

An AACR Special Conference in Cancer Research
Cancer Epigenetics

Conference Program

Wednesday, January 20

7:00 p.m.-8:30 p.m. Opening Session

Chairperson

Peter W. Laird, USC Epigenome Center, Los Angeles, CA

Keynote Address

Reprogramming of Somatic Cells to a Pluripotent State

Rudolph Jaenisch, Whitehead Institute for Biomedical Research,
 Massachusetts Institute of Technology, Cambridge, MA

8:30 p.m.-9:30 p.m. Opening Dessert Reception

Thursday, January 21

8:00 a.m.-10:00 a.m. Session 1: Epigenetics of Stemness and Differentiation
Chairperson: Kornelia Polyak, Dana-Farber Cancer Institute, Boston, MA

8:00 a.m.-8:30 a.m. Hematopoietic stem cells and epigenetic regulation
 Margaret A. Goodell, Center for Cell and Gene Therapy,
 Baylor College of Medicine, Houston, TX

8:30 a.m.-9:00 a.m. Epigenomics, stem cells, and disease
 Alexander Meissner, Broad Institute of Harvard and MIT,
 Cambridge, MA

9:00 a.m.-9:30 a.m. Epigenomic landscapes in pluripotent and lineage-committed human cells
 Bing Ren, Ludwig Institute for Cancer Research, University
 of California, San Diego, La Jolla, CA

9:30 a.m.-9:45 a.m. Genome-wide histone and DNA methylation profiles of human mammary epithelial progenitor and luminal epithelial cells*
Reo Maruyama, Dana-Farber Cancer Institute, Boston, MA

9:45 a.m.-10:00 a.m. Analysis of DNA methylation reprogramming in human gynogenetic and androgenetic conceptuses*
Keith Killian, National Cancer Institute, Bethesda, MD

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

10:30 a.m.-12:30 p.m. Session 2: Other Epigenomes

*Chairperson: Peter A. Jones, USC/Norris
Comprehensive Cancer Center, Los Angeles, CA*

10:30 a.m.-11:00 a.m. Cancer epigenomics
Peter A. Jones

11:00 a.m.-11:30 a.m. Chromatin assembly and disassembly
Jessica K. Tyler, University of Colorado Health Sciences Center, Denver, CO

11:30 a.m.-12:00 p.m. Eukaryotic transcriptomes: Complex, multifunctional, compartmentalized, and elegant
Thomas R. Gingeras, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

12:00 p.m.-12:15 p.m. Genome-wide analysis of transcription start sites of epigenetically silenced genes using next-generation sequencer*
Minoru Toyota, Sapporo Medical University, Sapporo, Japan

12:15 p.m.-12:30 p.m. The intrinsic kinetochore histone variant H2.AFZ identifies chromosomes that contain immortal DNA strands*
James L. Sherley, Boston Biomedical Research Institute, Watertown, MA

4:00 p.m.-7:00 p.m. Poster Session A

- 7:00 p.m.-9:00 p.m. Session 3: Readers and Writers**
*Chairperson: Paula M. Vertino, Emory University
 Winship Cancer Institute, Atlanta, GA*
- 7:00 p.m.-7:30 p.m. The role of polycomb group proteins and lysine demethylases in stem cell differentiation and cancer**
 Kristian Helin, Biotech Research and Innovation Centre, University of Copenhagen, Copenhagen, Denmark
- 7:30 p.m.-8:00 p.m. TDRD3 is an effector molecule for arginine methylated histone marks**
 Mark T. Bedford, UT M. D. Anderson Cancer Center, Smithville, TX
- 8:00 p.m.-8:30 p.m. Speaker to be announced**
- 8:30 p.m.-8:45 p.m. SUV4-20H2-mediated H4K20 trimethylation enforces promoter-proximal RNA polymerase II pausing by inhibition of hMOF-dependent H4K16 acetylation***
 Priya Kapoor, Winship Cancer Institute, Emory University, Atlanta, GA
- 8:45 p.m.-9:00 p.m. EZH2 drives prostate tumorigenesis and metastasis by suppressing a signaling scaffold that regulates Ras and NF- κ B***
 Karen Cichowski, Brigham and Women's Hospital, Boston, MA

Friday, January 22

- 8:00 a.m.-10:00 a.m. Session 4: Cancer Epigenomes**
Chairperson: Stephen B. Baylin, Johns Hopkins University School of Medicine, Baltimore, MD
- 8:00 a.m.-8:30 a.m. Genome-wide epigenetic patterns of normal human mammary epithelial cells**
 Kornelia Polyak, Dana-Farber Cancer Institute, Boston, MA
- 8:30 a.m.-9:00 a.m. The epigenetic progenitor hypothesis of cancer**
 Andrew P. Feinberg, Johns Hopkins University School of Medicine, Baltimore, MD

- 9:00 a.m.-9:30 a.m. The function of HOX genes in breast cancer and their epigenetic regulation by ncRNAs**
Saraswati Sukumar, Johns Hopkins University School of Medicine, Baltimore, MD
- 9:30 a.m.-9:45 a.m. Dissecting a primary colon tumor DNA methylome at single base pair resolution***
Benjamin P. Berman, USC Epigenome Center, Los Angeles, CA
- 9:45 a.m.-10:00 a.m. ChIP-Seq analysis of chromatin association to nuclear lamina in normal and cancer cells***
Marcos Estecio, UT M. D. Anderson Cancer Center, Houston, TX
- 10:00 a.m.-10:30 a.m. Coffee Break**
- 10:30 a.m.-12:45 p.m. Session 5: Clinical Implications**
Chairperson: Minoru Toyota, Sapporo Medical University, Sapporo, Japan
- 10:30 a.m.-11:00 a.m. Gene methylation for the early detection of cancer**
Paul Cairns, Fox Chase Cancer Center, Philadelphia, PA
- 11:00 a.m.-11:30 p.m. DNA methylation as a cancer risk marker that reflects our past lifestyle**
Toshikazu Ushijima, National Cancer Center Research Institute, Tsukiji, Japan
- 11:30 a.m.-12:00 p.m. DNA methylation as a predictive and prognostic biomarker**
James G. Herman, Johns Hopkins University School of Medicine, Baltimore, MD
- 12:00 p.m.-12:15 p.m. Identification and characterization of a cpg island methylator phenotype that defines a distinct clinical and molecular subgroup of glioma***
Houtan Noushmehr, University of Southern California, Los Angeles, CA

- 12:15 p.m.-12:30 p.m. Genomic DNA methylation scan identifies KRT13 and HOXB2 as key genes for invasive bladder cancer and poor patient survival***
Carmen J. Marsit, Brown University, Providence, RI
- 12:30 p.m.-12:45 p.m. Direct detection of DNA methylation through single-molecule, real-time (SMRTTM) DNA sequencing***
Benjamin Flusberg, Pacific Biosciences, Menlo Park, CA
- 4:00 p.m.-7:00 p.m. Poster Session B**
- 7:00 p.m.-9:00 p.m. Session 6: Epigenetic Therapies**
Chairperson: Steven A. Belinsky, Lovelace Respiratory Research Institute, Albuquerque, NM
- 7:00 p.m.-7:30 p.m. DNA methylation inhibitors for chemotherapy resensitization of solid tumors**
Kenneth P. Nephew, Indiana University School of Medicine, Bloomington, IN
- 7:30 p.m.-8:00 p.m. Combined therapy with agents targeted against deregulated epigenetic mechanisms in cancer**
Kapil N. Bhalla, MCG Cancer Center, Medical College of Georgia, Augusta, GA
- 8:00 p.m.-8:30 p.m. Role of histone methylation in leukemogenesis**
Yi Zhang, UNC Lineberger Comprehensive Cancer Center, University of North Carolina, Chapel Hill, NC
- 8:30 p.m.-8:45 p.m. A phase I and pharmacodynamic study of decitabine in combination with carboplatin in patients with recurrent, platinum-resistant, epithelial ovarian cancer***
Fang Fang, Medical Sciences, School of Medicine, Indiana University, Bloomington, IN
- 8:45 p.m.-9:00 p.m. My life with cytidine/uridine analogs: 5-fluorodeoxycytidine, tetrahydrouridine, and zebularine***
Sheldon Greer, University of Miami Miller School of Medicine, Miami, FL

Saturday, January 23

- 8:00 a.m.-10:00 a.m. Session 7: Establishing the Marks**
Chairperson: Jean-Pierre J. Issa, UT M. D. Anderson Cancer Center, Houston, TX
- 8:00 a.m.-8:30 a.m. Title to be announced**
 Stephen B. Baylin, Johns Hopkins University School of Medicine, Baltimore, MD
- 8:30 a.m.-9:00 a.m. Title to be announced**
 Arul M. Chinnaiyan, University of Michigan, Ann Arbor, MI
- 9:00 a.m.-9:30 a.m. Consolidation of epigenetic marks in cancer**
 Susan J. Clark, Garvan Institute of Medical Research, Sydney, Australia
- 9:30 a.m.-9:45 a.m. Global occupation-switching of epigenetically pre-established enhancers reprograms the androgen-responsive pathway in prostate cancer cells***
 Ivan Garcia-Bassets, Howard Hughes Medical Institute, University of California San Diego, La Jolla, CA
- 9:45 a.m.-10:00 a.m. Epigenetic antagonism between polycomb and SWI/SNF complexes during oncogenic transformation***
 Charles W. M. Roberts, Dana-Farber Cancer Institute, Boston, MA
- 10:00 a.m.-10:30 a.m. Coffee Break**
- 10:30 a.m.-12:30 p.m. Session 8: Environmental Effects on the Epigenome**
Chairperson: Robyn L. Ward, University of New South Wales, Sydney, Australia
- 10:30 a.m.-11:00 a.m. Interindividual epigenetic variation: Causes and consequences**
 Robert Waterland, Baylor College of Medicine, Houston, TX
- 11:00 a.m.-11:30 a.m. Epigenome and environment: Moving beyond one-carbon metabolism?**
 Cornelia M. Ulrich, Fred Hutchinson Cancer Research Center, Seattle, WA
- 11:30 a.m.-12:00 p.m. Title to be announced**
 Cheryl L. Walker, UT M. D. Anderson Cancer Center, Smithville, TX

- 12:00 p.m.-12:15 p.m. Epigenomic alterations and gene expression profiles in respiratory epithelia exposed to cigarette smoke condensate***
Fang Liu, National Institutes of Health/National Cancer Institute, Bethesda, MD
- 12:15 p.m.-12:30 p.m. Epigenetically driven epithelial to mesenchymal transition and reprogramming of the epigenome are pivotal for carcinogen-mediated transformation of bronchial epithelial cells***
Carmen S. Tellez, Lovelace Respiratory Research Institute, Albuquerque, NM
- 3:00 p.m.-5:00 p.m. Session 9: Technology and Bioinformatics**
Chairperson: Peter W. Laird, USC Epigenome Center, Los Angeles, CA
- 3:00 p.m.-3:30 p.m. Inferring epigenomic organization from high-throughput sequencing experiments**
Amos Tanay, The Weizmann Institute of Science, Rehovot, Israel
- 3:30 p.m.-4:00 p.m. A genomic view of epigenetic and transcriptional regulation in cancer**
Wei Li, Dan L. Duncan Cancer Center, Baylor College of Medicine, Houston, TX
- 4:00 p.m.-4:15 p.m. Development of a DNA methylation array normalization method for the recognition of large demethylating treatment effects in paired samples***
Floor A.M. Duijkers, Erasmus Medical Center, Rotterdam, The Netherlands
- 4:15 p.m.-4:30 p.m. Connectivity mapping identifies HDAC inhibition to reverse leukemia-specific proto-oncogene hypomethylation in t(4;11)-positive infant acute lymphoblastic leukemia***
Dominique J. P. M. Stumpel, Erasmus Medical Center, Sophia Children's Hospital, Rotterdam, The Netherlands
- 4:30 p.m.-4:45 p.m. Gene set-based module discovery decodes cis-regulatory codes generating transcriptomic diversity across human multiple tissues***
Atsushi Niida, Human Genome Center, Institute of Medical Science, University of Tokyo, Tokyo, Japan

- 4:45 p.m.-5:00 p.m.** **Combined approach using the Illumina Infinium methylation27 beadarray and Affymetrix tiling chip set: Preliminary results illustrate methylation differences in HPV(+) and HPV(-) head and neck cancers***
Maureen A. Sartor, University of Michigan, Ann Arbor, MI
- 5:00 p.m.-7:00 p.m.** **Session 10: Late Breaking News**
Chairpersons: Jean-Pierre J. Issa, UT M. D. Anderson Cancer Center, Houston, TX, and Kornelia Polyak, Dana-Farber Cancer Institute, Boston, MA
- 5:00 p.m.-5:30 p.m.** **GADD45 α and transcription in gene silencing following homology directed repair of double strand DNA breaks***
Mark Muller, University of Central Florida, Orlando, FL
- 5:30 p.m.-5:45 p.m.** **Epigenomic analysis in mice with humanized liver after hepatitis virus infection***
Yasuyuki Okamoto, Aichi Cancer Center Research Institute, Nagoya, Japan
- 5:45 p.m.-6:00 p.m.** **Azacytidine inhibits RNA methylation at DNMT2 target sites in human cancer cell lines***
Frank Lyko, German Cancer Research Center, Heidelberg, Germany
- 6:00 p.m.-6:15 p.m.** **Development of a new method, streptavidin bisulfite ligand methylation enrichment (SuBLIME) to enrich for methylated DNA prior to deep bisulfite genomic sequencing***
Jason P. Ross, Australian Commonwealth Scientific and Industrial Research Organization (CSIRO), North Ryde, Australia
- 6:15 p.m.-6:30 p.m.** **Genome-wide histone modification analysis identifies a network of aberrantly active developmental regulators in glioblastoma***
Esther Rheinbay, Massachusetts General Hospital, Boston, MA
- 6:30 p.m.-7:00 p.m.** Speaker to be announced

*Indicates proffered presentation from selected abstracts