

Announcing Keystone Symposia's
2015 conference on:

DNA Methylation

joint with the meeting on: *Epigenomics*

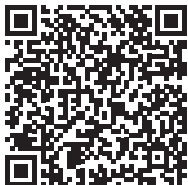
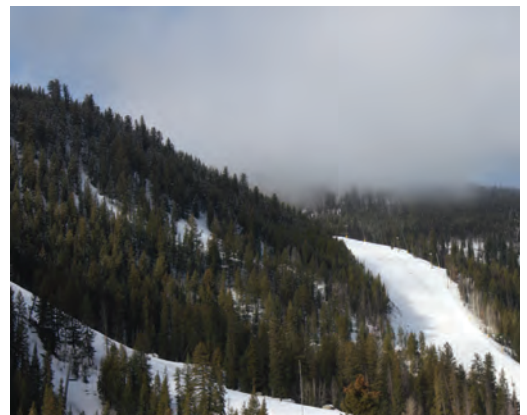
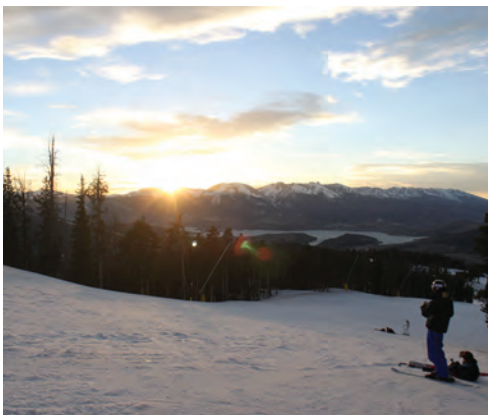
March 29 – April 3, 2015
Keystone Resort
Keystone, Colorado, USA

Scientific Organizers: Alexander Meissner and Dirk Schübeler

DNA methylation is essential for mammalian development and plays an important regulatory role in many organisms including plants. Major advances have been made in functionally studying the key players involved in establishing and maintaining DNA methylation as well as mapping its genome-wide location. Many gaps remain toward a complete understanding, in particular in diseases. In this meeting, experts in the field will provide the latest insights from plants to mammalian development. A further focus will be the relevance of DNA methylation for cancer biology and how it may lead to more advanced diagnostics and treatments in the clinic.

Session Topics:

- Genome-Wide DNA Methylation I & II (Joint)
- DNA Methylation in Early Development
- Regulation and Reading of DNA Methylation
- Intermediate and Allele-Specific DNA Methylation
- Perturbations of DNA Methylation in Disease
- DNA Methylation as a Biomarker
- DNA Methylation Turnover
- Workshop: Modeling DNA Methylation



Discounted Abstract/Scholarship Deadline: Dec 3, 2014
Abstract Deadline: Jan 8, 2015
Discounted Registration Deadline: Jan 29, 2015

To see the full program and for additional details,
visit www.keystonesymposia.org/15Z1.

KEYSTONE SYMPOSIA™
on Molecular and Cellular Biology
Accelerating Life Science Discovery

KEYSTONE SYMPOSIA

on Molecular and Cellular Biology

DNA Methylation (Z1)

Scientific Organizers: Alexander Meissner and Dirk Schübeler

Supported by the Directors' Fund

Epigenomics (Z2)

Scientific Organizers: Bing Ren and Daniel Zilberman

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SUNDAY, MARCH 29

Arrival and Registration

MONDAY, MARCH 30

Keynote Address (Joint)

*Daniel Zilberman, University of California, Berkeley, USA

Adrian P. Bird, University of Edinburgh, UK

DNA Methylation and Other CpG Signaling

Genome-Wide DNA Methylation I (Joint)

*Dirk Schübeler, Friedrich Miescher Institute for Biomedical Research, Switzerland

Alexander Meissner, Harvard University, Broad Institute, USA
DNA Methylation Dynamics in Development and Disease

Steven E. Jacobsen, HHMI/University of California, Los Angeles, USA
DNA Methylation in Flowering Plants

Ryan Lister, University of Western Australia, Australia

Short Talk: Large-Scale Interrogation of the Repressive Capacity of Human Promoter DNA Methylation by Genome-Wide Epigenomic Manipulation

Bradley R. Cairns, HHMI/University of Utah, USA

Chromatin-Transcription Dynamics in Developing Germline Stem Cells

Marie Classon, Genentech, Inc., USA

Short Talk: A Heterochromatic State Required for the Survival of Drug-Tolerant Cancer Cell Populations

Workshop 1: Roadmap Epigenomic Tutorial (Z2)

*Ting Wang, Washington University, USA

DNA Methylation in Early Development (Z1)

*Anne C. Ferguson-Smith, University of Cambridge, UK

Wolf Reik, Babraham Institute, UK

Epigenetic Reprogramming in Mammalian Development

Matthew C. Lorincz, University of British Columbia, Canada

Impact of LTR Retrotransposons on the Transcriptome and Methylome in the Mouse Germline

Jonathan I. Gent, University of Georgia, USA

Short Talk: RNA-Directed DNA Methylation in Suppression of Intronic Transposons: Minimizing Collateral Damage on Host Gene Expression

Marius Walter, Institut Curie, France

Short Talk: Transposon Regulation upon Acute Loss of DNA Methylation

Vincent Colot, École Normale Supérieure, France

Molecular and Developmental Basis of Progressive DNA Methylation across Generations

Nucleosome Dynamics (Z2)

*Barbara J. Meyer, University of California, Berkeley, USA

Steven Henikoff, Fred Hutchinson Cancer Research Center, USA
Nucleosome Barriers to Transcription

Alicia N. Schep, Stanford University, USA

Short Talk: NucleoATAC: Structured ATAC-seq Signal Around Nucleosomes Enables High-Resolution Nucleosome Positioning

B. Franklin Pugh, Pennsylvania State University, USA

Genome-Wide Organization of Chromatin

Jeffrey N. McKnight, Fred Hutchinson Cancer Research Center, USA

Short Talk: Global Relocalization of the Rpd3 Histone Deacetylase Drives Quiescence Entry in S. cerevisiae

Jason D. Lieb, University of Chicago, USA

Evidence for Lamin A Function at Enhancers, with Implications for Hutchinson-Gilford Progeria

Poster Session 1

TUESDAY, MARCH 31

Regulation and Reading of DNA Methylation (Z1)

*Margaret A. Goodell, Baylor College of Medicine, USA

Timothy H. Bestor, Columbia University College of Physicians and Surgeons, USA

FBXL10 Defends Polycomb-Bound Genes Against Hypermethylation

Xiaodong Cheng, Emory University, USA
Generation, Recognition and Erasure (GRE) of 5-Methylcytosine and its Oxidative Derivatives

Sriharsa Pradhan, New England Biolabs, USA

Regulation of DNMT1 Stability and Activity by Reader, Writer, Eraser and MicroRNA

Jiahao Huang, Babraham Institute, UK

Short Talk: Histone Modifiers Maintain Fidelity of de novo DNA Methylation in Growing Oocytes

Jafar Sharif, RIKEN IMS, Japan

Short Talk: Protracted NP95 Binding to Hemimethylated DNA Disrupts SETDB1-Mediated Proviral Silencing

Robert A. Martienssen, Cold Spring Harbor Laboratory, USA

Genome Reprogramming by Histone Variants and Small RNA

Manu J. Dubin, Gregor Mendel Institute, Austria

Short Talk: DNA Methylation Variation in Arabidopsis Has a Genetic Basis and Shows Evidence of Local Adaptation

Functional Chromatin Domains (Z2)

*Bas van Steensel, Netherlands Cancer Institute, Netherlands

Barbara J. Meyer, University of California, Berkeley, USA
Condensin-Driven Remodeling of X-Chromosome Topology during Dosage Compensation

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Elphège P. Nora, Gladstone Institute, USA

Short Talk: Life without CTCF (at Least for a Short While)

Sarah Elderkin, Babraham Institute, UK

Short Talk: Polycomb Repressive Complex PRC1 Spatially Constrains the Mouse Embryonic Stem Cell Genome to Regulate Pluripotency

Iestyn Whitehouse, Memorial Sloan Kettering Cancer Center, USA
Chromatin Assembly: A View from the Lagging Strand

Natasha E. Weiser, University of Michigan, USA

Short Talk: MORC-1 Regulates Endogenous Small RNAs, Chromatin Organization and Germline Immortality

Manolis Kellis, Massachusetts Institute of Technology / Broad Institute, USA

Interplay between Chromatin State, Regulator Binding and Regulatory Motifs

Intermediate and Allele-Specific DNA Methylation (Z1)

*Anjana Rao, La Jolla Institute for Allergy and Immunology, USA

Joseph F. Costello, University of California, San Francisco, USA
The Function of Intermediate DNA Methylation

Wenfeng An, South Dakota State University, USA

Short Talk: Retrotransposing Single-Copy Sequences into the Mouse Genome Reveals Sloping Shores: A Graded Influence of Hypomethylated CpG Islands on Flanking CpG Sites

Marisa S. Bartolomei, University of Pennsylvania Perelman School of Medicine, USA

Insulators, CTCF and DNA Methylation in Imprinted Gene Clusters

Anne C. Ferguson-Smith, University of Cambridge, UK
Genomic Imprinting and Parental-Origin Effects

Claude Becker, Max Planck Institute for Developmental Biology, Germany

Short Talk: Maternal Transmission of Increased Salt Stress Tolerance in Arabidopsis Is Linked to DNA Methylation

Chromatin Regulation of Development (Z2)

*Manolis Kellis, Massachusetts Institute of Technology / Broad Institute, USA

Joanna Wysocka, Stanford University School of Medicine, USA
Retroelement Reactivation in Human Preimplantation Development

Christopher W. Ng, Massachusetts Institute of Technology, USA
Short Talk: Epigenetic Ensembles Presage Transcriptional Changes in Differentiation and Disease

Karine G. Le Roch, University of California, Riverside, USA

Short Talk: Association between Chromatin Structure, Gene Regulation and Pathogenicity in the Human Malaria Parasite, Plasmodium falciparum

Andrew Dimond, Babraham Institute, UK

Short Talk: Developmental Gene Promoters Establish Poised Enhancer Contacts in Embryonic Stem Cells

Jeremie F. Poschmann, Genome Institute of Singapore, Singapore

Short Talk: Large-Scale Mapping of Chromatin-Altering Polymorphisms Reveals Molecular Drivers of Human Disease

John A. Stamatoyannopoulos, University of Washington, USA
Encoding Epigenesis

Poster Session 2

WEDNESDAY, APRIL 1

Perturbations of DNA Methylation in Disease (Z1)

Margaret A. Goodell, Baylor College of Medicine, USA
DNMT3A in Normal and Malignant Hematopoiesis

Peter A. Jones, Van Andel Research Institute, USA
Cancer Therapy

Benjamin Leadem, Johns Hopkins University, USA

Short Talk: Novel Inhibitors of KDM5 Family Proteins Synergize with DNMT Inhibitors to Regulate Gene Expression and Inhibit Proliferation of Breast Cancer Cells

Jeanne F. Loring, The Scripps Research Institute, USA
Dynamics of DNA Methylation in Human Pluripotent Stem Cell Differentiation

Ralf Gilsbach, University of Freiburg, Germany

Short Talk: Stage-Specific Gene Expression Programs in Cardiomyocytes Rely on Dynamic CpG-Methylation or Polycomb Repressive Marks

Amos Tanay, Weizmann Institute, Israel

Single-Cell Transcriptional and Epigenomic Approaches to Complex Cell Populations

Yvette A. Luyten, New England Biolabs, USA

Short Talk: Bacterial DNA Methyltransferases: A New "Class" of Type I Restriction Modification Enzymes Utilizing Two Distinct DNA Methyltransferase Genes

Higher-Order Chromatin Organization (Z2)

*Erez Lieberman-Aiden, Baylor College of Medicine, USA

Noam Kaplan, University of Massachusetts Medical School, USA
How the 1D Genome Encodes 3D Topologically Associating Domains

Edith Heard, Institut Curie, France

The Dynamics of X-Chromosome Structure and Activity during X Inactivation

Suhas S.P. Rao, Baylor College of Medicine, USA

Short Talk: Extremely High-Resolution 3D Maps of Human and Mouse Genomes Across Lineages and during Differentiation Reveal Principles of Chromatin Looping

Bas van Steensel, Netherlands Cancer Institute, Netherlands

Mapping Genome – Nuclear Lamina Interactions in Single Cells

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Peter Fraser, Babraham Institute, UK

Single Molecule Analyses of Chromosome Folding and Genome Organization by Single-Cell Hi-C

Robert A. Beagrie, MRC Clinical Sciences Centre, UK
Short Talk: Novel, Ligation-Free Method for Identifying Chromatin Interactions Genome-Wide

Workshop: Modeling DNA Methylation (Z1)

*Amos Tanay, Weizmann Institute, Israel

*Remo Rohs, University of Southern California, USA
Modeling of the Effect of DNA Methylation on DNA Shape and Protein-DNA Binding

Michael M. Hoffman, University of Toronto, Canada
Transcription Factor Binding in an Expanded Epigenetic Alphabet

Önder Kartal, University of Zürich, Switzerland
An Information-Theoretic Approach to Discover Differential DNA Methylation in Plants Suggests that Diversity Is Highest in the CG Context

Fabian Müller, Max Planck Institute for Informatics, Germany
Computational Methods for the DEEP Characterization of DNA Methylation BLUEPRINTs

Yaping Liu, Massachusetts Institute of Technology, USA
meQTLFinder: A Bayesian Model to Detect meQTL by Using Chromatin States and Chromatin Interaction Prior Information

David Gokhman, Hebrew University of Jerusalem, Israel
Paleo-Epigenetics: Reconstructing the DNA Methylation Maps of Archaic Hominins

DNA Methylation as a Biomarker (Z1)

*Peter A. Jones, Van Andel Research Institute, USA

Stephan Beck, University College London, UK
Insights from Methylome Analysis

Peter W. Laird, Van Andel Research Institute, USA
Cancer Methylomes

Michiel Vermeulen, Radboud University, Netherlands
Quantitative Interaction Proteomics for Epigenetics

Xueguang Sun, Zymo Research Corp, USA
Short Talk: Mirror Bisulfite Sequencing (Mirror-Seq): A Novel Sequencing Method for Genome-Wide Profiling of 5-Hydroxymethylcytosine with Single-Base Resolution

Shinji Maegawa†, Temple University, USA
Short Talk: DNA Methylation Drift as a Marker of Lifespan in Mammals

Small RNA (Z2)

*John L. Rinn, Harvard University, USA

Amy E. Pasquinelli, University of California, San Diego, USA
The Primary Target of let-7 MicroRNA

Haifan Lin, Yale University, USA

Multifaceted Roles of the Piwi-piRNA Pathway in Gene Regulation

Alla Grishok, Columbia University Medical Center, USA
Short Talk: Connecting Euchromatin and Endogenous RNAi in C. elegans

Sam (Guoping) Gu, Rutgers University, USA
Short Talk: siRNA-Mediated Chromatin Regulation and Multigenerational Homeostasis of Germline Gene Expression in C. elegans

Craig S. Pikaard, HHMI/Indiana University, USA
RNA Silencing and Epigenetic Inheritance

Poster Session 3

THURSDAY, APRIL 2

Genome-Wide DNA Methylation II (Joint)

*Alexander Meissner, Harvard University, Broad Institute, USA
Joseph R. Ecker, HHMI/The Salk Institute for Biological Studies, USA
Human Body Epigenome Maps Reveal Noncanonical DNA Methylation Variation

Bing Ren, University of California, San Diego, USA
Integrative Analysis of Haplotype-Resolved Epigenomes across Human Tissues

Daniel Zilberman, University of California, Berkeley, USA
Molecular Co-Evolution of Genomes and Chromatin

Andrew G. Clark, Cornell University, USA
Short Talk: Analysis of Novel Marsupial-Specific Imprinted Genes and their DMRs in the Opossum, Monodelphis domestica

Camila O. dos Santos, Cold Spring Harbor Laboratory, USA
Short Talk: An Epigenetic Memory of Pregnancy in the Mouse Mammary Gland

Dirk Schübeler, Friedrich Miescher Institute for Biomedical Research, Switzerland
Sequence and Chromatin Determinants of DNA Methylation

Workshop 2: ENCODE Datasets Tutorial (Z2)

*Feng Yue, Pennsylvania State University, USA

DNA Methylation Turnover (Z1)

*Xiaodong Cheng, Emory University, USA

Frédéric L. Chedin, University of California, Davis, USA
Epigenomics Signatures of R-Loop Forming Regions

Chuan He, University of Chicago, USA
Genome-Wide Sequencing of 5hmC and 5fC

Anjana Rao, La Jolla Institute for Allergy and Immunology, USA
TET Proteins, 5-Methylcytosine Oxidation and Cancer

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Salvatore Oliviero, Human Genetics Foundation, HuGeF, Italy

Short Talk: Single-Base Resolution Analysis of 5-Formyl and 5-Carboxyl Cytosine Reveals DNA Methylation/Demethylation Dynamics in the Mammalian Genome

Long Noncoding RNA (Z2)

*Amy E. Pasquinelli, University of California, San Diego, USA

John L. Rinn, Harvard University, USA

RNA-Binding Proteins Interact Specifically with Transposable Element Sequence in Human Genes

Jindan Yu, Northwestern University Feinberg School of Medicine, USA

Short Talk: LncRNA HOTAIR Enhances the Androgen Receptor-Mediated Transcriptional Program and Drives Castration-Resistant Prostate Cancer

L. Stirling Churchman, Harvard Medical School, USA

Short Talk: High-Resolution Architecture of Human Transcriptional Activity Revealed by Native Elongating Transcript Sequencing

Gilad Fuchs, Weizmann Institute of Science, Israel

Short Talk: Cotranscriptional Histone H2B Monoubiquitylation Is Tightly Coupled with RNA Polymerase II Elongation Rate

Mitchell Guttman, California Institute of Technology, USA

lncRNAs: Function and Mechanism in Controlling Cellular Identity

Meeting Wrap-Up: Outcomes and Future Directions (Organizers)
(Z1)

Meeting Wrap-Up: Outcomes and Future Directions (Organizers)
(Z2)

FRIDAY, APRIL 3

Departure