

Perspective

- Functional assays in *Drosophila* facilitate classification of variants of uncertain significance associated with rare diseases** 1473
Jung-Wan Mok, Shelley B. Gibson, Haley A. Dostalík, and Shinya Yamamoto

Research

- Genetic effects on chromatin accessibility uncover mechanisms of liver gene regulation and quantitative traits** 1485

Kevin W. Currin, Hannah J. Perrin, Gautam K. Pandey, Abdalla A. Alkhawaja, Swarooparani Vadlamudi, Annie E. Musser, Amy S. Etheridge, K. Elaine Broadaway, Jonathan D. Rosen, Arushi Varshney, Amarjit S. Chaudhry, Paul J. Gallins, Fred A. Wright, Yi-hui Zhou, Stephen C.J. Parker, Laura M. Raffield, Erin G. Schuetz, Federico Innocenti, and Karen L. Mohlke

- An iPSC-based model of 47,XXX Jacobs syndrome reveals a DNA methylation-independent transcriptional dysregulation shared with male X aneuploid cells** 1503^{OA}

Veronica Astro, Kelly Yojanna Cardona-Londoño, Lorena Viridiana Cortés-Medina, Rawan Alghamdi, Gustavo Ramírez-Calderón, Fotios Kefalas, Jair Dilmé-Capó, Santiago Radío, and Antonio Adamo

- Regeneration alters open chromatin and *cis*-regulatory landscape of erythroid precursors** 1518

Yichao Zhou, Venkatasai Rahul Dogiparthi, Hannah L. Harris, Suhita Ray, Avik Choudhuri, Song Yang, Yi Zhou, Leonard I. Zon, M. Jordan Rowley, and Kyle J. Hewitt

- Comprehensive functional annotation of ESRI-driven enhancers in breast cancer reveals hierarchical activity independent of genomic and epigenomic contexts** 1530

Yanis Zekri, Sebastian Gregoricchio, Elif Yapıcı, Chia-Chi Flora Huang, Tunç Morova, Umut Berkay Altıntaş, Gozde Korkmaz, Nathan A. Lack, and Wilbert Zwart

- Multi-species analysis of inflammatory response elements reveals ancient and lineage-specific contributions of transposable elements to NF-κB binding** 1544

Liangxi Wang, Tiegh Taylor, Kumaragurubaran Rathnakumar, Nadiya Khyzha, Minggao Liang, Azad Alizada, Laura F. Campitelli, Sara E. Pour, Zain M. Patel, Lina Antounians, Ian C. Tobias, Huayun Hou, Timothy R. Hughes, Sushmita Roy, Jennifer A. Mitchell, Jason E. Fish, and Michael D. Wilson

- Developmental transcriptomics in *Pristionchus* reveals the environmental responsiveness of a plasticity gene-regulatory network** 1560^{OA}

Shelley Reich, Tobias Loschko, Julie Jung, Samantha Nestel, Ralf J. Sommer, and Michael S. Werner

(continued)

Methods

- A new compression strategy to reduce the size of nanopore sequencing data** 1574^{OA}
Kavindu Jayasooriya, Sasha P. Jenner, Pasindu Marasinghe, Udith Senanayake, Hassaan Saadat, David Taubman, Roshan Ragel, Hasindu Gamaarachchi, and Ira W. Deveson
- Verkko2 integrates proximity-ligation data with long-read De Bruijn graphs for efficient telomere-to-telomere genome assembly, phasing, and scaffolding** 1583^{OA}
Dmitry Antipov, Mikko Rautiainen, Sergey Nurk, Brian P. Walenz, Steven J. Solar, Adam M. Phillippy, and Sergey Koren
- Highly accurate assembly polishing with DeepPolisher** 1595
Mira Mastoras, Mobin Asri, Lucas Brambrink, Prajna Hebbar, Alexey Kolesnikov, Daniel E. Cook, Maria Nattestad, Julian Lucas, Taylor S. Won, Pi-Chuan Chang, Andrew Carroll, Benedict Paten, Kishwar Shafin, and the Human Pangenome Reference Consortium
- Accurate short-read alignment through *r*-index-based pangenome indexing** 1609^{OA}
Rahul Varki, Massimiliano Rossi, Eddie Ferro, Marco Oliva, Erik Garrison, Ben Langmead, and Christina Boucher
- Spatial domain detection using contrastive self-supervised learning for spatial multi-omics technologies** 1621^{OA}
Jianing Yao, Jinglun Yu, Brian Caffo, Stephanie C. Page, Keri Martinowich, and Stephanie C. Hicks
- Tissular chromatin-state cartography based on double-barcoded DNA arrays that capture unloaded PA-Tn5 transposase** 1633^{OA}
Maria Grazia Mendoza-Ferri, Gwendoline Lozachmeur, Maximilien Duvina, Laetitia Perret, Didier Merciris, Anne Gigout, and Marco Antonio Mendoza-Parra
- Harnessing agent-based frameworks in CellAgentChat to unravel cell–cell interactions from single-cell and spatial transcriptomics** 1646^{OA}
Vishvak Raghavan, Yumin Zheng, Yue Li, and Jun Ding

Resource

- Integrated single-cell multiome analysis reveals muscle fiber-type gene regulatory circuitry modulated by endurance exercise** 1664
Aliza B. Rubenstein, Gregory R. Smith, Zidong Zhang, Xi Chen, Toby L. Chambers, Frederique Ruf-Zamojski, Natalia Mendelev, Wan Sze Cheng, Michel Zamojski, Mary Anne S. Amper, Venugopalan D. Nair, Andrew R. Marderstein, Stephen B. Montgomery, Olga G. Troyanskaya, Elena Zaslavsky, Todd Trappe, Scott Trappe, and Stuart C. Sealfon

^{OA}Open Access paper



Cover How single-cell biology reveals the intricate cellular responses to physical exercise is represented. The composition merges the dynamic forms of the human body running with a stylized data projection map, revealing a constellation of individual cell types and states. In this issue, single-cell transcriptome, chromatin, and regulatory circuit responses to acute endurance exercise in muscle are mapped, serving as a resource for understanding the molecular underpinnings of the metabolic and physiological effects of exercise. (Cover art was conceptualized by Antonio Cappuccio in collaboration with the authors of the article, Icahn School of Medicine at Mount Sinai. ChatGPT was used to generate figures aligned with the concept of combining a dynamic human form with a data projection map, which were then manually edited using Adobe Illustrator to correct anatomical proportions and improve clarity. [For details, see Rubenstein et al., pp. 1664–1677.]