

CONFERENCE PROGRAM

Monday, March 2

5:00 p.m.-7:00 p.m.

WELCOME AND OPENING KEYNOTE LECTURES

Legends 1-4

Introductions by **Cory Abate-Shen**, Columbia University Irving Comprehensive Cancer Center, New York, NY, and **Calvin J. Kuo**, Stanford University, Stanford, CA

5:00 p.m.-6:00 p.m.

Modeling and understanding tumor biologic mechanisms

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

6:00 p.m.-7:00 p.m.

Title to be announced

Toshiro Sato, Keio University, Tokyo, Japan

7:00 p.m.-9:00 p.m.

OPENING RECEPTION

Encore

Tuesday, March 3

7:00 a.m.-8:00 a.m.

BREAKFAST

Encore

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

PLENARY SESSION 1: LINEAGE PLASTICITY, STEM CELLS AND DEVELOPMENTAL PATHWAYS

Legends 1-4

Session Chairs: **Karuna Ganesh**, Memorial Sloan Kettering Cancer Institute, New York, NY, and **Elena Piskounova**, Weill Cornell Medicine, New York, NY

8:00 a.m.-8:30 a.m.

Neuroendocrine differentiation in prostate development and cancer

Michael M. Shen, Columbia University, New York, NY

8:30 a.m.-8:45 a.m.

Developmental reprogramming via Hedgehog pathway activation in nonmyogenic endothelial progenitors drives fusion-negative rhabdomyosarcoma*

Mark Hatley, St. Jude Children's Research Hospital, Memphis, TN

8:45 a.m.-9:15 a.m.

Stem cells: Coping with stress and cancer

Elaine Fuchs, Rockefeller University, New York, NY

**Short talk from proffered abstract*

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- 9:15 a.m.-9:30 a.m. **Matched metastatic pancreatic ductal adenocarcinoma biopsies and organoid models reveal tumor cell transcriptional plasticity and subtype-specific microenvironmental crosstalk***
Peter Winter, Massachusetts Institute of Technology, Cambridge, MA
- 9:30 a.m.-10:00 a.m. **Signaling networks in small-cell lung cancer**
Julien Sage, Stanford University, Stanford, CA
- 10:00 a.m.-10:30 a.m. BREAK**
Abbey Road
- 10:30 a.m.-12:30 p.m. PLENARY SESSION 2: MODELING THE IMMUNE RESPONSE AND THE TUMOR MICROENVIRONMENT**
Legends 1-4
Session Chairs: Alison Taylor, Columbia University Medical Center, New York, NY, and **Camila Dos Santos**, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
- 10:30 a.m.-11:00 a.m. **The tissue-specific microenvironment in primary tumors and metastases**
Zena Werb, University of California San Francisco, San Francisco, CA
- 11:00 a.m.-11:15 a.m. **Use of CRISPR knock-out screen to identify genes that regulate tumor cell sensitivity to NK cell-based immunotherapy***
Davide Bernareggi, University of California San Diego, San Diego, CA
- 11:15 a.m.-11:45 a.m. **Targeting the pancreas cancer microenvironment to therapeutic advantage**
Sunil R. Hingorani, Fred Hutchinson Cancer Research Center, Seattle, WA
- 11:45 a.m.-12:00 p.m. **Lymph node colonization promotes distant tumor metastasis through the induction of tumor-specific immunosuppression***
Nathan Reticker-Flynn, Stanford University, Stanford, CA
- 12:00 p.m.-12:30 p.m. **Organoid modeling of tumor and tissue microenvironments**
Calvin J. Kuo, Stanford University, Stanford, CA
- 12:30 p.m.-2:30 p.m. LUNCH ON OWN**
- 2:30 p.m.-4:30 p.m. PLENARY SESSION 3: MODELING DRUG SENSITIVITY AND ADAPTIVE RESPONSE**
Legends 1-4
Session Chairs: Hariharan Easwaran, The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins, Johns Hopkins University School of Medicine, Baltimore, MD, and **Jesse Boehm**, Broad Institute, Cambridge, MA
- 2:30 p.m.-3:00 p.m. **Tumor organoid cultures as a platform for functional genomics**
Mathew Garnett, Wellcome Sanger Institute, Cambridge, United Kingdom

**Short talk from proffered abstract*

- 3:00 p.m.-3:15 p.m. **A metabolomics discovery profiling approach identifies an E2F1-associated purine synthesis pathway as a major component of the MET-DNA damage response network***
Michaela Medová, Bern University Hospital, Bern, Switzerland
- 3:15 p.m.-3:45 p.m. **Modeling sensitivity and resistance to systemic therapies in lung cancer**
Katerina A. Politi, Yale University, New Haven, CT
- 3:45 p.m.-4:00 p.m. **An in vivo KRAS allelic series reveals distinct phenotypes of common oncogenic variants***
Maria Paz Zafra, Weill Cornell Medicine, New York, NY
- 4:00 p.m.-4:30 p.m. **The use of GEM tumor models to identify effective therapies against KRAS mutant tumors**
Mariano Barbacid, CNIO, Madrid, Spain
- 4:30 p.m.-4:40 p.m. POSTER HIGHLIGHTS A**
Legends 1-4

Introductions by **Cory Abate-Shen**, Columbia University Irving Comprehensive Cancer Center, New York, NY
- 4:30 p.m.-4:32 p.m. **Modeling the tissue-specific oncogenesis of mutant RAS**
Amanda Moore, Genentech, Inc., South San Francisco, CA
- 4:32 p.m.-4:34 p.m. **Androgen receptor blockade induces reprogramming to mesenchymal and stemlike prostate cancer and dependency on HER2/3 signaling**
Hyunho Han, The University of Texas MD Anderson Cancer Center, Houston, TX
- 4:34 p.m.-4:36 p.m. **Coordinate translational control of KRAS signaling pathway in pancreatic adenocarcinoma**
Kamini Singh, Memorial Sloan Kettering Cancer Center, New York, NY
- 4:36 p.m.-4:38 p.m. **A new somatic engineering-based model of small-cell lung cancer development**
Kwon-Sik Park, University of Virginia, Charlottesville, VA
- 4:38 p.m.-4:40 p.m. **Strategies to improve engineering cancer-associated SNVs with base editing**
Alyna Katti, Weill Cornell Medicine, New York, NY
- 4:40 p.m.-7:00 p.m. RECEPTION / POSTER SESSION A**
Encore/Legends 5-6

**Short talk from proffered abstract*

CONFERENCE PROGRAM

Wednesday, March 4

7:00 a.m.-8:00 a.m.

BREAKFAST

Encore

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

PLENARY SESSION 4: MODELING TUMOR EVOLUTION

Legends 1-4

Session Chairs: Katerina A. Politi, Yale University, New Haven, CT, and **Kwon-Sik Park**, University of Virginia, Charlottesville, VA

8:00 a.m.-8:30 a.m.

From mouse to man: Dissecting cancer mechanisms using mouse models

Cory Abate-Shen, Columbia University, New York, NY

8:30 a.m.-8:45 p.m.

Somatic tissue engineering in mouse models reveals an actionable role for WNT pathway alterations in prostate cancer metastasis*

Josef Leibold, Memorial Sloan Kettering Cancer Center, New York, NY

8:45 a.m.-9:15 a.m.

Identification, validation and therapeutic targeting of a driver gene in poor-prognosis breast cancer

Yibin Kang, Rutgers University, Princeton, NJ

9:15 a.m.-9:30 a.m.

Leveraging single-cell epigenomics to uncover regulatory programs in lung adenocarcinoma*

Lindsey LaFave, Massachusetts Institute of Technology, Cambridge, MA

9:30 a.m.-10:00 a.m.

Deconstructing the origins of PDAC development

Laura D. Attardi, Stanford University School of Medicine, Stanford, CA

10:00 a.m.-10:30 a.m.

BREAK

Abbey Road

10:30 a.m.-12:00 p.m.

MODEL FIDELITY FORUM

Legends 1-4

Moderator: Pier Paolo Pandolfi, Dana-Farber Cancer Center, Boston, MA

Embracing complexity: Changing how we use the mouse to model human cancer

Carol Bult, The Jackson Laboratory, Bar Harbor, ME

The International Human Cancer Models Initiative is generating models annotated with clinical and molecular data

Daniela S. Gerhard, National Cancer Institute, Bethesda, MD

A systematic approach to create patient-derived models of rare tumors*

Jesse Boehm, Broad Institute, Cambridge, MA

**Short talk from proffered abstract*

12:00 p.m.-1:00 p.m.	<p>SECOND KEYNOTE LECTURE Legends 1-4</p> <p>Introduction by Andrea Califano, Columbia University Medical Center, New York, NY</p> <p>Defining cancer dependency maps William C. Hahn, Dana-Farber Cancer Center, Boston, MA</p>
1:00 p.m.-1:10 p.m.	<p>POSTER HIGHLIGHTS B Legends 1-4</p> <p>Introductions by Cory Abate-Shen, Columbia University Irving Comprehensive Cancer Center, New York, NY</p>
1:00 p.m.-1:02 p.m.	<p>The zebrafish as a mechanical filter: Using zebrafish xenografts to model Ewing sarcoma metastasis in vivo Dagan Segal, The University of Texas Southwestern Medical Center, Dallas, TX</p>
1:02 p.m.-1:04 p.m.	<p>Impact of genetic diversity on the growth of human-derived xenografts Muneer Hasham, The Jackson Laboratory, Bar Harbor, ME</p>
1:04 p.m.-1:06 p.m.	<p>A hierarchical model of DNA repair inferred from omics-scale genetic interaction data reveals the dynamics of DNA damage induction Anton Kratz, University of California San Diego, San Diego, CA</p>
1:06 p.m.-1:08 p.m.	<p>Predictive modeling, applied to genetically engineered mouse models of breast or lung cancer, provides insights into major oncogenic pathways Bodo Lange, Alacris Theranostics GmbH, Berlin, Germany</p>
1:08 p.m.-1:10 p.m.	<p>Mechanism-based computational models to study interplay between EGFR inhibitors and KRAS mutants Edward Stites, Salk Institute for Biological Studies, La Jolla, CA</p>
1:10 p.m.-3:30 p.m.	<p>LUNCH / POSTER SESSION B Encore/Legends 5-6</p>
3:30 p.m.-5:15 p.m.	<p>PLENARY SESSION 5: FROM MODELS TO THE CLINIC Legends 1-4</p> <p>Session Chairs: Jinsong Liu, The University of Texas MD Anderson Cancer Center, Houston, TX, and Michael Shen, Columbia University Medical Center, New York, NY</p>
3:30 p.m.-4:00 p.m.	<p>Genetic dissection of breast cancer development and therapy resistance in mouse models Jos Jonkers, Netherlands Cancer Institute, Amsterdam, The Netherlands</p>
4:00 p.m.-4:15 p.m.	<p>A versatile ES cell-based melanoma mouse modeling platform* Florian Karreth, H. Lee Moffitt Cancer Center and Research Institute, Tampa, FL</p>

**Short talk from proffered abstract*

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- 4:15 p.m.-4:30 p.m. **MADR: Rapid generation of somatic mosaics with locus-specific, stably integrated transgenic elements for generation of “personalized” mouse models and human organoid tumor models***
Joshua Breunig, Cedars-Sinai Medical Center, Los Angeles, CA
- 4:30 p.m.-5:00 p.m. **Role of autophagy in cancer metabolism**
Eileen P. White, Rutgers Cancer Institute of New Jersey, New Brunswick, NJ
- 5:00 p.m.-5:15 p.m. **Dynamic single-cell imaging of human cancer growth and therapy responses following engraftment into immunodeficient zebrafish***
David Langenau, Massachusetts General Hospital Research Institute, Charlestown, MA
- 5:15 p.m.-5:45 p.m. **Modeling cancer in the mouse and its therapeutic implications**
Pier Paolo Pandolfi, Dana-Farber Cancer Center, Boston, MA
- 5:45 p.m. DINNER ON OWN**

Thursday, March 5

- 7:00 a.m.-8:00 a.m. BREAKFAST**
Encore
- 8:00 a.m.-10:00 a.m. PLENARY SESSION 6: SYSTEMS APPROACHES TO INTERROGATING DATA FROM MODELS**
Legends 1-4

Session Chairs: Andrew White, Cornell University, Ithaca, NY, and **Andrea Ventura**, Sloan Kettering Institute, New York, NY
- 8:00 a.m.-8:30 a.m. **Elucidating and targeting mechanisms of single-cell state maintenance: From N-of-1 to N-of-1-of-1 studies**
Andrea Califano, Columbia University Medical School, New York, NY
- 8:30 a.m.-8:45 a.m. **Polymerase-mediated ultramutagenesis: A new approach for modeling the high mutational load of human cancer***
Diego Castrillon, UT Southwestern Medical Center, Dallas, TX
- 8:45 a.m.-9:15 a.m. **Systems approach to rational combination therapy**
Gordon B. Mills, Oregon Health and Science University Knight Cancer Institute, Portland, OR
- 9:15 a.m.-9:30 a.m. **A multiscale map of recurrently mutated systems in cancer***
Fan Zheng, University of California San Diego, San Diego, CA

**Short talk from proffered abstract*

9:30 a.m.-10:00 a.m.	<p>Single-cell-resolution lineage tracing of tumors in a mouse xenograft model reveals rapid and multidirectional metastasis Jonathan S. Weissman, University of California San Francisco, San Francisco, CA</p>
10:00 a.m.-10:30 a.m.	<p>BREAK Abbey Road</p>
10:30 a.m.-12:30 p.m.	<p>PLENARY SESSION 7: LOOKING TO THE FUTURE OF CANCER MODELING Legends 1-4</p> <p>Session Chair: Jos Jonkers, Netherlands Cancer Institute, Amsterdam, The Netherlands</p>
10:30 a.m.-11:00 a.m.	<p>Interrogating therapy response and resistance in engineered preclinical models Lukas E. Dow, Weill Cornell Medicine, New York, NY</p>
11:00 a.m.-11:30 a.m.	<p>Modeling cancer in the CRISPR era Andrea Ventura, Sloan Kettering Institute, New York, NY</p>
11:30 a.m.-12:00 p.m.	<p>Multiplexed functional cancer genomics Monte M. Winslow, Stanford University, Stanford, CA</p>
12:00 p.m.-12:30 p.m.	<p>Title to be announced Tyler Jacks, The Koch Institute of MIT, Cambridge, MA</p>
12:30 p.m.	<p>CLOSING REMARKS Legends 1-4</p> <p>Jos Jonkers, Netherlands Cancer Institute, Amsterdam, The Netherlands</p>