

Review

- De novo gene birth and the conundrum of ORFan genes in bacteria 1679
Md. Hassan uz-Zaman and Howard Ochman

Research

- Oxygen-induced stress reveals context-specific gene regulatory effects in human brain organoids 1689^{OA}
Benjamin D. Umans and Yoav Gilad
- Wnt signaling activation induces CTCF binding and loop formation at *cis*-regulatory elements of target genes 1701^{OA}
Anna Nordin, Chaitali Chakraborty, Mattias Jonasson, Orgena Dano, Gianluca Zambanini, Pierfrancesco Pagella, Silvia Remeseiro, and Claudio Cantù
- Androgen receptor-mediated assisted loading of the glucocorticoid receptor modulates transcriptional responses in prostate cancer cells 1717^{OA}
Johannes Hiltunen, Laura Helminen, Niina Aaltonen, Kaisa-Mari Launonen, Hanna Laakso, Marjo Malinen, Einari A. Niskanen, Jorma J. Palvimo, and Ville Paakinaho
- Mitotic chromosomes harbor cell type- and species-specific structural features within a universal loop array conformation 1733^{OA}
Marlies E. Oomen, A. Nicole Fox, Inma Gonzalez, Amandine Molliex, Thaleia Papadopoulou, Pablo Navarro, and Job Dekker
- Dynamic barriers modulate cohesin positioning and genome folding at fixed occupancy 1745^{OA}
Hadi Rahmaninejad, Yao Xiao, Maxime M.C. Tortora, and Geoffrey Fudenberg
- Accurate genotyping of three major respiratory bacterial pathogens with ONT R10.4.1 long-read sequencing 1758
Nora Zidane, Carla Rodrigues, Valérie Bouchez, Martin Rethoret-Pasty, Virginie Passet, Sylvain Brisse, and Chiara Crestani
- Lambdoid phages with abundant Chi recombination hotspots reflect diverse viral strategies for recombination-dependent growth 1767^{OA}
Clarence Zheng, Sherwood R. Casjens, Alan R. Davidson, Susan K. Amundsen, and Gerald R. Smith
- ## Methods
- Uncovering methylation-dependent genetic effects on regulatory element function in diverse genomes 1781^{OA}
Rachel M. Petersen, Christopher M. Vockley, and Amanda J. Lea

(continued)

- A novel multislice framework for precision 3D spatial domain reconstruction and disease pathology analysis** 1794
Daijun Zhang, Ren Qi, Xun Lan, and Bin Liu
- Integration of hyperspectral imaging and transcriptomics from individual cells with SpectralSeq** 1809^{OA}
Yike Xie, Abbas Habibalahi, Ayad G. Anwer, Kanu Wahi, Jacqueline Bailey, Francis Lin, Catherine Gatt, Emma M.V. Johansson, Tatyana Chtanova, Jeff Holst, Ewa Goldys, and Fabio Zanini
- QuadST identifies cell–cell interaction–changed genes in spatially resolved transcriptomics data** 1821^{OA}
Xiaoyu Song, Yuqing Shang, Michelle E. Ehrlich, Panos Roussos, Guo-Cheng Yuan, and Pei Wang
- Batch correction methods used in single-cell RNA sequencing analyses are often poorly calibrated** 1832^{OA}
Sindri Emmanúel Antonsson and Páll Melsted
- Cancer driver topologically associated domains identify oncogenic and tumor-suppressive lncRNAs** 1842
Ziyan Rao, Min Zhang, Shaodong Huang, Chenyang Wu, Yuheng Zhou, Weijie Zhang, Xia Lin, and Dongyu Zhao
- Overcoming limitations to customize DeepVariant for domesticated animals with TrioTrain** 1859^{OA}
Jenna Kalleberg, Jacob Rissman, and Robert D. Schnabel
- A high-throughput screening method for selecting feature SNPs to evaluate breed diversity and infer ancestry** 1875^{OA}
Meilin Zhang, Heng Du, Yu Zhang, Yue Zhuo, Zhen Liu, Yahui Xue, Lei Zhou, Sixuan Zhou, Wanying Li, and Jian-Feng Liu

Resources

- A map of enhancer regions in primary human neural progenitor cells using capture STARR-seq** 1887
Sophia C. Gaynor-Gillett, Lijun Cheng, Manman Shi, Jason Liu, Gaoyuan Wang, Megan Spector, Qiuyu Guo, Le Qi, Mary Flaherty, Martha Wall, Ahyeon Hwang, Mengting Gu, Zhanlin Chen, Yuhang Chen, PsychENCODE Consortium, Jennifer R. Moran, Jing Zhang, Donghoon Lee, Mark Gerstein, Daniel Geschwind, and Kevin P. White
- CGCI, a new reference genome for *Caenorhabditis elegans*** 1902^{OA}
Kazuki Ichikawa, Massa J. Shoura, Karen L. Artilles, Dae-Eun Jeong, Chie Owa, Haruka Kobayashi, Yoshihiko Suzuki, Manami Kanamori, Yu Toyoshima, Yuichi Iino, Ann E. Rougvie, Lamia Wahba, Andrew Z. Fire, Erich M. Schwarz, and Shinichi Morishita

^{OA}Open Access paper



Cover The nematode worm *Caenorhabditis elegans*. Three life stages of *C. elegans* are shown: an adult hermaphrodite, a smaller larva, and ten newly laid eggs (with embryos developing inside them). These are all on a lawn of *Escherichia coli* bacteria (being eaten by the worms as food). The fully grown adult is roughly one millimeter long. (Cover photo credit: Marie-Anne Félix, Ecole Normale Supérieure, Paris, France. [For details, see Ichikawa et al., pp. 1902–1918.])