Conference Program

NOTE:

A = Session in the Translation of the Cancer Genome Conference

B = Session in the Computational and Systems Biology of Cancer Conference

A and B = Joint Session

Saturday, February 7

1:00 p.m.-3:00 p.m. **Session A1: Cancer Genomics and Epigenomics**
Grand Ballroom
Session Chairperson: Levi A. Garraway, Dana-Farber Cancer Institute, Boston, MA

Genomic heterogeneity in localized lung cancer
Andrew Futreal, The University of Texas MD Anderson Cancer Center, Houston, TX

Cancer genomics: Translational challenges
Elaine R. Mardis, Washington University, St. Louis, MO

The Pediatric Cancer Genome Project: Lessons learned
James R. Downing, St. Jude Children's Research Hospital, Memphis, TN

Identifying clinically important somatic mutations through a knowledge-based approach*
Benjamin J. Ainscough, Washington University in St. Louis School of Medicine, St. Louis, MO

Aneuploidy as a driver of liver cancer*
Lee Albacker, Harvard Medical School, Boston, MA

3:00 p.m.-3:30 p.m. **Break**
Grand Ballroom Foyer

3:30 p.m.-5:30 p.m. **Session A2: Clinical Applications of Cancer Genomics**
Grand Ballroom
Session Chairperson: Elaine R. Mardis, Washington University, St. Louis, MO

Clinical decision support in the era of genome-informed cancer medicine
Mia A. Levy, Vanderbilt University, Nashville, TN

Guiding principles of resistance to targeted therapeutics
Levi A. Garraway, Dana-Farber Cancer Institute, Boston, MA

Genomic medicine: Transforming cancer research and care
Lynda Chin, The University of Texas MD Anderson Cancer Center, Houston, TX

Pan-cancer analysis of the etiology and consequences of intratumor heterogeneity*
Noemi Andor, Stanford University School of Medicine, Stanford, CA

Cancer drug response networks built for comparative cancer pharmacogenomics identifies combination therapies for repositioning*
Gurkan Bebek, Case Western Reserve University, Cleveland, OH

*Short talks from proffered papers.

5:30 p.m.–8:00 p.m. **Poster Session A1 with Reception**
Gold Room/Venetian Room

Sunday, February 8

7:00 a.m.–8:00 a.m. **Breakfast**
Venetian Room

8:00 a.m.–10:00 a.m. **Session A3: Genomics and Target Discovery**
Grand Ballroom
Session Chairperson: Todd R. Golub, Broad Institute of MIT and Harvard, Cambridge, MA

Globally monitoring translation one codon at a time through ribosome profiling
Jonathan Weissman, University of California San Francisco, San Francisco, CA

Functional genomics to identify cancer targets
William C. Hahn, Dana-Farber Cancer Institute, Boston, MA

Therapy of lymphoma inspired by functional and structural genomics
Louis M. Staudt, National Cancer Institute, Bethesda, MD

Personalized medicine
René Bernards, Netherlands Cancer Institute, Amsterdam, The Netherlands

10:00 a.m.–10:30 p.m. **Break**
Grand Ballroom Foyer

10:30 a.m.–12:30 p.m. **Session A4: Genomics and Drug Discovery**
Grand Ballroom
Session Chairperson: Wendy Winckler, Novartis Institutes for BioMedical Research, Cambridge, MA

Tools for genomic approaches to drug discovery: PRISM and Connectivity Map
Todd R. Golub, Broad Institute of MIT and Harvard, Cambridge, MA

Functional genomic approaches to find the best cancer targets
Frank Stegmeier, Novartis, Cambridge, MA

Deconvoluting the molecular circuitry of cancerous cells with high-throughput experimentation
Lawrence Lum, UT Southwestern Medical Center, Dallas, TX

Using genome-scale CRISPR-mediated loss-of-function and gain-of-function screens to analyze gene-drug interactions in cancer*
Martin Kampmann, Howard Hughes Medical Institute, University of California, San Francisco, CA

Functional prioritization of rare gene aberration drivers of cancer*
Kenneth L. Scott, Baylor College of Medicine, Houston, TX

*Short talks from proffered papers.

12:30 p.m.–3:00 p.m. **Poster Session A2 with Lunch**
Gold Room/Venetian Room

3:00 p.m.–5:00 p.m. **Session A5: Genomics and Diagnostics**
Grand Ballroom
Session Chairperson: Louis M. Staudt, National Cancer Institute, Bethesda, MD

Single-cell sequencing in cancer genomics
Christopher Love, Massachusetts Institute of Technology, Cambridge, MA

Next-generation diagnostics for precision cancer medicine
Wendy Winckler, Novartis Institute for Biomedical Research, Cambridge, MA

Circulating tumor DNA
Luis A. Diaz, Johns Hopkins Kimmel Comprehensive Cancer Center, Baltimore, MD

Towards precision functional genomics via next-generation functional mapping of cancer variants*
Jesse S. Boehm, Broad Institute of Harvard and MIT, Cambridge, MA

In silico dissection of bulk tumors reveals immune subsets that predict cancer clinical outcomes*
Aaron M. Newman, Stanford University, Stanford, CA

5:00 p.m.–7:00 p.m. **Dinner on Own**

7:00 p.m.–8:00 p.m. **[JOINT SESSION] Welcome and Keynote Address**
Grand Ballroom

Spatial systems biology and cancer
Joe W. Gray, Oregon Health & Science University, Portland, OR

8:00 p.m.–9:30 p.m. **Reception**
Venetian Room

*Short talks from proffered papers.

Monday, February 9

7:00 a.m.-8:00 a.m. **Breakfast**
Venetian Room

8:00 a.m.-10:00 a.m. **[JOINT SESSION] Session A6, B1: Patient Stratification: Biomarker/Genomic Approaches**
Grand Ballroom
Session Chairperson: William R. Sellers, Novartis Institutes for BioMedical Research, Cambridge, MA

The application of integrative sequencing for precision oncology
Arul M. Chinnaiyan, University of Michigan, Ann Arbor, MI

Towards the next clinical option: Experience from a precision cancer medicine trial
Mark A. Rubin, Weill Cornell Medical College, New York, NY

Somatic mutations in human lung cancer
Matthew L. Meyerson, Dana-Farber Cancer Institute, Boston, MA

The prognostic landscape of genes and infiltrating immune cells across human cancers*
Andrew Gentles, Stanford University, Stanford, CA

Multiple Pathway Learning accurately predicts gene essentiality in the Cancer Cell Line Encyclopedia*
Vladislav Uzunangelov, University of California, Santa Cruz, CA

10:00 a.m.-10:30 a.m. **Break**
Grand Ballroom Foyer

10:30 a.m.-12:15 p.m. **[JOINT SESSION] Session A7, B2: Big Data in Clinical Applications**
Grand Ballroom
Session Chairperson: Andrea Califano, Columbia University, New York, NY

Modeling signaling systems in breast cancer cell lines
Paul T. Spellman, Oregon Health and Science University, Portland, OR

Network stratification of tumor mutations
Trey Ideker, University of California San Diego, La Jolla, CA

Genomic approaches for risk assessment in acute myeloid leukemia*
Allegra Petti, Washington University, St. Louis, MO

High-throughput gene expression profiling as a generalizable assay for determination of mutation impact on gene function*
Alice H. Berger, Broad Institute of MIT and Harvard, Cambridge, MA

Investigating the importance of low allele frequency mutations for cancer patient management*
Ken Chen, The University of Texas MD Anderson Cancer Center, Houston, TX

*Short talks from proffered papers.

12:15 p.m.-1:45 p.m. **Lunch on Own**

1:45 p.m.-4:00 p.m. **[JOINT SESSION] Session A8, B3: Network-Based Cancer Biology**
Grand Ballroom
Session Chairperson: Peter K. Jackson, Stanford University, Stanford, CA

Using single cell pharmacology to improve drug design
Peter K. Sorger, Harvard Medical School, Boston, MA

Interactome networks and cancer
Marc Vidal, Dana-Farber Cancer Institute, Boston, MA

Systematic elucidation and pharmacological targeting of non-oncogene dependencies in human malignancies
Andrea Califano, Columbia University, New York, NY

Nucleation of transcriptional super-enhancers at tumor oncogenes*
Brian J. Abraham, Whitehead Institute for Biomedical Research, Cambridge, MA

Functional analysis of diverse oncogenic driver mutations using an isogenic cell line library identifies novel drug responses and alterations in metabolism*
Andrei Goga, University of California, San Francisco, CA

New tools for mapping genetic modifiers of cancer risk in the tumor microenvironment*
Michael J. Flister, Medical College of Wisconsin, Milwaukee, WI

4:15 p.m.-5:00 p.m. **[JOINT SESSION] Keynote Talk 2**
Grand Ballroom

Cognitive computing for oncology
Eric W. Brown, IBM TJ Watson Research Center, Yorktown Heights, NY

5:00 p.m. -5:15 p.m. **Closing remarks for the attendees of the AACR Special Conference on Translation of the Cancer Genome**

*Short talks from proffered papers.