GENOME RESEARCH
Volume 34 Number 4 April 2024

Review

Navigating the landscape of epitranscriptomics and host immunity 515
Elaine Huang, Clara Frydman, and Xinshu Xiao

Perspective

Ribosome decision graphs for the representation of eukaryotic RNA translation complexity 530[OA]
Jack A.S. Tierney, Michał Świrski, Håkon Tjeldnes, Jonathan M. Mudge, Joanna Kufel, Nicola Whiffin, Eivind Valen, and Pavel V. Baranov

Research

Estrogen receptor 1 chromatin profiling in human breast tumors reveals high inter-patient heterogeneity with enrichment of risk SNPs and enhancer activity at most-conserved regions 539
Stacey E.P. Joosten, Sebastian Gregoricchio, Suzan Stelloo, Elif Yapıcı, Chia-Chi Flora Huang, Kerim Yavuz, Maria Donaldson Collier, Tunç Morova, Umut Berkay Altintaş, Yongsoo Kim, Sander Canisius, Cathy B. Moelans, Paul J. van Diest, Gozde Korkmaz, Nathan A. Lack, Michiel Vermeulen, Sabine C. Linn, and Wilbert Zwart

Suv39h-catalyzed H3K9me3 is critical for euchromatic genome organization and the maintenance of gene transcription 556[OA]
Christine R. Keenan, Hannah D. Coughlan, Nadia Iannarella, Andres Tapia del Fierro, Andrew Keniry, Timothy M. Johanson, Wing Fuk Chan, Alexandra L. Garnham, Lachlan W. Whitehead, Marnie E. Blewitt, Gordon K. Smyth, and Rhys S. Allan

Combinatorial microRNA activity is essential for the transition of pluripotent cells from proliferation into dormancy 572
Dhanur P. Iyer, Lambert Moyon, Lars Wittler, Chieh-Yu Cheng, Francisca R. Ringeling, Stefan Canzar, Annalisa Marsico, and Aydan Bulut-Karslioğlu

Transcriptional programs mediating neuronal toxicity and altered glial–neuronal signaling in a *Drosophila* knock-in tauopathy model 590[OA]
Hassan Bukhari, Vanitha Nithianandam, Rachel A. Battaglia, Anthony Cicalo, Souvarish Sarkar, Aram Comjean, Yanhui Hu, Matthew J. Leventhal, Xianjun Dong, and Mel B. Feany

Plant genome evolution in the genus *Eucalyptus* is driven by structural rearrangements that promote sequence divergence 606[OA]
Scott Ferguson, Ashley Jones, Kevin Murray, Rose Andrew, Benjamin Schwessinger, and Justin Borevitz

(continued)

Methods

Probabilistic association of differentially expressed genes with *cis*-regulatory elements 620
Brian S. Roberts, Ashlyn G. Anderson, E. Christopher Partridge, Gregory M. Cooper, and Richard M. Myers

Accelerated somatic mutation calling for whole-genome and whole-exome sequencing data from heterogenous tumor samples 633[OA]
Shuangxi Ji, Tong Zhu, Ankit Sethia, and Wenyi Wang

A new framework for exploratory network mediator analysis in omics data 642[OA]
Qingpo Cai, Yinghao Fu, Cheng Lyu, Zihe Wang, Shun Rao, Jessica A. Alvarez, Yun Bai, Jian Kang, and Tianwei Yu

[OA]Open Access paper

Cover *Eucalyptus* trees, commonly known as gum trees, are widespread throughout the Australian landscape. Containing over 800 species, *Eucalyptus* trees are adapted to diverse environments, provide habitat to a rich biodiversity of Australian wildlife, and are key to maintaining healthy ecosystems. A small number of species, such as *Eucalyptus viminalis* (manna gum), illustrated here, are the food source for koalas. A recent study across 33 *Eucalyptus* trees has revealed that their genomes exhibit a fascinating interplay between maintaining a stable structure and undergoing structural variations. These variations are driven by insertions, deletions, duplications, translocations, and inversions, which can shuffle genetic elements and accumulate genome divergence over time. The study provides valuable insights into how the architecture of plant genomes evolves, highlighting the interplay between stability and change. (Cover illustration by Kasey Pham, drawn and colored by hand in ProCreate for iPad. [For details, see Ferguson et al., pp. 606–619.])