

## In memoriam

Deborah A. Nickerson (1954–2021)

v

## Research

- Characteristics, origin, and potential for cancer diagnostics of ultrashort plasma cell-free DNA** 215<sup>OA</sup>  
Irena Hudecova, Christopher G. Smith, Robert Hänsel-Hertsch, Chandra S. Chilamakuri, James A. Morris, Aadhitthya Vijayaraghavan, Katrin Heider, Dineika Chandrananda, Wendy N. Cooper, Davina Gale, Javier Garcia-Corbacho, Simon Pacey, Richard D. Baird, Nitzan Rosenfeld, and Florent Mouliere
- Plasma cell-free RNA characteristics in COVID-19 patients** 228<sup>OA</sup>  
Yanqun Wang, Jie Li, Lu Zhang, Hai-Xi Sun, Zhaoyong Zhang, Jinjin Xu, Yonghao Xu, Yu Lin, Airu Zhu, Yuxue Luo, Haibo Zhou, Yan Wu, Shanwen Lin, Yuzhe Sun, Fei Xiao, Ruiying Chen, Liyan Wen, Wei Chen, Fang Li, Rijing Ou, Yanjun Zhang, Tingyou Kuo, Yuming Li, Lingguo Li, Jing Sun, Kun Sun, Zhen Zhuang, Haorong Lu, Zhao Chen, Guoqiang Mai, Jianfen Zhuo, Puyi Qian, Jiayu Chen, Huanming Yang, Jian Wang, Xun Xu, Nanshan Zhong, Jingxian Zhao, Junhua Li, Jincun Zhao, and Xin Jin
- Characterization of transcript enrichment and detection bias in single-nucleus RNA-seq for mapping of distinct human adipocyte lineages** 242  
Anushka Gupta, Farnaz Shamsi, Nicolas Altemose, Gabriel F. Dorlhiac, Aaron M. Cypess, Andrew P. White, Nir Yosef, Mary Elizabeth Patti, Yu-Hua Tseng, and Aaron Streets
- Mendelian randomization analyses implicate biogenesis of translation machinery in human aging** 258<sup>OA</sup>  
Sara Javidnia, Stephen Cranwell, Stefanie H. Mueller, Colin Selman, Jennifer M.A. Tullet, Karoline Kuchenbaecker, and Nazif Alic
- Gene by environment interaction mouse model reveals a functional role for 5-hydroxymethylcytosine in neurodevelopmental disorders** 266  
Ligia A. Papale, Andy Madrid, Qi Zhang, Kailei Chen, Lara Sak, Sündüz Keleş, and Reid S. Alisch
- Long-range promoter–enhancer contacts are conserved during evolution and contribute to gene expression robustness** 280  
Alexandre Laverré, Eric Tannier, and Anamaria Necsulea
- Limited allele-specific gene expression in highly polyploid sugarcane** 297  
Gabriel Rodrigues Alves Margarido, Fernando Henrique Correr, Agnelo Furtado, Frederik C. Botha, and Robert James Henry

(continued)

Resetting of the 24-nt siRNA landscape in rice zygotes 309  
Chenxin Li, Jonathan I. Gent, Hengping Xu, Hong Fu, Scott D. Russell, and Venkatesan Sundaresan

Reactivation of transposable elements following hybridization in fission yeast 324  
Sergio Tusso, Fang Suo, Yue Liang, Li-Lin Du, and Jochen B.W. Wolf

The asymmetric distribution of RNA polymerase II and nucleosomes on replicated daughter genomes is caused by differences in replication timing between the lagging and the leading strand 337  
Rahima Ziane, Alain Camasses, and Marta Radman-Livaja

## Methods

Accessible Region Conformation Capture (ARC-C) gives high-resolution insights into genome architecture and regulation 357<sup>OA</sup>  
Ni Huang, Wei Qiang Seow, Alex Appert, Yan Dong, Przemyslaw Stempor, and Julie Ahringer

A systematic genome-wide account of binding sites for the model transcription factor Gcn4 367  
Christopher T. Coey and David J. Clark

Antibody-free profiling of transcription factor occupancy during early embryogenesis by FitCUT&RUN 378  
Xiangxiu Wang, Wen Wang, Yiman Wang, Jia Chen, Guifen Liu, and Yong Zhang

## Resources

Integration of high-resolution promoter profiling assays reveals novel, cell type-specific transcription start sites across 115 human cell and tissue types 389  
Jill E. Moore, Xiao-Ou Zhang, Shaimae I. Elhajjajy, Kaili Fan, Henry E. Pratt, Fairlie Reese, Ali Mortazavi, and Zhiping Weng

Benchmarking small-variant genotyping in polyploids 403<sup>OA</sup>  
Daniel P. Cooke, David C. Wedge, and Gerton Lunter

<sup>OA</sup>Open Access paper



**Cover** An old man in a straw raincoat and cap represents tagging with the Fc region of rabbit immunoglobulin G. He is fishing using a rod without a hook, which represents pulling down transcription factors without using antibodies. In this issue, an antibody-free technology to profile transcription factor binding sites was developed to investigate zebrafish early embryogenesis. (Cover illustration by Yiqing Chen, [evaluna.y.c@gmail.com](mailto:evaluna.y.c@gmail.com). [For details, see Wang et al., pp. 378–388.]