**Evolution and Core Processes in Gene Regulation**  
**June 25 – 28, 2015**

**Meeting Location:** Washington University in St. Louis  
**Building:** Anheuser Busch Law School  
**Program/Badge Pick-Up:** Crowder Courtyard  
**Sessions:** Cullenbine Classroom  
**Posters:** Crowder Courtyard

**Thursday, June 25, 2015**

**Noon - 5:00 pm:** MEETING REGISTRATION CHECK-IN AND PROGRAM PICK-UP

**1:45 pm - 2:00 pm:** WELCOME AND MEETING INTRODUCTION  
David Arnosti, Michigan State University

**2:00 pm - 3:20 pm**  
**Session I**  
**NEW TECHNOLOGIES IN TRANSCRIPTION**  
Session Chair: Julia Zeitlinger, Stowers Institute for Medical Research

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<th>Time</th>
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<th>Speaker(s)</th>
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<td>2:00 pm - 2:20 pm</td>
<td>Probing Transcription Regulation by Single Molecule Imaging (1)</td>
<td>Robert Tjian, Janelia Research Campus, HHMI</td>
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<td>2:20 pm - 2:40 pm</td>
<td>Transcriptome-scale single molecule fluorescent in situ hybridization by MERFISH (2)</td>
<td>Alistair Boettiger, Howard Hughes Medical Institute, Dept. of Chemistry and Chemical Biology, Harvard University</td>
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<td>2:40 pm - 3:00 pm</td>
<td>Decoding transcriptional regulation in Drosophila (3)</td>
<td>Alexander Stark, Research Institute of Molecular Pathology (IMP)</td>
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<td>3:00 pm - 3:20 pm</td>
<td>Visualizing human transcription at nucleotide resolution by native elongating transcript sequencing (4)</td>
<td>L. Stirling Churchman, Harvard Medical School</td>
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<td>3:20 pm - 3:50 pm</td>
<td>Break</td>
<td>Crowder Courtyard</td>
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</table>
Thursday, June 25, 2015

3:50 pm - 5:30 pm:  **Session II**

**CIS-REGULATORY CODE AND EVOLUTION**
Session Chair: **Julia Zeitlinger**, Stowers Institute for Medical Research

3:50 pm - 4:10 pm:  *Sequence-based model of the Drosophila gap gene network and its application for analysis of polymorphism in the regulatory sequence* (5)
**Maria Samsonova**, St. Petersburg Polytechnic University, St. Petersburg, Russia

4:10 pm - 4:30 pm:  *Lessons from evolving enhancers — integrative studies of cis-regulatory function and evolution* (6)
**Saurabh Sinha**, Dept. of Computer Science, University of Illinois at Urbana-Champaign

4:30 pm - 4:50 pm:  *Evolution of Developmental Enhancers* (7)
**Emma Farley**, UC Berkeley

4:50 pm - 5:10 pm:  *Principles of epigenome conservation* (8)
**Ting Wang**, Washington University

5:10 pm - 5:30 pm:  *Comparing Hox binding sites and targets: A story in segments* (9)
**Robb Krumlauf**, Stowers Institute for Medical Research

5:30 pm - 8:30 pm:  Opening Reception and Dinner
**Crowder Courtyard**
Friday, June 26, 2015

7:00 am – 8:30 am: Breakfast for On-Campus Residents in Dining Hall
   Danforth University Center

8:00 am - 5:00 pm: MEETING REGISTRATION

9:00 am - 10:15 am: Session III
   MECHANISMS OF TRANSCRIPTION AND SPlicing
   Session Chair: David Arnosti, Michigan State University

9:00 am - 9:20 am: Gene expression control by transformer proteins (10)
   Irina Artsimovitch, Department of Microbiology, The Ohio State University

9:20 am - 9:40 am: Interplay between RNA Polymerase II activity and promoter architecture in specification of transcription start sites in Saccharomyces cerevisiae(11)
   Craig Kaplan, Texas A&M University, College Station

9:40 am - 9:55 am: H3 K36 methylation suppresses non-coding RNA transcription by resetting chromatin (12)
   Swaminathan Venkatesh, Stowers Institute for Medical Research

9:55 am - 10:15 am: Chromatin remodeling coordinates transcription and pre-messenger RNA splicing to regulate meiosis in Saccharomyces cerevisiae (13)
   Tracy Johnson, UCLA

10:15 am - 10:35 am: Break
   Crowder Courtyard
Evolution and Core Processes in Gene Regulation

Friday, June 26, 2015

10:35 am – 11:50 am: Session IV

POSTTRANSLATIONAL MECHANISMS AND EVOLUTION
Session Chair: David Arnosti, Michigan State University

10:35 am - 10:55 am: Sorting functional from junk RNAs through nuclear export. (14)
Alexander Palazzo, University of Toronto

10:55 am - 11:15 am: Mechanisms of mRNA surveillance defined by ribosome profiling and biochemistry (15)
Rachel Green, HHMI/Johns Hopkins University School of Medicine

11:15 am - 11:30 am: Drosophila X-linked genes have lower translational rates than autosomal genes (16)
Zhenguo Zhang, University of Rochester

11:30 am - 11:50 am: Evolution of cis-regulatory elements controlling mRNA translation (17)
Joel McManus, Carnegie Mellon University, Dept. of Biological Sciences

11:50 am - 12:00 pm: Session V

POSTER SNEAK PREVIEW
Presenters have one (1) minute to communicate the key message of their upcoming poster presentation.

11:51:00 am-11:52:00 am:
The effects of promoter divergence on expression and fitness of the gene MLS1 in yeast (18)
Andrew Bergen, Dept. of Genetics, Washington University in St. Louis

11:53 :00 am - 11:54:00 am:
Combinatorial control of temporal gene regulation in the Drosophila embryo (19)
Rhea Datta, New York University

11:55:00 am - 11:56:00 am:
Codon Usage Bias as a Mechanism for Restricting Tissue-specific Protein Translation (20)
Zhen Peng, Washington University in St. Louis
Evolution and Core Processes in Gene Regulation

Friday, June 26, 2015

11:50 am - 12:00 pm: Session V (continued)

POSTER SNEAK PREVIEW
Presenters have one (1) minute to communicate the key message of their upcoming poster presentation.

11:57:00 am - 11:58:00 am:
Widespread contribution of transposable elements to the innovation of gene regulatory networks (21)
Vasavi Sundaram, Washington University School of Medicine, St Louis

12:00 pm - 1:30 pm: Lunch
Crowder Courtyard

1:30 pm - 3:30 pm: POSTER SESSION
Posters located in Crowder Courtyard.
Presentations available on pages 11-13.

3:30 pm – 4:45 pm: Session VI
ENHANCER MECHANISMS
Session Chair: Alex Stark, Research Institute of Molecular Pathology (IMP)

3:30 pm - 3:50 pm: Enhancer priming and patterning in the early Drosophila embryo (22)
Julia Zeitlinger, Stowers Institute for Medical Research

3:50 pm - 4:10 pm: Macrophage-specific enhancers are kept accessible during macrophage differentiation by recruitment of the BAF/PBAF nucleosome remodeler (23)
Monique Floer, Michigan State University

4:10 pm - 4:25 pm: Determinants of nucleosome positioning and their influence on plant gene expression (24)
Ming-Jung Liu, Dept. of Plant Biology, Michigan State University, East Lansing

4:25 pm - 4:45 pm: Roles of sister chromatid cohesion proteins in metazoan enhancer function (25)
Dale Dorsett, Saint Louis University School of Medicine, Saint Louis
Friday, June 26, 2015

4:45 pm - 5:15 pm: Break
Crowder Courtyard

5:15 pm - 6:30 pm: Session VII
TRANSCRIPTION FACTORS AND ENHANCER EVOLUTION
Session Chair: Alex Stark, Research Institute of Molecular Pathology (IMP)

5:15 pm - 5:35 pm: “Soft” regulation of pleiotropic controls by transcriptional repressors: sources of evolutionary variation and innovations (26)
David Arnosti, Michigan State University

5:35 pm - 5:50 pm: DNA binding specificity changes in the evolution of forkhead transcription factors (27)
Julia Rogers, Brigham and Women's Hospital and Harvard Medical School, Division of Genetics, Boston

5:50 pm - 6:10 pm: A circuit-based view of gene regulatory network co-option reveals unexpected paths for the evolution of novelty (28)
Mark Rebeiz, University of Pittsburgh, Dept. of Biological Sciences

6:10 pm - 6:30 pm: Variation and Evolution of Gene Regulatory Networks (29)
Sergey Nuzhdin, University of Southern California

6:30 pm - 9:00 pm: Dinner
Crowder Courtyard
9:00 am - 10:20 am: Session VIII
PATTERN FORMATION AND ENHANCER EVOLUTION
Session Chair: Sergey Nuzhdin, University of Southern California

9:00 am - 9:20 am: Regulatory evolution and the diversification of pigmentation patterns in Drosophila: from nucleotide changes to novel phenotypes (30)
Nicolas Gompel, Ludwig-Maximilians Universität, Munich, Germany

9:20 am - 9:40 am: There are lots of ways to build a pattern: considering regulatory evolution at the locus level in Drosophila embryos. (31)
Angela DePace, Dept. of Systems Biology, Harvard Medical School

9:40 am - 10:00 am: Experimental and computational tests of cis-regulatory conservation (32)
Ilya Ruvinsky, University of Chicago

10:00 am - 10:20 am: Live imaging of eve stripe 2, shadow enhancers, and sensitized snail transgenes that provide evidence for transcriptional memory and allele interactions (33)
Mike Levine, UC Berkeley

10:20 am - 10:35 am: Break
Crowder Courtyard

10:35 am - 12:30 pm: Session IX
MUTATIONS AND EVOLUTION OF GENE NETWORKS
Session Chair: Sergey Nuzhdin, University of Southern California

10:35 am - 10:55 am: Genetic variation in gene expression dynamics (34)
Justin Fay, Washington University in St. Louis

10:55 am - 11:15 am: Disentangling the impacts of mutation and selection on regulatory variation (35)
Patricia Wittkopp, University of Michigan, Ann Arbor
Saturday, June 27, 2015

10:35 am - 12:30 pm: Session IX (continued)

**MUTATIONS AND EVOLUTION OF GENE NETWORKS**

Session Chair: **Sergey Nuzhdin**, University of Southern California

11:15 am - 11:35 am: *Non-allelic gene conversion enables rapid evolutionary change at multiple regulatory sites encoded by transposable elements* (36)

**Doris Bachtrog**, UC Berkeley


**Alberto Civetta**, University of Winnipeg

11:55 am – 12:10 pm: *Divergent Regulatory Mechanisms for Central Nervous System Development in Aedes aegypti and Drosophila melanogaster* (38)

**Kushal Suryamohan**, Dept. of Biochemistry, State University of New York at Buffalo

12:10 pm – 12:30 pm: *Evolution of Regulatory Networks Governing Bacterial Sporulation* (39)

**Lee Kroos**, Michigan State University, East Lansing

12:30 pm - 1:30 pm: Lunch

**Crowder Courtyard**

1:30 pm – 6:00 pm: Free-time to relax and explore Forest Park

First shuttle leaves from the Clock Tower at 2 pm and will circulate through the park with multiple stops.

6:00 pm – 9:00 pm: Dinner at the Boathouse located in Forest Park

- 5:30 pm: Shuttle leaves from the Clock Tower.
- Parking is available at the Boathouse in Forest Park.
- If you are in Forest Park, the shuttle will pick-up on its way to The Boathouse, beginning at 5:30 pm.
- 9:00 pm: Shuttle leaves Boathouse at end of dinner and drops-off at the Clock Tower.
Sunday, June 28, 2015

7:00 am – 8:30 am: Breakfast for On-Campus Residents in Dining Hall
Danforth University Center

8:00 am - 12:00 pm: MEETING REGISTRATION

9:00 am - 10:20 am: Session X
MAMMALIAN REGULATORY CODE AND EVOLUTION
Session Chair: Justin Fay, Washington University in St. Louis

9:00 am - 9:20 am: Why don't transcription factors get lost? (40)
Barak Cohen, Washington University in St. Louis School of Medicine, St. Louis

9:20 am - 9:40 am: An ancient yet flexible cis-regulatory architecture at the patched/PTCH1 locus allows tissue-specific tuning of Hedgehog signaling and morphological adaptation (41)
Scott Barolo, University of Michigan Medical School, Ann Arbor

9:40 am - 10:00 am: Enhanceosome transcription factors preferentially dimerize with high mobility group proteins (42)
Jerzy Tiuryn, University of Warsaw, Warsaw, Poland

10:00 am - 10:20 am: What we can learn from high resolution specificity determination (43)
Gary Stormo, Washington University School of Medicine, St Louis

10:20 am – 10:40 am: Break
Crowder Courtyard

10:40 am - 11:55 am: Session XI
MAMMALIAN SPECIALIZATION
Session Chair: Justin Fay, Washington University in St. Louis

10:40 am – 11:00 am: Essential role of linker histone H1 in transcriptional regulation during neural differentiation (44)
Yuhong Fan, School of Biology, Georgia Institute of Technology, Atlanta

11:00 am – 11:15 am: Exploring the Human Genome for Functional, Non-Coding Variation: Implications for Diseases of the Peripheral Nerve (45)
William Law, Dept. of Human Genetics, University of Michigan Medical School, Ann Arbor
Sunday, June 28, 2015

10:40 am - 11:55 am: Session XI (continued)

MAMMALIAN SPECIALIZATION
Session Chair: Justin Fay, Washington University in St. Louis

Joe Corbo, Washington University School of Medicine in St. Louis

11:35 am - 11:55 am: Meeting Wrap-up, Poster Award Announcements and Concluding Remarks
Organizers: David Arnosti, Michigan State University
Justin Fay, Washington University in St. Louis
Julia Zeitlinger, Stowers Institute for Medical Research

11:55 am: Box Lunches and Departures
Crowder Courtyard
# Poster Session in Crowder Courtyard

**Friday, June 26, 2015**

**1:30 pm - 3:30 pm: POSTER SESSION in Crowder Courtyard.**

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<tbody>
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<td>1</td>
<td>18</td>
<td>Andrew</td>
<td>Bergen</td>
<td>WUSTL</td>
<td>The effects of promoter divergence on expression and fitness of the gene MLS1 in yeast</td>
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<td>Rhea</td>
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<td>NYU</td>
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<td>Codon Usage Bias as a Mechanism for Restricting Tissue-specific Protein Translation</td>
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<tr>
<td>4</td>
<td>21</td>
<td>Vasavi</td>
<td>Sundaram</td>
<td>Washington Univ Sch of Med</td>
<td>Widespread contribution of transposable elements to the innovation of gene regulatory networks</td>
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<tr>
<td>5</td>
<td>47</td>
<td>Zachary</td>
<td>Burton</td>
<td>Michigan State Univ</td>
<td>A working model for RNA polymerase, promoter and general transcription factor evolution</td>
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<td>6</td>
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<td>Hemangi</td>
<td>Chaudhari</td>
<td>WUSTL</td>
<td>AP-1 binding site activity is sensitive to local sequence context.</td>
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<td>7</td>
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<td>Carly</td>
<td>Ching</td>
<td>Northeastern Univ</td>
<td>Investigating the regulation of recA in the emerging pathogen Acinetobacter baumannii</td>
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<td>8</td>
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<td>Bony</td>
<td>DE Kumar</td>
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<td>Hoxa1 - Regulator of signaling pathway during neural differentiation</td>
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<td>Rob</td>
<td>DeLong</td>
<td>Kansas State Univ</td>
<td>Biomolecular nanocomposite and engineered cell systems as new tools for the discovery of proteins and signaling patterns important in the growth of 3-D metastatic foci phenotype</td>
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<td>10</td>
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<td>Chetna</td>
<td>Gopinath</td>
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<td>Transcriptional Hierarchies Important for Myelination in the Peripheral Nervous System</td>
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<td>Kristen</td>
<td>Humphrey</td>
<td>SUNY at Buffalo</td>
<td>Sirtuins facilitate evolutionary adaptation</td>
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<td>13</td>
<td>55</td>
<td>Farzaneh</td>
<td>Khajouei</td>
<td>Univ of IL Urbana-Chamapaign</td>
<td>An information theoretic treatment of sequence-to-expression modeling, with application to enhancer evolution</td>
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<td>14</td>
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<td>David</td>
<td>Lorberbaum</td>
<td>Univ of Michigan</td>
<td>How a multi-modular, tissue specific cis-regulatory architecture controls a constitutive response to Hedgehog signaling</td>
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<td>15</td>
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<td>Katia</td>
<td>Los</td>
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<td>Regulation of resistance gene expression by ribosome targeting antibiotics</td>
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<td>58</td>
<td>Brett</td>
<td>Maricque</td>
<td>Washington Univ Sch of Med</td>
<td>Dissecting enhancer activity with a massively-parallel, genome-integrated reporter assay</td>
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<td>Moore</td>
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<td>Finding cis-regulatory elements that regulate plant defense response to insect herbivores</td>
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<td>De novo enhancer identification in differentiated Drosophila tissues</td>
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<td>Genome-wide effects of retinoblastoma family proteins on gene expression and chromatin state in Drosophila melanogaster development</td>
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<td>Ramya</td>
<td>Rajagopalan</td>
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<td>Evolution of a Sporulation Timer in Myxococcus xanthus</td>
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<td>Vivekanandan</td>
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<td>Regulation of RNA polymerase II recruitment during development</td>
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<td>Amol</td>
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<td>Epigenomic annotation of genetic variants using the Roadmap EpiGenome Browser</td>
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<td>Comparative Analysis of the DNA Methylome with Included and Excluded Alternatively Spliced Exons</td>
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<td>Alexander</td>
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<td>Using evolutionary computations to explore cis-regulatory modular organization and its relation to spatial gene expression domains</td>
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<td>Cynthia</td>
<td>Staber</td>
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<td>Devjanee</td>
<td>Swain Lenz</td>
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<td>Tanaka</td>
<td>Instituto Gulbenkian de Ciência, Lisbon, Portugal</td>
<td>Cis-regulatory basis of transcriptional divergence between recent gene duplicates</td>
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<td>Todd</td>
<td>Kansas State Univ</td>
<td>Dual DNA binding and co-activator modes of action for a Zn(II)2Cys6 transcription factor: a mechanism for promoter evolution?</td>
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<td>Uygun</td>
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<td>Wei</td>
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<td>Michael</td>
<td>White</td>
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<td>Bulk sum of transcription factor binding sites determines the compatibility of cis-regulatory elements with core promoters in photoreceptors</td>
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<td>Jinsong</td>
<td>Zhang</td>
<td>Saint Louis Univ Sch of Med</td>
<td>RNA polymerase II is a direct and functional target of the AML1-ETO leukemia fusion protein</td>
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