

# Program RegGenSIG 2012 .....AM

7:30 a.m.		Registration
8:30 a.m.	5 min	Welcome to SIG
	40 min	Keynote <b>Gary Stormo</b> , Washington University Medical School, USA <i>30 years of PWMs: Where are we now and what comes next?</i>
	20 min	<b>Quing Zhou</b> , University of California, Los Angeles, USA <i>Constructing sparse binding landscapes by penalized posterior sampling</i>
	20 min	<b>Saurabh Sinha</b> , University of Illinois, USA <i>Modeling transcription factor occupancy profiles in Drosophila</i>
	15 min	<b>Remo Rohs</b> , University of Southern California, USA <i>New approaches to genome analysis based on the integration of DNA sequence and shape</i>
10:15 a.m.	30 min	Morning Coffee Break
10:45 a.m.	20 min	<b>Wei Wang</b> , University of California, San Diego, USA <i>Delineation of epigenetic landscape in human cells</i>
	20 min	<b>Andrew Smith</b> , University of Southern California, USA <i>Precisely bounding genomic regulatory regions in mammals using high-resolution DNA-methylation data</i>
	15 min	<b>Siddarth Selvaraj</b> , University of California, USA <i>Identification and Characterization of Topological Domains in Mammalian Genomes</i>
	15 min	<b>Manoj Hariharan</b> , Stanford University, USA <i>Context-specific Combinatorial Interaction of Transcription Factors in Gene Regulation</i>
	15 min	<b>Yael Mandel-Gutfreund</b> , Israel Institute of Technology, Israel <i>An integrated regulatory network reveals pervasive cross-regulation among transcription and splicing factors</i>
	15 min	<b>Logan J. Everett</b> , University of Pennsylvania, USA <i>Cistromic analysis reveals novel insights into hepatic CREB regulatory mechanisms</i>

# Program RegGenSIG 2012.....PM

12:30 p.m.	60 min	Lunch / Poster Session
1:30 p.m.		Joint session RegGen SIG / AS-SIG - Room 104C <i>Systems approaches to modeling regulatory RNAs</i>
	5 min	Welcome
	20 min	<b>Alex Hartemink</b> , Duke University, USA <i>Toward a Mechanistic Understanding of Transcriptional Regulation: A Systems Perspective on Genome Occupancy</i>
	15 min	<b>An-Yuan Guo</b> , Huazhong Univ. of Science and Technology, China <i>MicroRNA and transcription factor co-regulatory network analysis reveals miR-19 inhibits CYLD in T-cell acute lymphoblastic leukemia</i>
	15 min	<b>Zhengqing Ouyang</b> , Stanford University, USA <i>SeqFold: Accurate genome-scale RNA structure reconstruction integrating experimental measurements provides insights into gene regulation</i>
	20min	<b>Steven Brenner</b> <i>Genome-wide analysis of RNA regulation in modENCODE</i>
	40 min	Panel Discussion: <i>From bench to bedside: The future of genomic medicine.</i> Moderator: <b>Klemens Hertel</b> , University of California - Irvine Panelists: <b>Steven Brenner, Tom Cooper, Alex Hartemink</b>
	5 min	Concluding remarks on joint session
3:30 p.m.	30 min	Afternoon Coffee Break / Posters
4:00 p.m.	40 min	Keynote <b>Harmen Bussemaker</b> , Columbia University, USA <i>Dissecting transcription factor networks using high-throughput sequencing and quantitative genetics</i>
	20 min	<b>Roderic Guigo</b> , Bioinformatics and Genomics, Centre for Genomic Regulation (CRG), Spain <i>Interrogating RNA heterogeneity</i>
	20 min	<b>Igor Zwir</b> , University of Granada, Spain <i>Mapping sequence to numbers: A quantitative model of promoter binding and gene transcription kinetics under DNA accessibility constrains</i>
	20 min	<b>Andrei Thomas-Tikhonenko</b> , University of Pennsylvania, USA <i>Quantitative transcriptome-wide analysis of the Myc-miR-17-92 axis</i>
	15 min	<b>Marit Ackermann</b> , TU Dresden, Germany <i>Assessing the impact of natural genetic variation on gene expression dynamics</i>
	5 min	Concluding remarks on SIG
6:00 p.m.		SIG Ends

# RegGenSIG 2012 .....Posters

Iris Dror, Tianyin Zhou, Lin Yang, Yael Mandel-Gutfreund, Remo Rohs	New approaches to genome analysis based on the integration of DNA sequence and shape (also see abstract for oral presentation by Remo Rohs)
Marie Trussart	The three-dimensional genome conformation of <i>Mycoplasma pneumoniae</i>
Christos Dimitrakopoulos, Marc Hulsman, Jeroen de Ridder	Scale-spaces from protein networks: how diffusion profiles reveal functional information in physical interaction topologies
Logan J. Everett, John Le Lay, Sabina Lukovac, David J. Steger, Diana Bernstein, Mitchell A. Lazar, and Klaus H. Kaestner	Cistromic analysis reveals novel insights into hepatic CREB regulatory mechanisms
Richard McEachin, Ashwini Bhasi, Trista Schagat, Aaron Goldstrohm	Identifying PUF co-regulators by RNA-Seq coupled with conserved motif search
R. Taylor Raborn, Krishnakumar Sridharan, Daniel S. Standage, John M. Logsdon Jr., Volker Brendel	Comparative genome-wide analysis of transcription initiation and promoter architecture in eukaryotes
Pilib Ó Broin, Terry Smith, Aaron Golden	A non-tree based approach to automated construction of familial binding profiles
Karsten Hokamp, Yuliana Pozdeeva, Juan-Pablo Labrador	A phylogenetic footprinting ensemble tool and a new scoring metric for evaluating the prediction of transcription factor binding sites in flies
Weronika Sikora Wohlfeld, Marit Ackermann, Eleni Christodoulou, Andreas Beyer	Predicting transcription factor target genes from ChIP-seq data
Alona Chubatiuk	Benchmarking of motif-finding algorithms
Dieter De Witte, Michiel Van Bel, Piet Demeester, Bart Dhoedt, Klaas Vandepoele and Jan Fostier	A high performance computing approach to the discovery of conserved motifs