

Research

V[DD]J recombination is an important and evolutionarily conserved mechanism for generating antibodies with unusually long CDR3s 1547
 Yana Safonova and Pavel A. Pevzner

Transposon expression in the *Drosophila* brain is driven by neighboring genes and diversifies the neural transcriptome 1559^{OA}
 Christoph D. Treiber and Scott Waddell

Active retrotransposons help maintain pericentromeric heterochromatin required for faithful cell division 1570
 Yajing Hao, Dongpeng Wang, Shuheng Wu, Xiao Li, Changwei Shao, Peng Zhang, Jia-Yu Chen, Do-Hwan Lim, Xiang-Dong Fu, Runsheng Chen, and Shunmin He

Large tandem duplications affect gene expression, 3D organization, and plant-pathogen response 1583^{OA}
 Ariadna Picart-Picolo, Stefan Grob, Nathalie Picault, Michal Franek, Christel Llauro, Thierry Halter, Tom R. Maier, Edouard Jobet, Julie Descombin, Panpan Zhang, Vijayalalani Paramasivan, Thomas J. Baum, Lionel Navarro, Martina Dvořáková, Marie Mirouze, and Frédéric Pontvianne

A systems genetics approach reveals environment-dependent associations between SNPs, protein coexpression, and drought-related traits in maize 1593
 Mélisande Blein-Nicolas, Sandra Sylvia Negro, Thierry Balliau, Claude Welcker, Llorenç Cabrera-Bosquet, Stéphane Dimitri Nicolas, Alain Charcosset, and Michel Zivy

An optogenetic switch for the Set2 methyltransferase provides evidence for transcription-dependent and -independent dynamics of H3K36 methylation 1605
 Andrew M. Lerner, Austin J. Hepperla, Gregory R. Keele, Hashem A. Meriesh, Hayretin Yumerefendi, David Restrepo, Seth Zimmerman, James E. Bear, Brian Kuhlman, Ian J. Davis, and Brian D. Strahl

Methods

Whole-genome analysis of noncoding genetic variations identifies multiscale regulatory element perturbations associated with Hirschsprung disease 1618
 Alexander Xi Fu, Kathy Nga-Chu Lui, Clara Sze-Man Tang, Ray Kit Ng, Frank Pui-Ling Lai, Sin-Ting Lau, Zhixin Li, Maria-Mercè Garcia-Barcelo, Pak-Chung Sham, Paul Kwong-Hang Tam, Elly Sau-Wai Ngan, and Kevin Y. Yip

Agonist-induced functional analysis and cell sorting associated with single-cell transcriptomics characterizes cell subtypes in normal and pathological brain 1633
 Sara Castagnola, Julie Cazareth, Kevin Lebrigand, Marielle Jarjat, Virginie Magnone, Sébastien Delhaye, Frederic Brau, Barbara Bardoni, and Thomas Maurin

(continued)

Identification of bona fide B2 SINE retrotransposon transcription through single-nucleus RNA-seq of the mouse hippocampus 1643

Sara B. Linker, Lynne Randolph-Moore, Kalyani Kottilil, Fan Qiu, Baptiste N. Jaeger, Jerika Barron, and Fred H. Gage

PRAM: a novel pooling approach for discovering intergenic transcripts from large-scale RNA sequencing experiments 1655^{OA}

Peng Liu, Alexandra A. Soukup, Emery H. Bresnick, Colin N. Dewey, and Sündüz Keleş

Accurate reconstruction of bacterial pan- and core genomes with PEPPAN 1667^{OA}

Zhemin Zhou, Jane Charlesworth, and Mark Achtman

Resource

Single-cell strand sequencing of a macaque genome reveals multiple nested inversions and breakpoint reuse during primate evolution 1680

Flavia Angela Maria Maggiolini, Ashley D. Sanders, Colin James Shew, Arvis Sulovari, Yafei Mao, Marta Puig, Claudia Rita Catacchio, Maria Dellino, Donato Palmisano, Ludovica Mercuri, Miriana Bitonto, David Porubský, Mario Cáceres, Evan E. Eichler, Mario Ventura, Megan Y. Dennis, Jan O. Korbel, and Francesca Antonacci

^{OA}Open Access paper



Cover An artistic representation of 3D genome organization, illustrating chromosome territories, nuclear compartments, as well as the emergence of structural variants due to genomic instability. In this issue, long-read sequencing in an *Arabidopsis thaliana* line with decreased ribosomal RNA (rRNA) gene copies shows features of genomic instability, including an accumulation of large tandem duplications, which lead to the duplication of hundreds of genes within a few generations. The authors investigate the impact of these duplications on 3D genome organization, gene expression, cytosine methylation, and plant phenotype, uncovering a potential link between these duplications and pathogen resistance. (Cover artwork by Clément Costarella, <https://spontart.com>, and conceptually inspired by Frédéric Pontvianne. [For details, see Picart-Picolo et al., pp. 1583–1592.])