This AACR Precision Medicine Series conference will focus on the critical points at which cancer becomes resistant to treatment. Research presented will address acquired resistance (secondary genetic alterations or changes in signaling pathways), adaptive resistance (DNA/RNA/protein or microenvironment-mediated), preexisting resistance from tumor heterogeneity or clonal selection, and lessons learned from “extreme” responders to therapy. This conference will also focus on new technologies, diagnostics, and noninterventional assessments to detect emerging resistance to treatment. Elucidating resistance mechanisms and exploiting cancer vulnerabilities to therapeutics will ultimately improve cancer therapy and patient care. This conference explores topics that will appeal to clinicians, as well as, basic, translational, and clinical scientists ranging from academics to industry.

The AACR would like to thank the following organizations for their generous support of this conference.

Professional Educational Grants

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The AACR thanks the following organizations for their generous support of the travel awards provided at this conference.

Award Supporters

AACR Precision Medicine Series
DRUG SENSITIVITY AND RESISTANCE: IMPROVING CANCER THERAPY
Conference Program

Wednesday, June 18

7:30 p.m.-8:30 p.m.   Opening Keynote Session
                      Grand Cypress Ballroom DEF

  Immunologic heterogeneity of cancer: Determinants of response and resistance to immunotherapy
  Suzanne L. Topalian, Johns Hopkins Kimmel Comprehensive Cancer Center, Baltimore, MD

8:30 p.m.-10:00 p.m. Opening Reception
                      Upper Pool Deck

Thursday, June 19

7:00 a.m.-8:00 a.m.  Continental Breakfast
                      Portico West

8:00 a.m.-10:00 a.m. Plenary Session 1: Adaptive Resistance
                      Grand Cypress Ballroom DEF
                      Session Chairperson: Matthew J. Ellis, Washington University Siteman Cancer Center, St. Louis, MO

  Matrix-dependent adaptive responses to targeted therapies
  Joan S. Brugge, Harvard Medical School, Boston, MA

  Mutations, drugs and breast cancer: How are we going to figure it out?
  Matthew J. Ellis

  Using comprehensive proteomic approaches to map signaling adaptations to BRAF and BRAF/MEK inhibition
  Keiran S.M. Smalley, Moffitt Cancer Center & Research Institute, Tampa, FL

  Adaptive resistance of patient-derived ovarian cancer cells to PI3K/mTOR inhibition*
  Ioannis Zervantonakis, Harvard Medical School, Boston, MA

10:00 a.m.-10:30 a.m. Break
                      Portico West

*Short talks from proffered papers.
10:30 a.m.-12:30 p.m.       Plenary Session 2: Noninterventional Assessment of Emerging Resistance or Increasing Tumor Burden
Grand Cypress Ballroom DEF
Session Chairperson: Nitzan Rosenfeld, Cancer Research UK Cambridge Research Institute, Cambridge, United Kingdom

Circulating tumor cells in lung cancer: Biomarkers, biology, and mouse models to study drug resistance
Caroline Dive, Cancer Research UK Manchester Institute, Manchester, United Kingdom

Monitoring the cancer genome in plasma using circulating tumor DNA
Nitzan Rosenfeld

Title to be announced
Jorge S. Reis-Filho, Memorial Sloan Kettering Cancer Center, New York, NY

12:30 p.m.-2:30 p.m.       Lunch on Own/Free Time

2:30 p.m.-4:00 p.m.        Panel Discussion – Barriers to Implementing Liquid Biopsy Monitoring
Grand Cypress Ballroom DEF

Panelists:
Caroline Dive, Cancer Research UK Manchester Institute, Manchester, United Kingdom
Nitzan Rosenfeld, Cancer Research UK Cambridge Research Institute, Cambridge, United Kingdom
Filip Janku, The University of Texas MD Anderson Cancer Center, Houston, TX
Howard I. Scher, Memorial Sloan Kettering Cancer Center, New York, NY
Elaine R. Mardis, Washington University School of Medicine, St. Louis, MO

4:00 p.m.-6:00 p.m.        Plenary Session 3: Extreme Resistance
Grand Cypress Ballroom DEF
Session Chairperson: David B. Solit, Memorial Sloan Kettering Cancer Center, New York, NY

Genetic predictors of drug sensitivity
David B. Solit

Title to be announced
José Baselga, Memorial Sloan Kettering Cancer Center, New York, NY

Kinase-impaired BRAF mutations as predictors of resistance and sensitivity
Faye M. Johnson, The University of Texas MD Anderson Cancer Center, Houston, TX

Identification of ERK1/2 mutations that confer resistance to MAPK pathway inhibitors*
Eva M. Goetz, Dana-Farber Cancer Institute, Boston, MA

*Short talks from proffered papers.
Friday, June 20

7:00 a.m.-9:30 a.m.  **Poster Session A and Continental Breakfast**  
Grand Cypress Ballroom GHI

9:30 a.m.-11:30 a.m.  **Plenary Session 4: Preexisting Resistance**  
Grand Cypress Ballroom DEF  
*Session Chairperson: Elaine R. Mardis, Washington University School of Medicine, St. Louis, MO*

Using genomics to study preexisting resistance  
Elaine R. Mardis

Correlating cancer heterogeneity to treatment response and relapse  
Elli Papaemmanuil, Wellcome Trust Sanger Institute, Cambridge, United Kingdom

Title to be announced  
Roger S. Lo, University of California, Los Angeles, CA

Identifying biomarkers of drug response and resistance using personalized Drosophila models of colorectal cancer*  
Erdem Bangi, Icahn School of Medicine at Mount Sinai, New York, NY

A melanoma transcriptional state distinction influences sensitivity to MAPK pathway inhibitors*  
Cory Johannessen, The Broad Institute of Harvard and MIT, Cambridge, MA

11:30 a.m.-1:30 p.m.  Lunch on Own / Free Time

1:30 p.m.-3:30 p.m.  **Plenary Session 5: Acquired Resistance**  
Grand Cypress Ballroom DEF  
*Session Chairperson: Gordon B. Mills, The University of Texas MD Anderson Cancer Center, Houston, TX*

Functionalizing the cancer genome  
Gordon B. Mills

Strategies to overcome acquired resistance to kinase inhibitors  
Gideon Bollag, Plexxikon, Inc., Berkeley, CA

Acquired resistance to targeted therapeutics in hematologic malignancies  
Neil P. Shah, University of California, San Francisco School of Medicine, San Francisco, CA

ERK pathway activation is associated with acquired resistance to AZD9291, a third-generation irreversible inhibitor targeting EGFR sensitizing (EGFRm+) and resistance (T790M) mutations in NSCLC*  
Cath Eberlein, AstraZeneca, Macclesfield, Cheshire, United Kingdom (not designated for CME credit)

A co-clinical assessment of patterns of BRAF inhibitor resistance*  
Lawrence N. Kwong, The University of Texas MD Anderson Cancer Center, Houston, TX

*Short talks from proffered papers.

**DRUG SENSITIVITY AND RESISTANCE: IMPROVING CANCER THERAPY**
Saturday, June 21

7:00 a.m.-8:00 a.m.  Continental Breakfast
Portico West

8:00 a.m.-10:00 a.m.  Plenary Session 6: Utility of Models in Predicting Resistance
Grand Cypress Ballroom DEF
Session Chairperson: Andrew E. Aplin, Thomas Jefferson University
Kimmel Cancer Center, Philadelphia, PA

Studying therapy response and resistance in mouse models of human breast cancer
Jos Jonkers, Netherlands Cancer Institute, Amsterdam, The Netherlands

ERK activity in mutant BRAF melanoma – A live report
Andrew E. Aplin

Modeling resistance to MAPK pathway inhibitors in melanoma preclinical models
Nancy K. Pryer, Novartis Institutes for BioMedical Research, Emeryville, CA

The strength of drug selection determines the maximum fitness cost of resistance mutations in culture and xenografts*
Lee A. Albacker, Harvard Medical School, Boston, MA

Microparticles derived from drug-resistant cells regulate miR-503 and PYK2 to promote migration and invasion in breast cancer*
Mary Bebawy, University of Technology Sydney, Ultimo, Australia

10:00 a.m.-10:15 a.m.  Break
Portico West

*Short talks from proffered papers.
10:15 a.m.-12:15 p.m.  Plenary Session 7: New Technologies and Diagnostics  
Grand Cypress Ballroom DEF  
Session Chairperson: Nicholas E. Navin, The University of Texas MD Anderson Cancer Center, Houston, TX

Molecular and genomic characterization of invasive circulating tumor cells (iCTCs) from men with metastatic castration-resistant prostate cancer (mCRPC)  
Pamela L. Paris, UCSF Helen Diller Family Comprehensive Cancer Center, San Francisco, CA

Enumeration of circulating tumor cells for studying cancer drug sensitivity  
Z. Hugh Fan, University of Florida, Gainesville, FL

Investigating breast cancer diversity and evolution with single-cell genomics  
Nicholas E. Navin

Single cell phosphoproteomics identifies adaptive network dynamics of mTOR inhibitor resistance and defines effective combination therapy in glioblastoma*  
Young Shik Shin, University of California, Los Angeles, CA

12:15 p.m.  Departure

*Short talks from proffered papers.