

# Systems Biology: Global Regulation of Gene Expression

## KEYNOTE SPEAKER

TUESDAY 3/23/2010, 7:30 PM

1 Henikoff Mapping genome-wide nucleosome dynamics 45

## Session 1 TRANSCRIPTION

TUESDAY 3/23/2010, 8:45 PM

T. Hughes

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
2	van Oudenaarden	Variability in gene expression underlies incomplete penetrance	20
3	Frise	Exploring relationships in data sets using spatial gene expression patterns for all <i>Drosophila</i> transcription factors	15
4	Brent	A quantitative model of glucose signaling in yeast reveals an incoherent feed forward loop leading to a specific, transient pulse of transcription	15
5	Tapscott	Genome-wide binding of MyoD in specified and differentiating muscle cells	15

## Session 2 TRANSCRIPTIONAL REGULATORY NETWORKS

WEDNESDAY 3/24/2010, 9:00 AM

X. Shirley Liu

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
6	Ideker	Biomarkers based on networks, not individual loci	20
7	Walhout	Functional modularity of nuclear hormone receptors in a <i>C. elegans</i> gene regulatory network	15
8	Young	New insights into global transcriptional control in embryonic stem cells and tumor cells	20
9	Regev	Unbiased reconstruction of a mammalian transcriptional network mediating the differential response to pathogens	20
10	Zhu	Profiling the human protein-DNA interactome identifies unconventional DNA-binding proteins	15
11	Kaufmann	From bolting to bloom—Genome-wide control of floral meristem initiation and differentiation	15
12	Andrews	Elucidating the structure of the transcriptional regulatory network with genetic interactions	15

## Session 3 POSTER SESSION I

WEDNESDAY 3/24/2010, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
13	Adar	Development of a genome-wide DNA damage detection assay	
14	Agius	Comprehensive modeling of microRNA targets predicts functional non-conserved and non-canonical sites	
15	Agius	High resolution models of transcription factor-DNA affinities improve in vitro and in vivo binding predictions	
16	Agius	Inferring transcriptional and microRNA-mediated regulatory programs in glioblastoma	
17	Albieri	A DNA-transposon based approach to functional screening in neural stem cells	

18	Arvey	Small RNA regulation is dependent on target concentration
19	Avraham	Fine tuning of signaling networks by microRNAs
20	Baek	Quantitative genome-wide analysis of chromatin-remodeling during 3T3-L1 adipocyte differentiation
21	Beckedorff	Intronic antisense noncoding RNA as a candidate regulator of RASSF1 genes
22	Benschop	A consensus of core protein complex compositions for <i>S. cerevisiae</i>
23	Bergstrom Lucas	Gene expression profiling of both protein-coding and non-coding RNA transcripts from small amounts of total RNA using a single microarray design
24	Boyle	Genome-wide DNase I footprinting in a diverse set of human cell-types
25	Brand	Altered genomic targeting of the oncogenic transcription factor TAL1/SCL in T-cell acute lymphoblastic leukemia
26	Bristow	Integrating heterogeneous datasets to predict active promoters, regions of regulatory importance, and characterize gene regulatory mechanisms in <i>Drosophila</i>
27	Brodsky	Quantitative analysis of the <i>Drosophila</i> segmentation regulatory network using pattern generating potentials
28	Busch	In vivo quantification of dynamic gene expression in the <i>Arabidopsis</i> root
29	Camargo	Effect of DNA methylation on the transcription of intronic noncoding RNAs in cancer cell lines
30	Charoensawan	Combinatorial binding codes of transcription factors and nucleosomes
31	Cheng	The limited sharing of factor occupancy between species is enriched for induction of gene expression
32	Cheng	NFκB p50 restricts the interferon response by binding IRE sequences
33	Chiba	A method for optimizing gene combination to induce adipocyte differentiation from mesenchymal stem cells
34	Christensen	Quantitative models of transcription factor specificity using high throughput sequencing and a Bacterial one hybrid assay
35	Conway	Nutrient signal integration through PKA in <i>S. cerevisiae</i>
36	Cotney	Global analysis of chromatin state and gene expression in developing mammalian tissues
37	Cramer	Globally uniform transitions in transcription complex composition
38	de Boer	Modeling yeast transcript definition
39	De Simone	Specific transcriptional regulatory circuits and nodes are affected in familial combined hyperlipidemia syndrome and upon statin treatment
40	Degner	Genome-wide mapping of the precise DNA binding locations for ~120 transcription factors using a single DNase-Seq assay
41	Deplancke	Primer-initiated sequence synthesis to identify and assemble sequence variants using next-generation sequencing data
42	Dresch	Predicting gene expression—From a graphical representation of protein interactions to a formula for gene expression

43	Fachel	Long intronic noncoding RNA signatures of malignancy and survival outcome in clear cell renal cell carcinoma
44	Fazlollahi	Harnessing natural sequence variation to dissect post-transcriptional networks in yeast
45	Firpi	Predicting enhancers using chromatin modifications and time-delay neural network
46	Foat	Industrial strength gene expression
47	Fujita	The impact of measurement errors in the identification of gene regulatory networks
48	Giresi	Regulatory elements that define breast cancer progression and subtypes
49	Gordan	Novel method for computing enrichment of DNA binding motifs provides clues to <i>C. albicans</i> pathogenicity
50	Gray	A global view of pre-mRNA processing suggests that splicing is slow relative to transcription
51	Grosse	MotifAdjuster—A tool for computational reassessment of transcription factor binding site annotations
52	Grosse	Genetic variation of the auxin signaling pathway and transcriptional auxin response networks in natural <i>A. thaliana</i> accessions
53	Guo	Branching process deconvolution algorithm reveals a detailed cell-cycle transcriptional program
54	Halfon	Flexible and accurate discovery of <i>cis</i> -regulatory elements in insects and mammals
55	Hatanaka	Characterization of GSE and GSE-interacting novel gene, GIAP, in primordial germ cells
56	Hawkins	Distinct epigenomic landscapes of human pluripotent and lineage-committed cells
57	Haynes	Applying reachability priors to regulatory network inference
58	Herrmann	Bioinformatic predictions, experimental validation and analysis of <i>cis</i> -regulatory modules—Application to <i>D.melanogaster's</i> cardiogenesis
59	Hickman	Discovery of promoter motifs in <i>A. thaliana</i> stress response genes
60	Hon	Identifying large and small chromatin domains from ChIP-Seq data
61	Huang	The -13kb A/G polymorphism in the LMX1A upstream regulatory region that potentially affects FOXF2/DEC2 binding is associated with osteoporosis
62	Hubank	Predicting transcriptional control patterns in complex genomic data
63	Hung	Discovery and characterization of ncRNAs involved in cell cycle regulation
64	Hyang Heun	Analysis of degraded maternal proteins by ubiquitin-proteasome pathway in mouse preimplantation embryos
65	Iborra	The origin of variation in transcription elongation
66	Ikegami	Characterization of genomic regions associated with the nuclear envelope in <i>C. elegans</i>
67	Imakaev	Dynamics of chromatin folding, looping and repositioning in a fractal globule
68	Ito	Computer analysis on the correlation between surface structure and gene transcription efficiency of the hyaluronic acid-coated DNA/polycation complex

69	Jacobsen	Systematic discovery of novel motifs which modulate microRNA regulation
70	Jene Sanz	Identification of altered regulatory pathways in cancer using IntOGen system
71	Ji	Regulation of alternative mRNA polyadenylation in cell reprogramming
72	Kainth	A genomic approach to map transcription pathways in <i>S. cerevisiae</i>
73	Karczewski	Discovering novel interactions between transcription factors—The allele binding cooperativity test
74	Kiddle	TCAP reveals transcriptional modules in <i>Arabidopsis</i>
75	Kinney	The biophysical basis of transcriptional regulation revealed through deep sequencing
76	Konig	iCLIP reveals the function of hnRNP particles in splicing at individual nucleotide resolution
77	Koohy	An alignment-free sequence comparison model for detection of functional conservation of regulatory sequences
78	Kundaje	A machine learning framework for integrative analysis of ENCODE II data
79	Ladunga	Nucleosome sliding and remodeling—Limits and patterns
80	Lam	C <sub>2</sub> H <sub>2</sub> zinc finger modules typically retain sequence specificity in modular assemblies
81	Lang	Understanding lysine acetylation signaling
82	Larson	Direct observation of transcription initiation and elongation control in living cells
83	Larson	Multi-gene chromatin domains found in mouse genome via hidden Markov models
84	Lee	Identifying the genetic determinants of transcription factor activity
85	Lei	Transcription regulatory network of Alzheimer's disease
86	Liao	Genome-wide analysis of FOXO1 occupancy in mouse neural stem cells using next-generation sequencing
87	Lightfoot	Predicting membership of regulatory protein complexes—Integrating protein interaction data with transcriptional regulation
88	Lin	Yeast axial element protein Red1 binds SUMO chains to promote meiotic interhomolog recombination and chromosome synapsis
89	Liu	Infer the transcription regulatory network in mouse intestine development from histone mark dynamics
90	Luksza	Significance-based clustering of gene expression data

#### KEYNOTE SPEAKER

WEDNESDAY 3/24/2010, 7:30 PM

91	Struhl	An epigenetic switch that links inflammation to cancer—Regulatory circuits and cancer	45
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#### Session 4 CHROMATIN

WEDNESDAY 3/24/2010, 8:45 PM

	R. Morse		
<b>#</b>	<b><u>Iname</u></b>	<b><u>Title</u></b>	<b><u>Talk Length</u></b>
		treatment	
92	Lieb	An atlas of open chromatin spanning diverse human cell types in health and disease	20

93	Sidow	Ultra-high resolution nucleosome organization maps and gene expression analysis in purified primary human cells	15
94	Ruan	Genome-wide long range chromatin interactions and transcription regulation networks	15
95	Van Berkum	Long-range gene regulatory architecture of human chromosome 21	15

**Session 5 EPIGENETICS**

THURSDAY 3/25/2010, 9:00 AM

J. Stamatoyannopoulos

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
96	Ren	Epigenomic landscapes of pluripotent and lineage-committed human cells	20
97	Lienert	Proximal promoter elements determine DNA methylation during somatic differentiation	15
98	Laurent	Whole-genome bisulfite sequencing of human pluripotent and differentiated cells reveals dynamic changes occurring during differentiation	15
99	Rando	Static and dynamic genome-wide views of yeast chromatin	20
100	Mendenhall	Combined computational and experimental approaches pinpoint a GC-rich element sufficient for the recruitment of Polycomb Complexes in ES Cells.	15
101	Hebenstreit	Bimodality in gene expression levels correlates with an epigenetic module	15
102	Chang	Programming chromatin states by long noncoding RNAs	20

**Session 6 POSTER SESSION II**

THURSDAY 3/25/2010, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
103	MacNeil	A protein-DNA interaction network regulating responses to reactive oxygen species	
104	Maranville	The impact of genetic polymorphism on the transcriptional pathway underlying glucocorticoid response	
105	Marinov	Genome-wide characterization of the transcriptome in ENCODE cell lines	
106	Martincorena	Evidence of bet-hedging in the spatial variation of mutation rate along bacterial genomes	
107	Matsui	Proviral silencing in ES cells requires the histone methyltransferase ESET	
108	Mayer	High-resolution ChIP-chip profiling reveals uniform transitions in transcription complex composition	
109	Meneghini	Rpb2 ortholog Jhd2 mediates global histone demethylation and gene expression to control spore differentiation timing during budding yeast gametogenesis	
110	Meuleman	Dynamics and evolution of genome - nuclear lamina interactions	
111	Mirny	Nucleosome-mediated cooperativity between transcription factors	
112	Mo	A novel Bayesian segmentation model for ChIP-seq data analyses	
113	Mogno	TATA is a modular component of synthetic promoters	
114	Mokry	Nucleotide resolution protein-DNA binding characteristics by double fragmentation ChIP-Seq	

115	Morohashi	An incoherent feed forward loop defines the pattern of <i>AGO4</i> expression during early <i>A. thaliana</i> trichome development
116	Morse	Extensive role of the general regulatory factors, Abf1 and Rap1, in determining genome-wide chromatin structure in budding yeast
117	Mortazavi	Integrative analysis of ChIP-seq and RNA-seq data using Self-Organizing Maps
118	Murray	A cellular resolution atlas of embryonic gene expression identifies dynamic temporal control of temporal identity and fate
119	Naef	Rhythmic protein-DNA interactomes and circadian transcription regulatory networks
120	Nie	Using c-Myc-GFP knock-in mice to study the regulation and function of c-Myc in normal cells, in vivo
121	Onichtchouk	Oct4/Pou5f1-dependent transcriptional networks in temporal control of early development
122	Orlov	Genome wide nucleosome occupancy and affinity of transcription factors binding—Yeast study
123	Ouyang	Combinatorial regulation of transcription factors and histone modifications revealed from integrated modeling of genome-wide ChIP-Seq and gene expression data
124	Pasquali	Genome-wide organization of open chromatin in human pancreatic islets
125	Pott	Genome-wide mapping of PPAR $\gamma$ /RXR binding in macrophages connects the transcription factor PU.1 to the selection of tissue-specific target genes
126	Qian	Global analysis of phosphorylation networks in humans
127	Qin	Detection and refinement of transcription factor binding sites using Hybrid Monte Carlo method
128	Rajagopal	H3.3 levels at enhancers and the 3' ends of genes correlate with gene expression
129	Reimers	Statistical analysis reveals fine scale patterns in methylation and expression of genes in the NCI 60 panel
130	Riley	Binding-site affinity modeling of positional dependencies and context-sensitive nucleotide insertions and deletions
131	Rodrigues	Comparative genomics of HSF-1 regulated activity
132	Rynditch	Regulation of intersectin family gene expression
133	Sanchez Garcia	Associations between genomic alterations in cancer
134	Schimpf-Linzenbold	Identification of allelic expression differences in retinal expressed disease genes
135	Schmid	Coordinate transcriptional regulation of the response to environmental extremes
136	Schroth	Studying gene structure, expression and regulation using the Illumina HiSeq2000 system
137	Schulze	Histone H3 methylation and H2B ubiquitination signatures in the yeast genome and their roles in cell cycle control, transcription, and mRNA splicing.
138	Schumacher	Genome instability in aging and longevity
139	Sealfon	Predicting enhancer regions and transcription factor binding sites in <i>D. melanogaster</i> using supervised learning approaches

140	Selimyan	Localized DNA demethylation marks recombination intermediates during immunoglobulin heavy chain gene assembly
141	Severino	MicroRNA-196-mediated regulation of gene expression and molecular networks in oral squamous cell carcinoma
142	Shiff	Differences in p53 binding upon acetylation
143	Shin	Analysis of transcriptional regulators governing establishment of cell-to-cell reprogramming network
144	Shiraishi	Inferring cis-regulatory network via differently perturbed multiple time-course gene expression data
145	Siggers	Precise temporal control of the eye regulatory gene Pax6 via enhancer binding site affinity
146	Szczurek	Model- and knowledge-based analysis of gene deregulation
147	Tanaka	Adipogenesis induced by short interference RNAs predicted by informatics
148	Tanasa	Nuclear receptor-induced DNA breaks that can underlie specific translocations in cancers
149	Taylor	Transcriptional regulatory subnetworks in the mouse brain as derived from data sets in the Allen Mouse Brain Atlas
150	Tepper	A novel meta-analysis identifies DAF-16/FOXO transcription factor target genes
151	Tillo	High nucleosome occupancy is encoded at human regulatory sequences
152	Trcek	Single molecule analysis in yeast cells reveals cell-cycle dependent mRNA degradation
153	Tsankov	The role of nucleosome positioning in the evolution of gene regulation
154	Tuomela	Novel insights into the gene regulatory networks regulating human T helper (Th) cell differentiation
155	Ule	iCLIP RNA maps elucidate TIA1 and TIAL1 as master regulators of RNA splicing
156	van Arensbergen	Selective derepression Polycomb targets during pancreatic organogenesis creates a neural program in insulin-producing $\beta$ -cells.
157	van Bakel	Most "dark matter" transcripts are associated with known genes
158	Vastenhouw	Chromatin signature of embryonic pluripotency is established during zygotic genome activation
159	Wan	Genome-wide probing of RNA structure in yeast
160	Wang	Genome-wide prediction of transcription factor binding sites using an integrated model
161	Wang	Co-evolution of transcription factor and its binding sites
162	Wang	DNA methylome map reveals conserved role of DNA methylation in regulating alternative promoters
163	Ward	Promiscuous, stress-responsive binding of transcription factors to yeast ncRNA genes and nucleosome-depleted regions
164	Weirauch	"Pfam-wide" determination and inference of transcription factor DNA sequence specificities
165	White	Geometric perspectives on uncertainty minimization for fuzzy spectral clustering

166	Wilczynski	Understanding transcriptional regulation during development using a probabilistic model
167	Wu	Epigenomic landscape of erythroid maturation
168	Yadon	Genome-wide reduction of NFR size and suppression of cryptic RNA transcription by an ATP-dependent chromatin remodeling enzyme
169	Yu	From TMPRSS2-ERG gene fusion to prostate cancer
170	Yue	Systematic discovery of cis-regulatory elements in the mouse genome
171	Zang	Identification of large-scale chromatin domains from ChIP-Seq data— A coarse-graining approach
172	Zhang	Integrative discovery and analysis of a global splicing-regulatory network in mouse brain
173	Zhang	Functional analysis of the C-terminal Binding Protein (CtBP) in <i>Drosophila</i>
174	Zhao	Estimating binding energies from protein binding microarray experiments
175	Zhou	Determinants of Transcription factor binding and regulation
176	Zhu	Differential gene expression in tissues with different tropism for foot-and-mouth disease virus
177	Zwang	The regulatory program of EGF-induced S-phase entry

**Session 7 CIS REGULATORY LOGIC**

THURSDAY 3/25/2010, 7:30 PM

L. Mirny

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
178	Siggia	Geometry, genetics and evolution	20
179	Furlong	Making global predictions of cis-regulatory activity	20
180	Bussemaker	Elucidating the intrinsic sequence specificity of DNase I using high-throughput sequencing	15
	Stathopoulos	Title only: Patterning mechanisms supporting differential gene expression within fields of cells	20
181	Kaplan	What shapes the landscape of transcription factor binding during early <i>Drosophila</i> development?	15
182	Wold	Integrating and testing ChIP-seq and RNA-seq data	20

**Session 8 POST-TRANSCRIPTIONAL REGULATION**

FRIDAY 3/26/2010, 9:00 AM

M. Walhout

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
183	Burge	Global analysis of RNA processing in mouse models of myotonic dystrophy	20
184	Younger	Transcriptional silencing by micro-RNAs that target gene promoters	15
185	Bartel	MicroRNAs and their regulatory targets	20
186	Gingeras	Eukaryotic transcriptomes—Complex, multifunctional, compartmentalized and elegant	20
187	Tsvetanova	Proteome-wide search for novel RBP-RNA interactions in <i>S. cerevisiae</i> using protein microarrays	15

188	Gerber	Systematic identification of RNA-binding proteins in yeast proposes dual functions for enzymes	15
189	Rinn	Chromatin associated large intergenic non-coding RNAs (lincRNAs) in cancer and stem cells	20

**Session 9 EMERGING TECHNOLOGY**

FRIDAY 3/26/2010, 2:00 PM

B. Andrews

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
190	Bulyk	High-throughput experimental identification of tissue/cell-type-specific cis regulatory modules in <i>Drosophila</i>	15
191	Levo	Transcriptional Lego—Tuning expression levels in a predictable manner by manipulating promoter building blocks	15
192	Hemberg	Widespread transcription at thousands of enhancers during activity-dependent gene expression in neurons	15
193	Zenklusen	Studying transcription dynamics in yeast—A single molecule approach	15
194	Braunschweig	A combinatorial protein code defines new principal chromatin types in <i>Drosophila</i>	15
195	Kouzine	Global correlation of transcription and DNA conformation reveals new modes of gene regulation	15
196	Lieberman-Aiden	Chromatin on the megabase scale—The fractal globule architecture and its physical properties	15
197	Dekker	The three-dimensional folding of the $\beta$ -globin gene domain reveals formation of chromatin globules	15

**Session 10 VARIATION AND EVOLUTION**

SATURDAY 3/27/2010, 9:00 AM

M. Bulyk

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
198	Kellis	Regulatory genomics and epigenomics of multiple human cell lines	20
199	Bourque	Transposable elements have rewired the core regulatory network of human embryonic stem cells	15
200	Irizarry	Stochastic epigenetic variation as a driving force of development, evolutionary adaptation, and disease	20
201	Bejerano	Human-specific loss of regulatory DNA and the evolution of human-specific traits	15
202	Yun	Single Base Matters—A systematic approach for detecting expression variation at single nucleotide resolution	15
203	Stark	Comparative regulatory genomics in <i>Drosophila</i>	15
204	Snyder	Transcription binding variation in eucaryotes	15