

## Research

- The human ribosomal DNA array is composed of highly homogenized tandem clusters** 1971<sup>OA</sup>  
Yutaro Hori, Akira Shimamoto, and Takehiko Kobayashi
- Embryonic LTR retrotransposons supply promoter modules to somatic tissues** 1983  
Kosuke Hashimoto, Eeva-Mari Jouhilahti, Virpi Tökönen, Piero Carninci, Juha Kere, and Shintaro Katayama
- Mutational bias in spermatogonia impacts the anatomy of regulatory sites in the human genome** 1994<sup>OA</sup>  
Vera B. Kaiser, Lana Talmane, Yatendra Kumar, Fiona Semple, Marie MacLennan, Deciphering Developmental Disorders Study, David R. FitzPatrick, Martin S. Taylor, and Colin A. Semple
- Nuclease deficiencies alter plasma cell-free DNA methylation profiles** 2008<sup>OA</sup>  
Diana S.C. Han, Meng Ni, Rebecca W.Y. Chan, Danny K.L. Wong, Linda T. Hiraki, Stefano Volpi, Peiyong Jiang, Kathy O. Lui, K.C. Allen Chan, Rossa W.K. Chiu, and Y.M. Dennis Lo
- RBFOX splicing factors contribute to a broad but selective recapitulation of peripheral tissue splicing patterns in the thymus** 2022<sup>OA</sup>  
Kathrin Jansen, Noriko Shikama-Dorn, Moustafa Attar, Stefano Maio, Maria Lopopolo, David Buck, Georg A. Holländer, and Stephen N. Sansom
- Positive selection in noncoding genomic regions of vocal learning birds is associated with genes implicated in vocal learning and speech functions in humans** 2035<sup>OA</sup>  
James A. Cahill, Joel Armstrong, Alden Deran, Carolyn J. Khoury, Benedict Paten, David Haussler, and Erich D. Jarvis
- Genome-wide oscillations in G + C density and sequence conservation** 2050  
Zarmik Moqtaderi, Susan Brown, and Welcome Bender
- Cellular abundance shapes function in piRNA-guided genome defense** 2058  
Pavol Genzor, Parthena Konstantinidou, Daniel Stoyko, Amirhossein Manzhourolajdad, Celine Marlin Andrews, Alexandra R. Elchert, Constantinos Stathopoulos, and Astrid D. Haase
- Shared evolutionary trajectories of three independent neo-sex chromosomes in *Drosophila*** 2069<sup>OA</sup>  
Masafumi Nozawa, Yohei Minakuchi, Kazuhiro Satomura, Shu Kondo, Atsushi Toyoda, and Koichiro Tamura

(continued)

## Methods

Effective sequence similarity detection with strobemers 2080<sup>OA</sup>  
Kristoffer Sahlin

Cancer-associated dynamics and potential regulators of intronic polyadenylation revealed by IPAfinder using standard RNA-seq data 2095<sup>OA</sup>  
Zhaozhao Zhao, Qiushi Xu, Ran Wei, Weixu Wang, Dong Ding, Yu Yang, Jun Yao, Liye Zhang, Yue-Qing Hu, Gang Wei, and Ting Ni

Variational inference using approximate likelihood under the coalescent with recombination 2107  
Xinhao Liu, Huw A. Ogilvie, and Luay Nakhleh

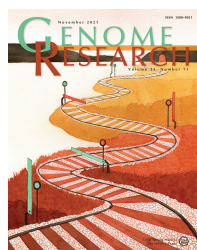
Targeted regulation of transcription in primary cells using CRISPRa and CRISPRi 2120  
Trine I. Jensen, Nanna S. Mikkelsen, Zongliang Gao, Johannes Foßelteder, Gabriel Pabst, Esben Axelgaard, Anders Laustsen, Saskia König, Andreas Reinisch, and Rasmus O. Bak

Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes 2131  
George Armstrong, Kalen Cantrell, Shi Huang, Daniel McDonald, Niina Haiminen, Anna Paola Carrieri, Qiyun Zhu, Antonio Gonzalez, Imran McGrath, Kristen L. Beck, Daniel Hakim, Aki S. Havulinna, Guillaume Méric, Teemu Niiranen, Leo Lahti, Veikko Salomaa, Mohit Jain, Michael Inouye, Austin D. Swafford, Ho-Cheol Kim, Laxmi Parida, Yoshiki Vázquez-Baeza, and Rob Knight

## Resource

A systematic analysis of *Trypanosoma brucei* chromatin factors identifies novel protein interaction networks associated with sites of transcription initiation and termination 2138<sup>OA</sup>  
Desislava P. Staneva, Roberta Carloni, Tatsiana Auchynnikava, Pin Tong, Juri Rappsilber, A. Arockia Jeyaparakash, Keith R. Matthews, and Robin C. Allshire

<sup>OA</sup>Open Access paper



**Cover** Cell-free DNA in plasma consists of fragments of DNA and has been used for noninvasive prenatal testing, cancer liquid biopsies, and transplantation monitoring. In this issue, Han et al. demonstrate the interrelationships between nucleases, cell-free DNA fragmentation, and DNA methylation, which are depicted in this artistic illustration. The railroad (representing DNA) enters a red tunnel (representing a blood vessel) in the distant mountain. The railroad has red and green sign posts, denoting methylated cytosines and unmethylated cytosines on the DNA, respectively. Barriers of different colors are different nucleases, preferring to cleave (down position) or not cleave (up position) the DNA. DNASE1 (red barriers) prefers to cleave at unmethylated cytosines, while DNASE1L3 (green barriers) prefers to cleave at methylated cytosines. Thus, nuclease-mediated cell-free DNA fragmentation is informed by underlying DNA methylation. (Cover art using watercolor and colored pencils on paper by Carmen Ng [<https://www.carmen-ng.com/>], based on a concept from Dennis Lo. [For details, see Han et al., pp. 2008–2021.]