

CONFERENCE PROGRAM

Thursday, March 1, 2018

- 5:00 p.m.–6:00 p.m.** **WELCOME AND OPENING KEYNOTE**
Grand Ballroom AB
- Epigenetic therapy: Bench to bedside**
Jean-Pierre J. Issa, Fels Institute for Cancer Research & Molecular Biology, Temple University, Philadelphia, PA
- 6:00 p.m.–8:30 p.m.** **WELCOME RECEPTION**
Grand Ballroom DEF

Friday, March 2, 2018

- 7:00 a.m.–8:00 a.m.** **BREAKFAST**
Grand Ballroom Foyer
- 8:00 a.m.–10:00 a.m.** **PLENARY SESSION 1: DNA METHYLATION AND CHROMATIN CROSSTALK**
Grand Ballroom AB
- Session Chair: Bradley E. Bernstein**, Massachusetts General Hospital/Harvard Medical School, Boston, MA
- Detecting and interpreting DNA methylation marks**
Xiaodong Cheng, The University of Texas MD Anderson Cancer Center, Houston, TX
- Activation of oncogenes by misfolded chromosomes**
Bradley E. Bernstein
- Epigenetic regulation through UHRF proteins**
Scott B. Rothbart, Van Andel Research Institute, Grand Rapids, MI
- DNA and histone methyltransferase inhibitors cooperate to increase viral mimicry in cancer cells***
Minmin Liu, Van Andel Research Institute, Grand Rapids, MI
- Investigating the mechanisms by which ZBTB38 recognizes methylated DNA and modulates transcription***
Nicholas Hudson, University of Utah, Salt Lake City, UT
- 10:00 a.m.–10:30 a.m.** **BREAK**
Grand Ballroom Foyer

**Short talk from proffered abstract*

CONFERENCE PROGRAM

- 10:30 a.m.–12:30 p.m.** **PLENARY SESSION 2: ENVIRONMENT, INFLAMMATION, AND DNA REPAIR**
Grand Ballroom AB
Session Chair: Susan J. Clark, Garvan Institute of Medical Research, Sydney, NSW, Australia
- Enduring epigenetic landmarks define the cancer microenvironment**
Susan J. Clark
- Epigenome response to the environment, inflammation, and DNA repair: A critical player for the early events in tumorigenesis?**
Stephen B. Baylin, Johns Hopkins University School of Medicine, Baltimore, MD
- Enhancing antitumor immune response by DNA-demethylating agents**
Daniel De Carvalho, Princess Margaret Cancer Centre, Toronto, ON, Canada
- Mismatch repair proteins initiate epigenetic alterations during inflammation-driven tumorigenesis***
Heather O'Hagan, Indiana University School of Medicine, Bloomington, IN
- DNA methylation patterns separate senescence from transformation potential and indicate cancer risk***
Hariharan Easwaran, The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins, The Johns Hopkins University School of Medicine, Baltimore, MD
- 12:30 p.m.–2:30 p.m.** **LUNCH ON OWN**
- 2:30 p.m.–4:30 p.m.** **PLENARY SESSION 3: DNMTS IN NORMAL AND MALIGNANT HEMATOPOIESIS**
Grand Ballroom AB
Session Chair: Margaret A. Goodell, Baylor College of Medicine, Houston, TX
- How do DNMT3A mutations initiate AML?**
Timothy J. Ley, Washington University School of Medicine, McDonnell Genome Institute, St. Louis, MO
- Immortal HSCs and their regulation by DNA methylation**
Margaret A. Goodell
- Restraining the mutagenic influence of 5-methylcytosine**
Ian Majewski, The Walter and Eliza Hall Institute of Medical Research, Parkville, VIC, Australia
- Genome-wide 5-hydroxymethylcytosine alterations in medulloblastoma***
Hyerim Kim, Emory University, Atlanta, GA
- Relapsing and refractory acute myeloid leukemia patients reveal converging genetic and epigenetic features suggesting common treatment strategies and response biomarkers***
Timothy Triche, Van Andel Research Institute, Grand Rapids, MI
- 4:30 p.m.–7:00 p.m.** **RECEPTION AND POSTER SESSION A**
Grand Ballroom DEF

**Short talk from proffered abstract*

Saturday, March 3, 2018

- 7:00 a.m.–8:00 a.m.** **BREAKFAST**
Grand Ballroom Foyer
- 8:00 a.m.–10:00 a.m.** **PLENARY SESSION 4: TETS AND 5HMC AND REGULATION OF GENE EXPRESSION**
Grand Ballroom AB
Session Chair: Lucy A. Godley, University of Chicago, Chicago, IL
- TET methylcytosine oxidases, immune responses, and cancer**
Anjana Rao, La Jolla Institute for Allergy & Immunology, La Jolla, CA
- Regulation of neuroblastoma phenotype by hypoxia and 5-hydroxymethylcytosine**
Lucy A. Godley
- DNA modifications: From mechanisms to genome-wide profiling in cancers**
François Fuks, Université libre de Bruxelles, Brussels, Belgium
- Synthetic lethal targeting of TET2 loss in myeloid malignancies by TOP1 inhibitors***
Chang-Bin Jing, Dana-Farber Cancer Institute, Boston, MA
- Identification of specific readers of epigenetic modifications in human bronchial epithelial cells using a quantitative proteomics approach***
Jenna Fernandez, Masonic Cancer Center, Minneapolis, MN
- 10:00 a.m.–10:30 a.m.** **BREAK**
Grand Ballroom Foyer
- 10:30 a.m.–12:30 p.m.** **PLENARY SESSION 5: TARGETING DNA METHYLATION IN THE CLINIC**
Grand Ballroom AB
Session Chair: Maria E. Figueroa, Sylvester Comprehensive Cancer Center, University of Miami, Miami, FL
- DNA-hypomethylating agents in acute myeloid leukemia (AML): The role of combination therapies and their curative potential**
Michael Lübbert, University Freiburg Medical Centre, Freiburg, Germany
- Modulation of the immune system in myeloid cancers by epigenetic therapy**
Kirsten Grønbaek, University of Copenhagen, Rigshospitalet, Copenhagen, Denmark
- DNA methylation in myelodysplastic syndromes: From clinical biomarkers to therapeutic targeting**
Maria E. Figueroa
- Discovery of selective, noncovalent small-molecule inhibitors of DNMT1***
Melissa Pappalardi, GlaxoSmithKline, Collegeville, PA
(not eligible for CME credit)
- Targeting CDK9 reactivates epigenetically silenced genes in cancer***
Hanghang Zhang, Fels Institute for Cancer Research & Molecular Biology, Temple University School of Medicine, Philadelphia, PA

**Short talk from proffered abstract*

CONFERENCE PROGRAM

- 12:30 p.m.–3:00 p.m.** **LUNCH AND POSTER SESSION B**
Grand Ballroom DEF
- 3:00 p.m.–5:15 p.m.** **PLENARY SESSION 6: EPIGENETIC MODULATION IN THE DEVELOPMENT OF CANCER**
Grand Ballroom AB
Session Chair: Benjamin P. Berman, Cedars-Sinai Medical Center, Los Angeles, CA
- Cancer methylation at the intersection of diverse chromatin processes**
Benjamin P. Berman
- Characterizing and modulating epigenetic events during melanoma initiation**
Charles K. Kaufman, Washington University School of Medicine, St. Louis, MO
- Epigenetic field induced by vicious combination of inflammatory signals**
Toshikazu Ushijima, National Cancer Center Research Institute, Tokyo, Japan
- p16 epimutation: Function in intestinal tumorigenesis and as a target for therapy***
Lanlan Shen, Baylor College of Medicine, Houston, TX
- Inhibition of histone methyltransferases EHMT1 and EHMT2 reduces PARP inhibitor resistance in high-grade serous ovarian cancer***
Zachary Watson, University of Colorado, Aurora, CO
- Targeted disruption of SIN3 chromatin regulator complex function inhibits metastasis and improves survival in triple-negative breast cancer***
Samuel Waxman, Icahn School of Medicine at Mount Sinai, New York, NY
- 5:15 p.m.** **EVENING OFF**

Sunday, March 4, 2018

- 7:00 a.m.–8:00 a.m.** **BREAKFAST**
Grand Ballroom Foyer
- 8:00 a.m.–10:00 a.m.** **PLENARY SESSION 7: SINGLE-CELL EPIGENOMIC ANALYSIS**
Grand Ballroom AB
Session Chair: Wolf Reik, Babraham Institute, Cambridge, United Kingdom
- Single-cell epigenome landscape of mammalian development and aging**
Wolf Reik
- Single-cell approaches for studying DNA methylation heterogeneity in tumors**
Amos Tanay, Weizmann Institute of Science, Rehovot, Israel
- iPS cell technology, gene editing, and disease research**
Rudolf Jaenisch, MIT Whitehead Institute for Biomedical Research, Cambridge, MA

**Short talk from proffered abstract*

CONFERENCE PROGRAM

Reprogramming of DNA and histone methylome by cancer-associated histone H3 mutations*

Chao Lu, Columbia University, New York, NY

CRISPR screening to assess genetic vulnerabilities in mutant IDH1-dependent models of different lineages*

Lindsey Rodrigues, Novartis Institutes for Biomedical Research, Cambridge, MA

10:00 a.m.–10:30 a.m.

BREAK

Grand Ballroom Foyer

10:30 a.m.–12:30 p.m.

PLENARY SESSION 8: REGULATION OF THE NONCODING GENOME

Grand Ballroom AB

Session Chair: Paula M. Vertino, Emory University Winship Cancer Institute, Atlanta, GA

Switching roles for DNA and histone methylation depend on evolutionary ages of human endogenous retroviruses

Peter A. Jones, Van Andel Research Institute, Grand Rapids, MI

Transposable elements in cancer epigenome

Ting Wang, Washington University School of Medicine, McDonnell Genome Institute, St. Louis, MO

Epigenetic regulation of transcriptional plasticity: Implications for cancer biology and therapy

Paula M. Vertino

The role of long noncoding RNA-mediated disruption of SWI/SNF in prostate cancer*

Jesse Raab, UNC Chapel Hill, Chapel Hill, NC

Epigenetic regulation of noncoding RNA in cancer and its effects on the immune microenvironment*

Katherine Chiappinelli, The George Washington University, Washington, DC

12:30 p.m.

CLOSING REMARKS

**Short talk from proffered abstract*