Research

Sumoylation at chromatin governs coordinated repression of a transcriptional program essential for cell growth and proliferation

Hélène Neyret-Kahn, Moussa Benhamed, Tao Ye, Stéphanie Le Gras, Jack-Christophe Cossec, Pierre Lapasset, Oliver Bischof, Maia Ouspenskaia, Mary Dasso, Jacob Seeler, Irwin Davidson, and Anne Dejean

Lamin A/C-promoter interactions specify chromatin state–dependent transcription outcomes

Eivind Lund, Anja R. Oldenburg, Erwan Delbarre, Christel T. Freberg, Isabelle Duband-Goulet, Ragnhild Eskeland, Brigitte Buendia, and Philippe Collas

GC skew at the 5’ and 3’ ends of human genes links R-loop formation to epigenetic regulation and transcription termination

Paul A. Ginno, Yoong Weam Lim, Paul L. Lott, Ian Korf, and Frédéric Chédin

De novo DNA demethylation and noncoding transcription define active intergenic regulatory elements

Felix Schlesinger, Andrew D. Smith, Thomas R. Gingeras, Gregory J. Hannon, and Emily Hodges

Frac-seq reveals isoform-specific recruitment to polyribosomes

Timothy Sterne-Weiler, Rocio Teresa Martinez-Nunez, Jonathan M. Howard, Ivan Cvitovik, Sol Katzman, Muhammad A. Tariq, Nader Pourmand, and Jeremy R. Sanford

Genome-wide and parental allele-specific analysis of CTCF and cohesin DNA binding in mouse brain reveals a tissue-specific binding pattern and an association with imprinted differentially methylated regions

Adam R. Prickett, Nikolaos Barkas, Ruth B. McCole, Siobhan Hughes, Samuele M. Amante, Reiner Schulz, and Rebecca J. Oakey

Global analyses of UPF1 binding and function reveal expanded scope of nonsense-mediated mRNA decay

Jessica A. Hurt, Alex D. Robertson, and Christopher B. Burge

The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA

Michael Regulski, Zhenyuan Lu, Jude Kendall, Mark T.A. Donoghue, Jon Reinders, Victor Llaca, Stephane Deschamps, Andrew Smith, Dan Levy, W. Richard McCombie, Scott Tingey, Antoni Rafalski, James Hicks, Doreen Ware, and Robert A. Martienssen

Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population

Robert J. Schmitz, Yupeng He, Oswaldo Valdés-López, Saad M. Khan, Trupti Joshi, Mark A. Urich, Joseph R. Nery, Brian Diers, Dong Xu, Gary Stacey, and Joseph R. Ecker

(continued)
Methods

Pathoscope: Species identification and strain attribution with unassembled sequencing data

Integrated detection of natural antisense transcripts using strand-specific RNA sequencing data
Song Li, Louisa M. Liberman, Neelanjan Mukherjee, Philip N. Benfey, and Uwe Ohler

Resources

Coelacanth genomes reveal signatures for evolutionary transition from water to land

The million mutation project: A new approach to genetics in Caenorhabditis elegans
Owen Thompson, Mark Edgley, Pnina Strasbourger, Stephane Flibotte, Brent Ewing, Ryan Adair, Vinci Au, Iasha Chaudhry, Lisa Fernando, Harald Hutter, Armelie Kieffer, Joanne Lau, Norris Lee, Angela Miller, Greta Raymant, Bin Shen, Jay Shendure, Jon Taylor, Emily H. Turner, LaDeana W. Hillier, Donald G. Moerman, and Robert H. Waterston

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Cover Barbara McClintock’s early work on epigenetic gene control involved the transposable element Suppresser Mutator (Spm). Spotted kernels have active transposition during kernel development, detected as mutations from a1 to A1, and weak (pale) expression of the A1 (anthocyanin) gene, which is under epigenetic control. In this issue a high resolution map of the maize methylome is reported, revealing widespread epigenetic control of gene expression and inheritance. (Courtesy of Cold Spring Harbor Laboratory Archives. Photo: Thomas Adams. [For details, see Regulski et al., pp. 1651–1662.])