

Perspective

- Decrypting noncoding RNA interactions, structures, and functional networks 1377^{OA}
Muller Fabbri, Leonard Girnita, Gabriele Varani, and George A. Calin

Research

- The 22q11 low copy repeats are characterized by unprecedented size and structural variability 1389
Wolfram Demaerel, Yulia Mostovoy, Feyza Yilmaz, Lisanne Vervoort, Steven Pastor, Matthew S. Hestand, Ann Swillen, Elfi Vergaelen, Elizabeth A. Geiger, Curtis R. Coughlin, Stephen K. Chow, Donna McDonald-McGinn, Bernice Morrow, Pui-Yan Kwok, Ming Xiao, Beverly S. Emanuel, Tamim H. Shaikh, and Joris R. Vermeesch
- Genome-wide analysis of polymerase III–transcribed *Alu* elements suggests cell-type–specific enhancer function 1402
Xiao-Ou Zhang, Thomas R. Gingeras, and Zhiping Weng
- Replication timing networks reveal a link between transcription regulatory circuits and replication timing control 1415
Juan Carlos Rivera-Mulia, Sebo Kim, Haitham Gabr, Abhijit Chakraborty, Ferhat Ay, Tamer Kahveci, and David M. Gilbert
- Estrogen-independent molecular actions of mutant estrogen receptor 1 in endometrial cancer 1429
Zannel Blanchard, Jeffery M. Vahrenkamp, Kristofer C. Berrett, Spencer Arnesen, and Jason Gertz
- Targeted delivery of CRISPR interference system against *Fabp4* to white adipocytes ameliorates obesity, inflammation, hepatic steatosis, and insulin resistance 1442
Jee Young Chung, Qurrat Ul Ain, Yoonsung Song, Seok-Beom Yong, and Yong-Hee Kim
- A high resolution A-to-I editing map in the mouse identifies editing events controlled by pre-mRNA splicing 1453^{OA}
Konstantin Licht, Utkarsh Kapoor, Fabian Amman, Ernesto Picardi, David Martin, Prajakta Bajad, and Michael F. Jantsch
- Distinct types of short open reading frames are translated in plant cells 1464
Igor Fesenko, Ilya Kirov, Andrey Kniazev, Regina Khazigaleeva, Vassili Lazarev, Daria Kharlampieva, Ekaterina Grafkskaia, Viktor Zgoda, Ivan Butenko, Georgy Arapidi, Anna Mamaeva, Vadim Ivanov, and Vadim Govorun

(continued)

Unique genetic basis of the distinct antibiotic potency of high acetic acid production in the probiotic yeast *Saccharomyces cerevisiae* var. *boulardii* 1478^{OA}
Benjamin Offei, Paul Vandecruys, Stijn De Graeve, María R. Foulquié-Moreno, and Johan M. Thevelein

Large-scale genome analysis of bovine commensal *Escherichia coli* reveals that bovine-adapted *E. coli* lineages are serving as evolutionary sources of the emergence of human intestinal pathogenic strains 1495^{OA}
Yoko Arimizu, Yumi Kirino, Mitsuhiro P. Sato, Koichi Uno, Toshio Sato, Yasuhiro Gotoh, Frédéric Auvray, Hubert Brugere, Eric Oswald, Jacques G. Mainil, Kelly S. Anklam, Dörte Döpfer, Shuji Yoshino, Tadasuke Ooka, Yasuhiro Tanizawa, Yasukazu Nakamura, Atsushi Iguchi, Tomoko Morita-Ishihara, Makoto Ohnishi, Koichi Akashi, Tetsuya Hayashi, and Yoshitoshi Ogura

Methods

Identifying loci under positive selection in complex population histories 1506
Alba Refoyo-Martínez, Rute R. da Fonseca, Katrín Halldórsdóttir, Einar Árnason, Thomas Mailund, and Fernando Racimo

Profiling the long noncoding RNA interaction network in the regulatory elements of target genes by chromatin in situ reverse transcription sequencing 1521^{OA}
Shilin Zhang, Yichen Wang, Lin Jia, Xue Wen, Zhonghua Du, Cong Wang, Yajing Hao, Dehai Yu, Lei Zhou, Naifei Chen, Jingcheng Chen, Huiling Chen, Hui Zhang, Ilkay Celik, Günhan Gülsoy, Jianjun Luo, Baoming Qin, Xueling Cui, Zhonghui Liu, Songling Zhang, Miguel A. Esteban, Ferhat Ay, Wei Xu, Runsheng Chen, Wei Li, Andrew R. Hoffman, Ji-Fan Hu, and Jiuwei Cui

Discovering human transcription factor physical interactions with genetic variants, novel DNA motifs, and repetitive elements using enhanced yeast one-hybrid assays 1533
Shaleen Shrestha, Jared Allan Sewell, Clarissa Stephanie Santoso, Elena Forchielli, Sebastian Carrasco Pro, Melissa Martinez, and Juan Ignacio Fuxman Bass

Direct RNA nanopore sequencing of full-length coronavirus genomes provides novel insights into structural variants and enables modification analysis 1545
Adrian Viehweger, Sebastian Krautwurst, Kevin Lamkiewicz, Ramakanth Madhugiri, John Ziebuhr, Martin Hölzer, and Manja Marz

Resource

Pediatric Cancer Variant Pathogenicity Information Exchange (PeCanPIE): a cloud-based platform for curating and classifying germline variants 1555^{OA}
Michael N. Edmonson, Aman N. Patel, Dale J. Hedges, Zhaoming Wang, Evadnie Rampersaud, Chimene A. Kesserwan, Xin Zhou, Yanling Liu, Scott Newman, Michael C. Rusch, Clay L. McLeod, Mark R. Wilkinson, Stephen V. Rice, Thierry Soussi, J. Paul Taylor, Michael Benatar, Jared B. Becksfort, Kim E. Nichols, Leslie L. Robison, James R. Downing, and Jinghui Zhang

(continued)

Corrigenda

Corrigendum: Mutational signatures of DNA mismatch repair deficiency in *C. elegans* and human cancers 1566

Bettina Meier, Nadezda V. Volkova, Ye Hong, Pieta Schofield, Peter J. Campbell, Moritz Gerstung, and Anton Gartner

Corrigendum: A long-term demasculinization of X-linked intergenic noncoding RNAs in *Drosophila melanogaster* 1566

Ge Gao, Maria D. Vibranovski, Li Zhang, Zheng Li, Min Liu, Yong E. Zhang, Xinmin Li, Wenxia Zhang, Qichang Fan, Nicholas W. VanKuren, Manyuan Long, and Liping Wei

^{OA}Open Access paper



Cover A baker produces very long strings of icing (RNA molecules) with a piping bag (representative of Oxford Nanopore's MinION technology) filled with complete viruses. RNA virus genome sequences can be read in one string of icing. In this issue, a full-length, direct RNA sequencing approach is used to characterize viral RNAs produced in cells infected with a human coronavirus. (Cover art by Beetlebum, jojo@beetlebum.de. [For details, see Viehweger et al., pp. 1545–1554.]