Research

Incomplete lineage sorting patterns among human, chimpanzee, and orangutan suggest recent orangutan speciation and widespread selection
   Asger Hobolth, Julien Y. Dutheil, John Hawks, Mikkel H. Schierup, and Thomas Mailund

Age-dependent gain of alternative splice forms and biased duplication explain the relation between splicing and duplication
   Julien Roux and Marc Robinson-Rechavi

Interactome mapping suggests new mechanistic details underlying Alzheimer’s disease
   Montserrat Soler-López, Andreas Zanzoni, Ricart Lluis, Ulrich Stelzl, and Patrick Aloy

Bubble-chip analysis of human origin distributions demonstrates on a genomic scale significant clustering into zones and significant association with transcription

Global impact of RNA polymerase II elongation inhibition on alternative splicing regulation
   Joanna Y. Ip, Dominic Schmidt, Qun Pan, Arun K. Ramani, Andrew G. Fraser, Duncan T. Odom, and Benjamin J. Blencowea

Cln4-2 genomic structure differs between the X locus in Mus spretus and the autosomal locus in Mus musculus: AT motif enrichment on the X

Nucleotide composition-linked divergence of vertebrate core promoter architecture
   Simon J. van Heeringen, Waseem Akhtar, Ulrike G. Jacobi, Robert C. Akkers, Yutaka Suzuki, and Gert Jan C. Veenstra

Dioxin receptor and SLUG transcription factors regulate the insulator activity of B1 SINE retrotransposons via an RNA polymerase switch

Genome-scale RNAi on living-cell microarrays identifies novel regulators of Drosophila melanogaster TORC1–S6K pathway signaling

(continued)
Methods

Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data

Roger Pique-Regi, Jacob F. Degner, Athma A. Pai, Daniel J. Gaffney, Yoav Gilad, and Jonathan K. Pritchard

High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells


A novel approach identifies new differentially methylated regions (DMRs) associated with imprinted genes

Sanaa Choufani, Jonathan S. Shapiro, Martha Susiarjo, Darci T. Butcher, Daria Grafodatskaya, Youliang Lou, Jose C. Ferreira, Dalila Pinto, Stephen W. Scherer, Lisa G. Shaffer, Philippe Coullin, Isabella Caniggia, Joseph Beyene, Rima Slim, Marisa S. Bartolomei, and Rosanna Weksberg

Selective ploidy ablation, a high-throughput plasmid transfer protocol, identifies new genes affecting topoisomerase I–induced DNA damage

Robert J.D. Reid, Sergio González-Barrera, Ivana Sunjevaric, David Alvaro, Samantha Ciccone, Marisa Wagner, and Rodney Rothstein

Resources

Adaptive seeds tame genomic sequence comparison

Szymon M. Kiełbasa, Raymond Wan, Kengo Sato, Paul Horton, and Martin C. Frith

Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons

Brian J. Haas, Dirk Gevers, Ashlee M. Earl, Mike Feldgarden, Doyle V. Ward, Georgia Giannoukos, Dawn Ciulla, Diana Tabbaa, Sarah K. Highlander, Erica Sodergren, Barbara Methé, Todd Z. DeSantis, The Human Microbiome Consortium, Joseph F. Petrosino, Rob Knight, and Bruce W. Birren

OA Open Access paper.