

## Perspective

- Realizing the potential of blockchain technologies in genomics 1255<sup>OA</sup>  
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## Research

- Noncanonical secondary structures arising from non-B DNA motifs are determinants of mutagenesis 1264  
Ilias Georgakopoulos-Soares, Sandro Morganella, Naman Jain, Martin Hemberg, and Serena Nik-Zainal
- Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding 1272<sup>OA</sup>  
Ian C. McDowell, Alejandro Barrera, Anthony M. D'Ippolito, Christopher M. Vockley, Linda K. Hong, Sarah M. Leichter, Luke C. Bartelt, William H. Majoros, Lingyun Song, Alexias Safi, D. Dewran Koçak, Charles A. Gersbach, Alexander J. Hartemink, Gregory E. Crawford, Barbara E. Engelhardt, and Timothy E. Reddy
- Tracing human stem cell lineage during development using DNA methylation 1285<sup>OA</sup>  
Lucas A. Salas, John K. Wiencke, Devin C. Koestler, Ze Zhang, Brock C. Christensen, and Karl T. Kelsey
- Natural genetic variation in *C. elegans* identified genomic loci controlling metabolite levels 1296<sup>OA</sup>  
Arwen W. Gao, Mark G. Sterken, Jelmi uit de Bos, Jelle van Creijl, Rashmi Kamble, Basten L. Snoek, Jan E. Kammenga, and Riekelt H. Houtkooper
- Death of new microRNA genes in *Drosophila* via gradual loss of fitness advantages 1309  
Guang-An Lu, Yixin Zhao, Hao Yang, Ao Lan, Suhua Shi, Zhongqi Liufu, Yumei Huang, Tian Tang, Jin Xu, Xu Shen, and Chung-I Wu
- Hidden variation in polyploid wheat drives local adaptation 1319<sup>OA</sup>  
Laura-Jayne Gardiner, Ryan Joynson, Jimmy Omony, Rachel Rusholme-Pilcher, Lisa Olohan, Daniel Lang, Caihong Bai, Malcolm Hawkesford, David Salt, Manuel Spannagl, Klaus F.X. Mayer, John Kenny, Michael Bevan, Neil Hall, and Anthony Hall
- Plant 24-nt reproductive phasiRNAs from intramolecular duplex mRNAs in diverse monocots 1333  
Atul Kakrana, Sandra M. Mathioni, Kun Huang, Reza Hammond, Lee Vandivier, Parth Patel, Siwaret Arikat, Olga Shevchenko, Alex E. Harkess, Bruce Kingham, Brian D. Gregory, James H. Leebens-Mack, and Blake C. Meyers

## Methods

- High-throughput single-cell DNA sequencing of acute myeloid leukemia tumors with droplet microfluidics 1345<sup>OA</sup>  
Maurizio Pellegrino, Adam Sciambi, Sebastian Treusch, Robert Durruthy-Durruthy, Kaustubh Gokhale, Jose Jacob, Tina X. Chen, Jennifer A. Geis, William Oldham, Jairo Matthews, Hagop Kantarjian, P. Andrew Futreal, Keyur Patel, Keith W. Jones, Koichi Takahashi, and Dennis J. Eastburn

- Single-cell RNA-seq analysis identifies markers of resistance to targeted BRAF inhibitors in melanoma cell populations** 1353  
Yu-Jui Ho, Naishitha Anaparthi, David Molik, Grinu Mathew, Toby Aicher, Ami Patel, James Hicks, and Molly Gale Hammell
- Whole-genome bisulfite sequencing with improved accuracy and cost** 1364  
Masako Suzuki, Will Liao, Frank Vos, Andrew D. Johnston, Justin DeGrazia, Jennifer Ishii, Toby Bloom, Michael C. Zody, Soren Germer, and John M. Greally
- Genome-scale identification of cellular pathways required for cell surface recognition** 1372<sup>OA</sup>  
Sumana Sharma, S. Josefin Bartholdson, Amalie C.M. Couch, Kosuke Yusa, and Gavin J. Wright
- Variant antigen repertoires in *Trypanosoma congolense* populations and experimental infections can be profiled from deep sequence data using universal protein motifs** 1383<sup>OA</sup>  
Sara Silva Pereira, Aitor Casas-Sánchez, Lee R. Haines, Moses Ogugo, Kihara Absolomon, Mandy Sanders, Steve Kemp, Álvaro Acosta-Serrano, Harry Noyes, Matthew Berriman, and Andrew P. Jackson
- GrapeTree: visualization of core genomic relationships among 100,000 bacterial pathogens** 1395<sup>OA</sup>  
Zheming Zhou, Nabil-Fareed Alikhan, Martin J. Sergeant, Nina Luhmann, Cátia Vaz, Alexandre P. Francisco, João André Carriço, and Mark Achtman
- Resources**
- Human proteins that interact with RNA/DNA hybrids** 1405<sup>OA</sup>  
Isabel X. Wang, Christopher Grunseich, Jennifer Fox, Joshua Burdick, Zhengwei Zhu, Niema Ravazian, Markus Hafner, and Vivian G. Cheung
- High resolution annotation of zebrafish transcriptome using long-read sequencing** 1415  
German Nudelman, Antonio Frasca, Brandon Kent, Kirsten C. Sadler, Stuart C. Sealfon, Martin J. Walsh, and Elena Zaslavsky
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- Corrigendum: Large-scale analysis of genome and transcriptome alterations in multiple tumors unveils novel cancer-relevant splicing networks** 1426  
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<sup>OA</sup>Open Access paper



**Cover** An artistic representation of an R-loop bound by a protein. An R-loop is a three-stranded nucleic acid structure that comprises an RNA/DNA hybrid with a displaced single-stranded DNA. In this issue, Wang et al. identified hundreds of proteins that interact with R-loops in human cells. (Cover artwork by Colleen K. McGarry. [For details, see Wang et al., pp. 1405–1414.] )