Conference Program

Wednesday, June 19

7:00 p.m.-8:30p.m. Keynote Talks

Salon DEF

Transcriptional and epigenetic control of oncogenes

Richard A. Young, MIT Whitehead Institute for Biomedical Research, Cambridge, MA

Varying and poisoning the "Histone Code": A role of the histone variant H3.3 in human cancers

C. David Allis, Rockefeller University, New York, NY

8:30 p.m.-10:00 p.m. Dessert Reception

The Terrace & Ellington Prefunction

Thursday, June 20

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

Overlook

8:00 a.m.-10:15 a.m. Session 1: Chromatin Regulators Mutated in Cancer

Session Chair: Suzanne J. Baker, St. Jude Children's Research

Hospital, Memphis, TN

Salon DEF

Effective epigenetic therapy for CIMP positive childhood ependymoma

Michael Taylor, PBTF Institute at Sick Children's Hospital, Toronto, ON, Canada

ATRX mutations in human carcinogenesis

Nickolas E. Papadopoulos, Johns Hopkins Medical Institutes, Baltimore, MD

Mutations converging on histone H3 in pediatric high-grade glioma

Suzanne J. Baker

Global chromatin profiling identifies NSD2 mutations in pediatric acute lymphoblastic leukemia*

Frank Stegmeier, Novartis Institutes for BioMedical Research, Cambridge, MA

Epigenetics of hormone dependence#

Myles Brown, Dana-Farber Cancer Institute, Boston, MA

*Short talks from proffered papers

#Invited abstract IA15



10:15 a.m.-10:30 a.m. Break

Ellington Prefunction

10:30 a.m.-12:30 p.m. Session 2: Histone Modifiers

Session Chair: Sharon Y. R. Dent, The University of Texas MD

Anderson Cancer Center, Houston, TX

Salon DEF

Epigenetic regulation and heterogeneity in cancer

Bradley E. Bernstein, Massachusetts General Hospital, Boston, MA

New functions for histone modifying enzymes

Sharon Y. R. Dent

Targeting histone methylation in leukemia

Scott A. Armstrong, Memorial Sloan-Kettering Cancer Center, New York, NY

Variation in chromatin accessibility in human kidney cancer links H3K36 methyltransferase loss with widespread RNA processing defects* lan Davis, University of North Carolina at Chapel Hill, Chapel Hill, NC

Multivalent histone engagement by the linked tandem Tudor and PHD domains of UHRF1 is required for DNA methylation maintenance*

Scott B. Rothbart, University of North Carolina at Chapel Hill, NC

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

2:30 p.m.-4:30 p.m. Session 3: Polycomb Complexes

Session Chair: Kristian Helin, University of Copenhagen, Copenhagen, Denmark Salon DEF

Nucleotide biosynthetic enzyme GMP Synthase is a relay of p53 stabilization in response to genomic stress

Peter Verrijzer, Erasmus University Medical Center, The Netherlands

Mechanisms regulating polycomb group proteins to target genes Kristian Helin

The epigenetic stability of pluripotent and somatic cell states
Jacob H. Hanna, The Weizmann Institute of Science, Rehovot, Israel

Genomic and epigenomic interactions of an Ewing sarcoma-specific long noncoding RNA*

Sheetal A. Mitra, Children's Hospital Los Angeles, Los Angeles, CA

Reversing the oncogenic roles of misdirected chromatin remodeling: Disruption of mSWI/SNF (BAF) complexes by the SS18-SSX fusion in human synovial sarcoma* Cigall Kadoch, Stanford University, Stanford, CA

4:30 p.m.-6:30 p.m. Poster Session A and Reception
Overlook



Friday, June 21

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

Overlook

8:00 a.m.-10:00 a.m. Session 4: SWI/SNF (BAF) Complexes

Session Chair: Charles W. M. Roberts, Dana-Farber Cancer

Institute, Boston, MA

Salon DEF

SWI/SNF (BAF) complexes in tumor suppression

Charles W. M. Roberts

Chromatin regulation: New concepts and methods

Gerald R. Crabtree, Stanford University, Stanford, CA

Histone variant H2A.Z sets the stage for ESC differentiation

Keji Zhao, National Institutes of Health, Bethesda, MD

CARM1 methylates BAF155 and perturbs chromatin remodeling machinery to enhance tumor progression*

Wei Xu, University of Wisconsin-Madison, Madison, WI

SNF5 is an essential executor of epigenetic regulation during differentiation*

Minmin Liu, USC Norris Comprehensive Cancer Center, Los Angeles, CA

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

Ellington Prefunction

10:30 a.m.-12:30 p.m. Session 5: Chromatin Dynamics and Transcriptional Regulation

Session Chair: Peter A. Jones, USC Norris Comprehensive Cancer Center, Los Angeles, CA Salon DEF

Reactivating epigenetically silenced genes

Peter A. Jones

mSWI/SNF (BAF) complexes facilitate decatentation of DNA by topoisomerase II* Emily Dykhuizen, Stanford University, Stanford, CA

Unraveling intricate relationship between chromatin remodeling, transcription, and cancer*

Michael Y. Tolstorukov, Massachusetts General Hospital, Boston, MA

Modulation of chromatin structure and transcription by the SWI/SNF complex in acute lymphoblastic leukemia*

Jennifer Wu, Dana-Farber Cancer Institute, Boston, MA

Doxorubicin enhances nucleosome turnover around active gene promoters* Fan Yang, Fred Hutchinson Cancer Research Center, Seattle, WA

CHD5 is required for neurogenesis and has a dual role in facilitating gene expression and polycomb gene repression*

Adrian P. Bracken, Trinity College Dublin, Dublin, Ireland

12:30 p.m.-2:30 p.m. Poster Session B and Lunch
Overlook



2:30 p.m.-4:30 p.m. Session 6: Reprogramming and Development

Session Chair: George Q. Daley, Boston Children's Hospital, Boston, MA Salon DEF

The stem cell factor LIN28 in pediatric cancer

George Q. Daley

Genetic and epigenetic control of transcription in hematopoiesis

Stuart H. Orkin, Dana-Farber Cancer Institute, Boston, MA

In vivo RNAi screening for polycomb targets in glioblastoma

Maarten Van Lohuizen, Netherlands Cancer Institute, Amsterdam, The Netherlands

Comparison of the gene regulatory programs controlled by the mutually exclusive SWI/SNF subunits ARID1A and ARID2*

Jesse Raab, University of North Carolina at Chapel Hill, Chapel Hill, NC

Dissecting the role of the histone variant macroH2A in reprogramming and breast cancer*

Alexandre Maia, Icahn School of Medicine at Mount Sinai, New York, NY

4:30 p.m.-5:30 p.m. Panel Discussion: Inferring Mechanism from Human

Genetics and Genomic Analysis of Cancer

Moderator: Gerald R. Crabtree, Stanford University, Stanford, CA

Salon DEF

Panelists:

Jesse J. Smith, Epizyme, Inc., Cambridge, MA Charles W. M. Roberts, Dana-Farber Cancer Institute, Boston, MA Stuart H. Orkin, Dana-Farber Cancer Institute, Boston, MA

Saturday, June 22

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

Overlook

8:00 a.m.-10:00 a.m. Session 7: DNA Methylation

Session Chair: Ari M. Melnick, Weill Cornell Medical College of Cornell University, New York, NY Salon DEF

Epigenetic deregulation of gene expression

Ari M. Melnick

Translational implication of DNA methylation changes in the cancer epigenome

Stephen B. Baylin, Johns Hopkins University School of Medicine, Baltimore, MD

Cancer as a single process of a dysregulated epigenome

Andrew P. Feinberg, Johns Hopkins University School of Medicine, Baltimore, MD

Functional and structural studies of HP1 heterochromatin

Geeta Narlikar, University of California, San Francisco, CA

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

Ellington Prefunction

10:15 a.m.-12:15 p.m. Session 8: Drugging the Epigenome

Session Chair: James E. Bradner, Dana-Farber Cancer Institute, Boston, MA Salon DEF

Histone methyltransferase inhibitors as therapeutic agents in genetically defined cancers

Jesse J. Smith, Epizyme, Inc., Cambridge, MA

Linking genetic features of human cancers and histone-modifying enzymes for future cancer therapies

Stuart L. Schreiber, Howard Hughes Medical Institute, Cambridge, MA

Clinical translation of bromodomain inhibition

James E. Bradner

SUZ12: A novel tumor suppressor and potential biomarker for efficacy of BRD4 inhibition*

Thomas De Raedt, Brigham and Women's Hospital, Boston, MA

A new class of small molecule acetyltransferase inhibitors discovered through high-throughput screening are potent anticancer agents with cancer-type-specific activity* Daiqing Liao, University of Florida College of Medicine, Gainesville, FL

12:15 p.m.-12:30 p.m. Closing Remarks and Departure

Salon DEF

*Short talks from proffered papers

