

# Keystone Symposia: Dynamics of Eukaryotic Transcription during Development

April 7–12, 2010 • Big Sky Resort • Big Sky, Montana • USA

Scientific Organizers: Karen Adelman and Marc Timmers

## PROGRAM FACULTY & TALKS

- Karen Adelman**, NIEHS, National Institutes of Health, USA  
*Pol II Stalling Potentiates Expression of Stress-Responsive Genes*
- Wendy A. Bickmore**, MRC Human Genetics Unit, UK  
*Recruitment of Genes to Nuclear Periphery*
- Stephen Buratowski**, Harvard Medical School, USA  
*Coupling Transcription with mRNA Processing and Chromatin*
- Joan W. Conaway**, Stowers Institute for Medical Research, USA  
*Mechanisms for Recruiting Chromatin Remodeling Complexes to Their Targets*
- David S. Gilmour**, Pennsylvania State University, USA  
*Regulation of Transcription Elongation in Drosophila*
- Hiroshi Handa**, Tokyo Institute of Technology, Japan  
*The Role of Transcription Elongation Factors in Genome Expression*
- Steven Henikoff**, Fred Hutchinson Cancer Research Center, USA  
*Histone Replacement during Transcription*
- Frank Holstege**, University Medical Center, Utrecht, The Netherlands  
*Understanding Regulatory Circuitry using DNA Microarray Expression-Profile Phenotypes*
- Katherine A. Jones**, The Salk Institute, USA  
*Co-Transcriptional Activities of the Spt6:Iws1 Complex on the RNAPII CTD*
- Jennifer F. Kugel**, University of Colorado, Boulder, USA  
*Regulation of Early Steps of Transcription by Small ncRNAs*
- Michael S. Levine**, University of California, Berkeley, USA  
*Gene Activation during Development and Differentiation in Drosophila*
- John T. Lis**, Cornell University, USA  
*Imaging Transcription Factors Dynamics in vivo before and during Gene Activation*
- Susan E. Mango**, University of Utah, USA  
*Investigating the Transcriptional Mechanisms that Govern the Progression of C. elegans Development*
- Jane Mellor**, University of Oxford, UK  
*Transcription Elongation on a Chromatin Template*
- Stuart H. Orkin**, Dana-Farber Cancer Institute, USA  
*Epigenetic Regulation of Hematopoietic Stem Cells and mES Cell Pluripotency and Differentiation*
- Barbara Panning**, University of California, San Francisco, USA  
*Tip60-p400 as a Regulator of Embryonic Stem Cell Identity*
- B. Franklin Pugh**, Pennsylvania State University, USA  
*Global Interplay between the Transcription Machinery and Chromatin*
- Danny F. Reinberg**, NYU-School of Medicine, USA  
*How Histone Modifications Affect Gene Expression*
- Robert G. Roeder**, Rockefeller University, USA  
*Function of Coactivators in Stimulating Pre-Initiation Complex Formation*
- Ali Shilatifard**, Stowers Institute for Medical Research, USA  
*Histone Methylation Pathways*
- Kevin Struhl**, Harvard Medical School, USA  
*Transcriptional and Epigenetic Mechanisms in Yeast and Cancer Cells*
- Marc Timmers**, University Medical Centre Utrecht, Netherlands  
*Dynamic Regulation of the Basal Transcription Machinery*
- Laszlo Tora**, Institut de Genetique et de Biologie Moleculaire et Cellulaire, France  
*Transcription Factors Involved in Mammalian Oogenesis and Early Embryogenesis*
- Jessica K. Tyler**, University of Colorado Health Sciences Center, USA  
*Mechanisms of Chromatin Assembly and Disassembly during Transcription*
- Ali Shilatifard**, Stowers Institute for Medical Research, USA  
*Histone Methylation Pathways*
- Bas van Steensel**, Netherlands Cancer Institute, The Netherlands  
*Architecture and Function of Genome – Nuclear Lamina Interactions*
- Fiona M. Watt**, Cambridge Research Institute, UK  
*Proliferation and Differentiation of Epidermal Stem Cells*
- Jonathan Widom**, Northwestern University, USA  
*DNA-Encoded Nucleosome Organization of Eukaryotic Genomes*
- Richard A. Young**\*, Whitehead Institute for Biomedical Research, USA  
*Programming Embryonic Stem Cell State*
- Kenneth S. Zaret**, University of Pennsylvania, USA  
*Pioneer Transcription Factors in Programming of Liver and Pancreas Progenitors: Lessons for Stem Cell Differentiation*

\*Keynote speaker. Program subject to change. Current as of November 2, 2009.



Gene expression in eukaryotes is regulated primarily at the level of transcription. Although much is known about the basic building blocks required to recruit RNA polymerase II to a gene promoter and establish a pre-initiation complex, recent data reveals that a great deal of regulation occurs during transcription elongation, and involves dynamic interactions between the transcription machinery and chromatin structure. This meeting is intended to explore these recently appreciated mechanisms for gene regulation and to showcase the novel techniques that have permitted these advances. Of particular interest are the use of comprehensive, genomic approaches, and their use towards understanding the different patterns of gene expression in different model systems, including stem cells and developing tissues, as well as the application of novel molecular probing and cell imaging techniques to investigate the global nuclear architecture and its impact on gene expression.

## PROGRAM PLENARY SESSIONS & WORKSHOPS:

- Genomic Approaches to Understanding Gene Expression
- Transcription Regulation in Stem Cells and during Development
- Transcription Regulation – From Pol II Recruitment to Early Elongation
- Workshop 1: Genomic Approaches: Discovery of Transcription Modulators as Drug Targets and High-Throughput Techniques for Investigating Changes in Gene Expression
- Regulation of Transcription Elongation
- The Effects of Chromatin Structure on Transcription
- Workshop 2: New and Noteworthy
- Activators and Co-Regulatory Complexes
- Co- and Post-Transcriptional RNA Processing
- Imaging and Probing Global Nuclear Architecture

## DEADLINES:

Abstract & Scholarship: December 7, 2009

Late-Breaking Abstract: January 5, 2010

Early Registration: February 5, 2010

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