15 p.m.

Room 119, Pennsylvania Convention Center
Extracellular Vesicles in Cancer: Isolation and Function

Chairperson: Robert J. Coffey, Vanderbilt University Medical Center, Nashville, TN

This session is intended to discuss recent advances in the study of extracellular vesicles in cancer. Extracellular vesicles are often divided into smaller sized vesicles termed exosomes and larger vesicles termed microvesicles. There will be an update on a National Cancer Institute-funded U19, Extracellular RNA Biogenesis, Biodistribution, Uptake, and Effector Function, which provides a website detailing methods of isolation and characterization of these vesicles. There will be three talks from leading investigators in this field that will highlight methods employed in their studies. The session will end with a discussion of challenges and opportunities in this field.

3:15 p.m.   **NCI U19 extracellular RNA: Resources and tools**
Robert J. Coffey Jr., Vanderbilt University Medical Center, Nashville, TN

3:35 p.m.   **Discussion**

3:40 p.m.   **Oncogene regulation of extracellular RNAs**
Andrei Goga, University of California, San Francisco, CA

4:00 p.m.   **Discussion**

4:05 p.m.   **Biology and function of exosomes in cancer**
Raghu Kalluri, The University of Texas MD Anderson Cancer Center, Houston, TX

4:25 p.m.   **Discussion**

4:30 p.m.   **Stromal-tumor cross talk through exosomes**
Rama Khokha, University of Toronto Ontario Cancer Institute, Toronto, ON, Canada

4:50 p.m.   **Discussion**

4:55 p.m.   **General Discussion: Challenges and opportunities**

Terrace Ballroom IV (400 Level), Pennsylvania Convention Center
Methods Advances in Clinical Cancer Genomics for Personalized Oncology

Chairperson: Marc Ladanyi, Memorial Sloan Kettering Cancer Center, New York, NY

In the new paradigm of molecular oncology and precision medicine, the identification of "driver" genetic alterations in key oncogenes and tumor suppressor genes plays an essential role in the diagnosis and treatment of many cancers. This process helps to match patients to a rapidly increasing number of targeted therapies, approved or under clinical investigation, that specifically inhibit the tumorigenic effects of the aberrant proteins resulting from these genetic alterations. It has thus become crucial to develop accurate, sensitive and high throughput genomic analysis methods to support the increasingly genotype-based practice of clinical oncology. Assays based on massively parallel "next-generation" sequencing (NGS) technology enable the unbiased identification of mutations across the genome or across more targeted regions with high sensitivity and specificity. This session will present a variety of current NGS-based strategies in clinical cancer genomics testing for personalized oncology, along with their technical challenges and limitations.

3:15 p.m.   **Personalized genomic analyses for cancer mutation discovery and interpretation**
Victor E. Velculescu, Johns Hopkins Kimmel Comprehensive Cancer Center, Baltimore, MD

3:45 p.m.   **Discussion**

3:55 p.m.   **Detection of gene fusions in cancer**
Anthony John Iafrate, Massachusetts General Hospital, Boston, MA

4:25 p.m.   **Discussion**

4:35 p.m.   **The MSK-IMPACT Program: Prospective clinical cancer genomics to enable personalized oncology and advance the clinical development of targeted therapies**
Marc Ladanyi, Memorial Sloan Kettering Cancer Center, New York, NY

5:05 p.m.   **Discussion**

Terrace Ballroom I (400 Level), Pennsylvania
Convention Center

Systems Approaches to Cancer Metabolism

Chairperson: Ralph J. DeBerardinis, UT Southwestern Medical Center, Dallas, TX

Metabolic reprogramming is a hallmark of cancer and a potential source of informative biomarkers and therapeutic targets. Technological advances, particularly in mass spectrometry, nuclear magnetic resonance spectroscopy, and metabolic imaging, have made it possible to examine metabolic states in greater detail than ever before. A current challenge in cancer metabolism is to understand how best to deploy these advanced technologies to address the most pressing questions in tumor biology and clinical oncology. In particular, because metabolism is highly linked to functional cellular outputs such as survival, growth, and proliferation, we now have an incredible opportunity to merge metabolic data with other informative and clinically relevant aspects of systems biology (genomics, proteomics, etc.). This Methods Workshop will cover emerging techniques in metabolic assessment and how these techniques are being used to understand cancer biology.

3:15 p.m.   **Untargeted metabolomics: Technologies to study cancer metabolism at the global scale**
Gary Patti, Washington University in St. Louis, St. Louis, MO

3:35 p.m.   **Discussion**

3:45 p.m.   **Understanding metabolic heterogeneity in cancer cells and human tumors**
Ralph J. DeBerardinis, UT Southwestern Medical Center, Dallas, TX

4:05 p.m.   **Discussion**

4:15 p.m.   **Similarity and diversity in cancer cell metabolism**
Dennis Vitkup, Columbia University, New York, NY

4:35 p.m.   **Discussion**

4:45 p.m.   **Integrating metabolomics with transcriptional profiling: Statistical aspects of hypothesis generating systems data analysis**
Edward Driggers, General Metabolics, Winchester, MA

5:05 p.m.   **Discussion**

MEET-THE-EXPERT SESSIONS

Saturday, 4:30 p.m.-5:30 p.m.

Room 118, Pennsylvania Convention Center
Curative Potential of T Cell Immunotherapy for Cancer

Steven A. Rosenberg, National Cancer Institute, Bethesda, MD

Adoptive cell therapy (ACT) involves the administration, to the cancer bearing patient, of immune cells with direct anticancer activity. A major factor limiting the successful utilization of ACT in humans is the identification of cells that can target antigens selectively expressed on the cancer and not on essential normal tissues. ACT uses T cells that can naturally be found in the patient or can be genetically engineered ex vivo. Effective ACT has been applied to patients with melanoma, multiple hematologic tumors, as well as sarcomas and cervical cancers. The ideal targets for ACT are the unique mutations that occur in cancers. We have recently reported a new approach to ACT using deep exomic sequencing along with immunologic testing to identify immune mutations that give rise to cancer-reactive T cells. This approach was used to treat a patient with metastatic bile duct cancer who has ongoing shrinkage of lung and liver metastases one year after treatment. Since virtually all cancers contain mutations this approach is now being vigorously studied to expand the current reach of cancer immunotherapy to common epithelial cancers.

Room 103, Pennsylvania Convention Center
Large-Scale Experimental Approaches Applied to Translation Drug Discovery

William R. Sellers, Novartis Institutes for BioMedical Research, Cambridge, MA

Cancer remains among the most complex of medical illnesses. Nearly every distinct cell type undergoes transformation to yield tumors that harbor somatic genetic alterations in the context of lineage-related signaling networks and lineage-specific stromal interactions. As cancers evolve they can undergo genetic divergence that yields distinct subclonal populations. These populations become prominent during therapeutic pressure or through subselection during metastasis. Over the past decade, experimental systems have allowed us to begin to approach this complexity experimentally. Model systems used at great depth and diversity along with next-generation sequencing enabled experimentation allow us to model drug response and genetic inactivation across hundreds of cell lines, hundreds of primary tumor xenografts, and millions of individually bar coded cells. The use of these tools and their application to cancer drug discovery will be the focus of the lecture.

Room 204, Pennsylvania Convention Center
Lgr5 Stem Cells in Self-Renewal and Cancer

Hans Clevers, Hubrecht Institute, Utrecht, The Netherlands

The intestinal epithelium is the most rapidly self-renewing tissue in adult mammals. We originally defined Lgr5 as a Wnt target gene, transcribed in colon cancer cells. Two knock-in alleles revealed exclusive expression of Lgr5 in cycling, columnar cells at the crypt base. Using lineage tracing experiments in adult mice, we found that these Lgr5+ve crypt base columnar cells (CBC) generated all epithelial lineages throughout life, implying that they represent the stem cell of the small intestine and colon. Lgr5 was subsequently found to represent an exquisitely specific and almost "generic" marker for stem cells, including in hair follicles, kidney, liver, mammary gland, inner ear, tongue, and stomach epithelium. Single sorted Lgr5+ve stem cells can initiate ever-expanding crypt-villus organoids, or so called "mini-guts" in 3-D culture. The technology is based on the observation that Lgr5 is the receptor for a potent stem cell growth factor, R-spondin. Similar 3-D cultures systems have been developed for the Lgr5+ve stem cells of stomach, liver, pancreas, and kidney. Using CRISPR/Cas9 technology, the CFTR locus has been corrected in intestinal organoids of cystic fibrosis patients.

Room 115, Pennsylvania Convention Center
Triple-Negative Breast Cancer: Biologic Advances but a Therapeutic Impasse

Lisa A. Carey, UNC Lineberger Comprehensive Cancer Center, Chapel Hill, NC

Triple-negative breast cancer, which comprises about 20% of incident breast cancers, is defined by negative clinical assays for the estrogen and progesterone receptors and HER2, leaving only chemotherapy for treatment. For this reason it carries a significantly poorer outcome than other clinical subtypes. Molecular studies clearly illustrate the biologic heterogeneity of this disease, which is comprised of all intrinsic subtypes although is dominated by the basal-like subtype, which itself may include multiple biologic variants. Epidemiologic studies confirm the unique biology of the basal-like subtype, which has different risk factors as well as different metastatic site tropism from other subtypes. The therapeutic challenges posed by this subtype are considerable, and are among the most intensive areas of breast cancer research.

AACR ANNUAL MEETING 2015

AACR-IRVING WEINSTEIN LECTURE

Saturday, 5:30 p.m.-6:30 p.m.

Grand Ballroom (300 Level), Pennsylvania Convention Center
Eleventh Annual AACR-Irving Weinstein Foundation Distinguished Lecture
MicroRNAs, Leukemia, and Hematopoietic Stem Cell Homeostasis

David Baltimore, PhD, FAACR

President Emeritus and Robert Andrews Millikan Professor of Biology
California Institute of Technology, Pasadena, CA

The AACR-Irving Weinstein Foundation Distinguished Lectureship was established in 2004 to honor an individual whose outstanding innovations in science and whose position as a thought leader have the potential to inspire creative thinking and new directions in cancer research.

Dr. David Baltimore is honored for his groundbreaking research in numerous fields of biomedical research, including immunology, virology, and cancer research. In 1975, he was awarded the Nobel Prize in Physiology or Medicine for his work on viral replication and his discovery of reverse transcriptase, which revolutionized molecular biology and has been essential to understanding the lifecycle of retroviruses such as HIV.

Dr. Baltimore pioneered the use of recombinant DNA technology, which members of his laboratory used to advance understanding of the immune system, including discovering NF-κB and the recombination activating genes RAG-1 and RAG-2. He has also contributed significantly to the use of gene therapy methods to treat not only cancer, but other diseases such as AIDS.

The research in his laboratory is currently focused on furthering knowledge of the development and function
of the mammalian immune system and using viral vectors to carry new genes into immune cells to increase the range of pathogens effectively fought by the immune system and to make the immune system resist cancer growth more effectively.

Dr. Baltimore graduated with a bachelor's degree in chemistry from Swarthmore College in Swarthmore, Pennsylvania, and received his doctorate from Rockefeller University in New York, where he also once served as president and professor of biology. He served on the faculty at the Massachusetts Institute of Technology for more than 30 years, including as founding director of the Whitehead Institute for Biomedical Research. He is also a former president of the American Association for the Advancement of Science.

Dr. Baltimore has received numerous honors and accolades including the National Medal of Science, the AMA Scientific Achievement Award, and the Warren Alpert Foundation Scientific Prize from Harvard Medical School. He is also an elected member of the Institute of Medicine, the American Academy of Arts and Sciences, and the National Academy of Sciences, as well as a foreign member of the Royal Society in the United Kingdom and the French Academy of Sciences.

PROFESSIONAL ADVANCEMENT SESSION *(not eligible for CME credit)*

Saturday, 5:30 p.m.-6:30 p.m.

Room 119, Pennsylvania Convention Center
Social Media for Scientists

Chairperson: Rick Buck, American Association for Cancer Research, Philadelphia, PA

Basic, translational, and clinical investigators can use social media platforms such as Twitter and LinkedIn to support their research efforts in a myriad of ways. They can follow the musings of thought leaders in their field, discover articles of interest from respected colleagues, engage and recruit patients for clinical trials, and create working groups around the topics that interest them. Two AACR members who are longtime users of social media–Wafik El-Deiry (@weldeiry) and Emil Lou (@cancerassassin1)–will discuss the professional and personal benefits they derive from incorporating social media into their daily research activities. In addition, patient advocate AnneMarie Ciccarella (@chemobrainfog) will discuss the benefits of social media from a patient's perspective and how investigators can use these platforms to engage and empower their patients.

For AACR members, all 2015 Professional Advancement Sessions are free with your Annual Meeting registration (except for the Grant Writing Workshop) and are an added benefit of your membership. For nonmembers, there is an additional fee of $50 ($95 for the Grant Writing Workshop) for attendance at each session. If you are not an AACR member, we strongly encourage you to join and take advantage of the many benefits of membership, which include attendance at these sessions. Participation is on a first-come, first-served basis, and space is limited. Nonmembers are required to pay on site.

5:30 p.m.   **Using Twitter and LinkedIn to lead and follow your field**
Wafik S. El-Deiry, Fox Chase Cancer Center, Philadelphia, PA

5:45 p.m.   **Engaging with patients and colleagues on social media**
Emil Lou, University of Minnesota, Minneapolis, MN

6:00 p.m.   **Engaging with investigators on social media: What patients are looking for**
AnneMarie Ciccarella, Independent Advocate, Glen Head, NY

6:15 p.m.   **Questions and Discussion**

AACR-WICR CHARLOTTE FRIEND LECTURE

Saturday, 5:30 p.m.-6:45 p.m.

Terrace Ballroom II-III (400 Level), Pennsylvania Convention Center
Eighteenth Annual AACR-Women in Cancer Research
Charlotte Friend Memorial Lectureship
Cancer Cell Invasion and Metastasis

Sara A. Courtneidge, PhD, DSc (hc)
Professor, Department of Cell Development & Cancer Biology
Oregon Health & Science University, Collaborative Life Sciences Building, Portland, OR

The AACR-Women in Cancer Research Charlotte Friend Memorial Lectureship was established in 1998 in honor of renowned virologist and discoverer of the Friend virus, Dr. Charlotte Friend, for her pioneering research on viruses, cell differentiation, and cancer. The lectureship recognizes an outstanding scientist who has made meritorious contributions to the field of cancer research and who has, through leadership or by example, furthered the advancement of women in science.

Sara A. Courtneidge, PhD, is honored for her contributions to our understanding of the roles of Src-family kinases in tumor development. As a leader in kinase biology and drug development, Dr. Courtneidge has made outstanding contributions to cancer research in both academia and the biotechnology industry. Over the years, she gave numerous keynote addresses and plenary lectures to share her exciting and important discoveries with national and international cancer research communities. In addition to these accomplishments, and of special relevance for this award, Sara is a passionate and committed advocate for women in science. Not only does she exemplify the highest standards in her own work, she serves the community tirelessly.

Dr. Courtneidge's research has focused on the first oncogene to be discovered, Src, and how its dysregulation contributes to cancer. She is known for her research on oncologic transformation, including her discovery that the RSV v-Src transforming protein and its cellular counterpart, c-Src, are plasma membrane-associated, anchored to the membrane via an N-terminal myristoyl group. She discovered that the middle T antigen of polyomavirus is associated with c-Src, a finding that revolutionized the DNA tumor virus field. Dr. Courtneidge also found that c-Src is activated by association with the PDGF receptor tyrosine kinase, and is required for mitogenic signaling in a pathway that leads to c-Myc.

Recently, Dr. Courtneidge identified the Tks4 and Tks5 adaptor proteins as Src substrates and showed that they function through Nox-mediated ROS generation at the surface of tumor cells where they trigger formation of invadopodia, which control the proteases essential for tumor cell invasion through normal tissue.

Dr. Courtneidge has been an active AACR member, having served on the board of directors, the nominating committee, as program chair of the Annual Meeting 2003, and as a scientific editor of several journals. She is currently on the editorial board of *Cancer Today,* the AACR's consumer-oriented publication. She is also an adjunct professor at Sanford-Burnham Medical Research Institute in La Jolla, California, and the University of California, San Diego. A native of the United Kingdom, Dr. Courtneidge graduated from the University of Leeds and received her doctorate from the National Institute for Medical Research in London. Prior to joining OHSU in 2014, Dr. Courtneidge was director of the tumor microenvironment and metastasis program and academic affairs at Sanford-Burnham Medical Research Institute.

PROFESSIONAL ADVANCEMENT SESSION *(not eligible for CME credit)*

Saturday, 5:30 p.m.-7:30 p.m.

Grand Ballroom Salons C-E (Level 5), Philadelphia Marriott Downtown

Careers in Clinical and Translational Cancer Research

Chairperson: A. William Blackstock, Jr., Wake Forest University School of Medicine, Winston-Salem, NC

This session is offered to postdoctoral and clinical fellows, and graduate and medical students interested in careers in clinical and translational research. Dr. A. William Blackstock, Jr., will open the session with a brief introduction, followed by presentations by recognized leaders in clinical and translational research to respond to the needs of researchers in training. These senior investigators will describe their own career experiences and the successes that helped them establish their career paths. They will also provide personal perspectives to direct clinical and translational researchers on successful careers. The presentations will be followed by mentored roundtable discussions. Mentors will be preassigned to each of the tables to promote dialog and respond to questions from interested young clinical investigators. Limited space is available and admission will be on a first-come, first-served basis. The program will begin promptly at 5:30 p.m. For AACR members, Professional Advancement Sessions are free with your Annual Meeting registration and are an added benefit of your membership. For nonmembers, there is an additional fee of $50 for attendance at each session to be paid onsite.

5:30 p.m.	**Introduction** A. William Blackstock, Jr., Wake Forest University School of Medicine, Winston-Salem, NC
5:45 p.m.	Beverly A. Teicher, National Cancer Institute, Bethesda, MD
6:00 p.m.	Steven D. Averbuch, Bristol-Myers Squibb Co., Princeton, NJ
6:15 p.m.	Dan Theodorescu. University of Colorado Cancer Center, Aurora, CO
6:30 p.m.	General Discussion with Mentors

Mentors:

Cory Abate-Shen, Columbia University Irving Comprehensive Cancer Center, New York, NY

Steven D. Averbuch, Bristol-Myers Squibb Co., Princeton, NJ

Susan E. Bates, National Cancer Institute, Bethesda, MD

A. William Blackstock, Wake Forest University School of Medicine, Winston-Salem, NC

James E. Bradner, Dana-Farber Cancer Institute, Boston, MA

Johann S. De Bono, Institute of Cancer Research, Sutton, United Kingdom

Robert S. DiPaola, Rutgers Cancer Institute of New Jersey, New Brunswick, NJ

James H. Doroshow, National Cancer Institute-DCTD, Bethesda, MD

Lee M. Ellis, The University of Texas MD Anderson Cancer Center, Houston, TX

Susan M. Galbraith, AstraZeneca, Macclesfield, United Kingdom

Tona M. Gilmer, GlaxoSmithKline, Research Triangle Park, NC

Lee J. Helman, National Cancer Institute, Bethesda, MD

Sandra J. Horning, Genentech, Inc., San Francisco, CA

Richard M. Marais, Cancer Research UK Manchester Institute, Manchester, United Kingdom

Douglas M. Noonan, University of Insubria, Varese, Italy

William Pao, Roche Pharma Early Research and Development, Basel, Switzerland

Yves G. Pommier, National Cancer Institute-CCR, Bethesda, MD

Joseph D. Rosenblatt, University of Miami Sylvester Comprehensive Cancer Center, Miami, FL

Eric H. Rubin, Merck Research Laboratories, North Wales, PA

Edward A. Sausville, University of Maryland Greenebaum Cancer Center, Baltimore, MD

Geoffrey I. Shapiro, Dana-Farber Cancer Institute, Boston, MA

Lillian L. Siu, University Health Network Princess Margaret Hospital, Toronto, ON, Canada

Beverly A. Teicher, National Cancer Institute, Bethesda, MD

Dan Theodorescu, University of Colorado Cancer Center, Aurora, CO

Giampaolo Tortora, University of Verona, Verona, Italy

Louis M. Weiner, Georgetown Lombardi Comprehensive Cancer Center, Washington, DC

Cheryl L. Willman, University of New Mexico Cancer Research and Treatment Center, Albuquerque, NM

MEET AND GREET *(not eligible for CME credit)*

Saturday, 6:30 p.m.-8:30 p.m.

Hall E Foyer (200 Level), Pennsylvania Convention Center
New Member Networking Mixer

The New Member Mixer at the AACR Annual Meeting provides an excellent opportunity for AACR's leadership to welcome and recognize new AACR members. The purpose of this event is to provide an informal gathering where new members will be welcomed into the AACR, learn more about AACR programs and upcoming activities, and have the opportunity to network with other members. Members of AACR leadership, including representatives from AACR Association Groups, will be present. Refreshments will be served.

Special Remarks

2015-2016 AACR President
José Baselga, Memorial Sloan Kettering Cancer Center, New York, NY