

Research

- A-to-I RNA editing occurs at over a hundred million genomic sites, located in a majority of human genes** 365^{OA}
Lily Bazak, Ami Haviv, Michal Barak, Jasmine Jacob-Hirsch, Patricia Deng, Rui Zhang, Farren J. Isaacs, Gideon Rechavi, Jin Billy Li, Eli Eisenberg, and Erez Y. Levanon
- The genetic basis for individual differences in mRNA splicing and APOBEC1 editing activity in murine macrophages** 377
Musa A. Hassan, Vincent Butty, Kirk D.C. Jensen, and Jeroen P.J. Saeij
- Functional and topological characteristics of mammalian regulatory domains** 390
Orsolya Symmons, Veli Vural Uslu, Taro Tsujimura, Sandra Ruf, Sonya Nassari, Wibke Schwarzer, Laurence Ettwiller, and François Spitz
- Principles of nucleation of H3K27 methylation during embryonic development** 401^{OA}
Simon J. van Heeringen, Robert C. Akkers, Ila van Kruijsbergen, M. Asif Arif, Lars L.P. Hanssen, Nilofar Sharifi, and Gert Jan C. Veenstra
- Evolution at two levels of gene expression in yeast** 411
Carlo G. Artieri and Hunter B. Fraser
- Ribosome profiling reveals post-transcriptional buffering of divergent gene expression in yeast** 422^{OA}
C. Joel McManus, Gemma E. May, Pieter Spealman, and Alan Shteyman
- Regulatory modules controlling maize inflorescence architecture** 431
Andrea L. Eveland, Alexander Goldshmidt, Michael Pautler, Kengo Morohashi, Christophe Liseron-Monfils, Michael W. Lewis, Sunita Kumari, Susumu Hiraga, Fang Yang, Erica Unger-Wallace, Andrew Olson, Sarah Hake, Erik Vollbrecht, Erich Grotewold, Doreen Ware, and David Jackson
- Genome-wide identification of long noncoding natural antisense transcripts and their responses to light in *Arabidopsis*** 444
Huan Wang, Pil Joong Chung, Jun Liu, In-Cheol Jang, Michelle J. Kean, Jun Xu, and Nam-Hai Chua

Methods

- Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome** 454^{OA}
Jakob Skou Pedersen, Eivind Valen, Amhed M. Vargas Velazquez, Brian J. Parker, Morten Rasmussen, Stinus Lindgreen, Berit Lilje, Desmond J. Tobin, Theresa K. Kelly, Søren Vang, Robin Andersson, Peter A. Jones, Cindi A. Hoover, Alexei Tikhonov, Egor Prokhortchouk, Edward M. Rubin, Albin Sandelin, M. Thomas P. Gilbert, Anders Krogh, Eske Willerslev, and Ludovic Orlando

(continued)

- A fine-scale recombination map of the human–chimpanzee ancestor reveals faster change in humans than in chimpanzees and a strong impact of GC-biased gene conversion** 467
Kasper Munch, Thomas Mailund, Julien Y. Dutheil, and Mikkel Heide Schierup
- Most parsimonious reconciliation in the presence of gene duplication, loss, and deep coalescence using labeled coalescent trees** 475^{OA}
Yi-Chieh Wu, Matthew D. Rasmussen, Mukul S. Bansal, and Manolis Kellis
- A mobile insulator system to detect and disrupt *cis*-regulatory landscapes in vertebrates** 487
José Bessa, Mario Luengo, Solangel Rivero-Gil, Ana Ariza-Cosano, António H.F. Maia, Francisco J. Ruiz-Ruano, Pablo Caballero, Silvia Naranjo, Jaime J. Carvajal, and José Luis Gómez-Skarmeta
- From single-cell to cell-pool transcriptomes: Stochasticity in gene expression and RNA splicing** 496^{OA}
Georgi K. Marinov, Brian A. Williams, Ken McCue, Gary P. Schroth, Jason Gertz, Richard M. Myers, and Barbara J. Wold

Resources

- Endothelial, epithelial, and fibroblast cells exhibit specific splicing programs independently of their tissue of origin** 511
Pierre Mallinoud, Jean-Philippe Villemin, Hussein Mortada, Micaela Polay-Espinoza, François-Olivier Desmet, Samaan Samaan, Emilie Chautard, Léon-Charles Tranchevent, and Didier Auboeuf
- A biochemical landscape of A-to-I RNA editing in the human brain transcriptome** 522
Masayuki Sakurai, Hiroki Ueda, Takanori Yano, Shunpei Okada, Hideki Terajima, Toutai Mitsuyama, Atsushi Toyoda, Asao Fujiyama, Hitomi Kawabata, and Tsutomu Suzuki
- An unbiased resource of novel SNP markers provides a new chronology for the human Y chromosome and reveals a deep phylogenetic structure in Africa** 535
Rosaria Scozzari, Andrea Massaia, Beniamino Trombetta, Giovanna Bellusci, Natalie M. Myres, Andrea Novelletto, and Fulvio Cruciani

^{OA}Open Access paper



Cover A portrait representative of a Paleo-Eskimo individual of the Saqqaq culture from Greenland. Recent advances in ancient DNA research have allowed the sequencing of complete ancient genomes from short DNA molecules preserved in the fossil record for thousands, and sometimes even hundreds of thousands, of years. It was unknown, however, whether ancient epigenomes could be reconstructed. In this issue, the first ancient epigenome is reconstructed using DNA sequence information retrieved from the hairs of a 4000-yr-old Paleo-Eskimo individual. (Cover illustration by Nuka Konrad Gotfredsen, www.andala.dk. [For details, see Pedersen et al., pp. 454–466.]