Special Sessions ROOM 312

Sunday, July 11

SS1 10:45 A.M. – 12:40 P.M.  
CHROMATIN & GENE REGULATION I: NUCLEOSOMES

10:45 A.M. – 11:10 A.M.  
Nucleosome positioning from archaeabacteria to man  
Jonathan Widom

11:15 A.M. – 11:40 A.M.  
Global Interplay between the Transcription Machinery & Chromatin  
Frank Pugh

11:45 A.M. – 12:10 P.M.  
Transcriptional Lego: Predictable fine tuning of gene expression by manipulating nucleo-some positioning signals  
Eran Segal

12:15 P.M. – 12:40 P.M.  
Chromatin dynamics during the cell cycle in S. cerevisiae  
Oliver Rando

SS2 2:30 P.M. – 4:25 P.M.  
CHROMATIN & GENE REGULATION II: EPIGENOMICS

2:30 P.M. – 2:55 P.M.  
Dynamics of chromatin states across nine human ENCODE cell lines  
Manolis Kellis

3:00 P.M. – 3:25 P.M.  
Unsupervised inference of chromatin domain structure from multiple functional genomics data sets  
William Stafford Noble

3:30 P.M. – 3:55 P.M.  
The Epigenome of Pluripotent Cells: Variations of a Common Theme  
Christoph Bock

4:00 P.M. – 4:25 P.M.  
Inferring in vivo transcription factor binding from histone mark dynamics  
Shirley Liu

Monday, July 12

SS3 10:45 A.M. – 12:40 P.M.  
COMPUTATIONAL APPROACHES IN PHARMACOGENOMICS

10:45 A.M. – 11:10 A.M.  
Identification & Pharmacogenomic Characterization of Liver Membrane Transporter Enhancers  
Nadav Ahituv

11:15 A.M. – 11:40 A.M.  
Can high-throughput genomics data identify new therapeutic targets in cancer?  
Rachel Karchin

11:45 A.M. – 12:10 P.M.  
Genetic factors affecting severe adverse effects for common drugs  
Itsik Pe’er

12:15 P.M. – 12:40 P.M.  
The Genome Commons  
Steven E. Brenner

SS4 2:30 P.M. – 3:55 P.M.  
THE FUTURE OF SCIENTIFIC PUBLISHING

2:30 P.M. – 3:25 P.M.  
Opening remarks by panelists  
Theo Bloom (PLoS), Jen Boyd (OUP), Rachel Burley (Wiley), Matt Cockerill (BMC), Anita de Waard (Elsevier)

3:30 P.M. – 3:55 P.M.  
Open discussion with panelists

Tuesday, July 13

SS5 10:45 A.M. – 12:40 P.M.  
VISUALIZATION OF BIOLOGICAL NETWORKS

10:45 A.M. – 11:10 A.M.  
Introduction – Tools & their features for biological network analysis & visualization  
Igor Jurisica

11:15 A.M. – 11:40 A.M.  
Visualization of large networks  
Frank van Ham

11:45 A.M. – 12:10 P.M.  
Visual interpretation of biological data using networks  
Gary Bader

12:15 P.M. – 12:40 P.M.  
Visualization & analysis of signaling pathways  
Lincoln Stein

SS6 2:30 P.M. – 4:25 P.M.  
DATA ANALYSIS IN GENOME-SCALE RNAI RESEARCH

2:15 P.M. – 2:40 P.M.  
Methods for the Efficient Implementation of siRNA HighThroughput Screens  
Shane Marine

2:45 P.M. – 3:10 P.M.  
Massively Parallel Phenotyping by High-throughput RNAI  
Michael Boutros

3:15 P.M. – 3:40 P.M.  
Development of analytic methods in genome-scale RNAi researches  
Xiaohua Douglas Zhang

3:45 P.M. – 4:10 P.M.  
Computational Assessment of Screening Statistics for RNAI  
Amanda Birmingham