

In memoriam

Haig H. Kazazian, Jr. (1937–2022) v

Commentary

Implications of the first complete human genome assembly 595^{OA}

Perspectives

Short arms of human acrocentric chromosomes and the completion of the human genome sequence 599

Stylianos E. Antonarakis

The genetics and epigenetics of satellite centromeres 608^{OA}

Paul B. Talbert and Steven Henikoff

Research

Chromosome-specific telomere lengths and the minimal functional telomere revealed by nanopore sequencing 616

Samantha L. Sholes, Kayarash Karimian, Ariel Gershman, Thomas J. Kelly, Winston Timp, and Carol W. Greider

MYC overexpression leads to increased chromatin interactions at super-enhancers and MYC binding sites 629^{OA}

Yi Xiang See, Kaijing Chen, and Melissa J. Fullwood

Somatic structural variant formation is guided by and influences genome architecture 643^{OA}

Nikos Sidiropoulos, Balca R. Mardin, F. Germán Rodríguez-González, Ivan D. Bochkov, Shilpa Garg, Adrian M. Stütz, Jan O. Korb, Erez Lieberman Aiden, and Joachim Weischenfeldt

A hidden layer of structural variation in transposable elements reveals potential genetic modifiers in human disease-risk loci 656^{OA}

Elisabeth J. van Bree, Rita L.F.P. Guimarães, Mischa Lundberg, Elena R. Blujdea, Jimi L. Rosenkrantz, Fred T.G. White, Josse Poppinga, Paula Ferrer-Raventós, Anne-Fleur E. Schneider, Isabella Clayton, David Haussler, Marcel J.T. Reinders, Henne Holstege, Adam D. Ewing, Colette Moses, and Frank M.J. Jacobs

Accumulation and ineffective silencing of transposable elements on an avian W Chromosome 671

Vera M. Warmuth, Matthias H. Weissensteiner, and Jochen B.W. Wolf

The role of insulators and transcription in 3D chromatin organization of flies 682^{OA}

Keerthi T. Chathoth, Liudmila A. Mikheeva, Gilles Crevel, Jareth C. Wolfe, Ioni Hunter, Saskia Beckett-Doyle, Sue Cotterill, Hongsheng Dai, Andrew Harrison, and Nicolae Radu Zabet

(continued)

GC content, but not nucleosome positioning, directly contributes to intron splicing efficiency in *Paramecium* 699
Stefano Gnan, Mélody Matelot, Marion Weiman, Olivier Arnaiz, Frédéric Guérin, Linda Sperling, Mireille Bétermier, Claude Thermes, Chun-Long Chen, and Sandra Duharcourt

Broad domains of histone marks in the highly compact *Paramecium* macronuclear genome 710
Franziska Drews, Abdulrahman Salhab, Sivarajan Karunanithi, Miriam Cheaib, Martin Jung, Marcel H. Schulz, and Martin Simon

Methods

Sequencing of individual barcoded cDNAs using Pacific Biosciences and Oxford Nanopore Technologies reveals platform-specific error patterns 726^{OA}
Alla Mikheenko, Andrey D. Prjibelski, Anoushka Joglekar, and Hagen U. Tilgner

Pan-human consensus genome significantly improves the accuracy of RNA-seq analyses 738^{OA}
Benjamin Kaminow, Sara Ballouz, Jesse Gillis, and Alexander Dobin

Identification of phenotype-specific networks from paired gene expression–cell shape imaging data 750^{OA}
Charlie George Barker, Eirini Petsalaki, Girolamo Giudice, Julia Sero, Emmanuel Nsa Ekpenyong, Chris Bakal, and Evangelia Petsalaki

A framework to score the effects of structural variants in health and disease 766^{OA}
Philip Kleinert and Martin Kircher

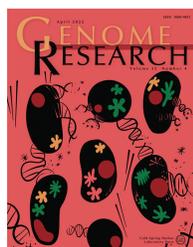
An association test of the spatial distribution of rare missense variants within protein structures identifies Alzheimer’s disease–related patterns 778^{OA}
Bowen Jin, John A. Capra, Penelope Benchek, Nicholas Wheeler, Adam C. Naj, Kara L. Hamilton-Nelson, John J. Farrell, Yuk Yee Leung, Brian Kunkle, Badri Vadarajan, Gerard D. Schellenberg, Richard Mayeux, Li-San Wang, Lindsay A. Farrer, Margaret A. Pericak-Vance, Eden R. Martin, Jonathan L. Haines, Dana C. Crawford, and William S. Bush

Variations in antibody repertoires correlate with vaccine responses 791
Yana Safonova, Sung Bong Shin, Luke Kramer, James Reecy, Corey T. Watson, Timothy P.L. Smith, and Pavel A. Pevzner

Erratum

Erratum: Genome biology of the darkedged splitfin, *Girardinichthys multiradiatus*, and the evolution of sex chromosomes and placentation 805
Kang Du, Martin Pippel, Susanne Kneitz, Romain Feron, Irene da Cruz, Sylke Winkler, Brigitta Wilde, Edgar G. Avila Luna, Gene Myers, Yann Guiguen, Constantino Macias Garcia, and Manfred Schartl

^{OA}Open Access paper



Cover Genes are interrupted by introns that must be accurately spliced from messenger RNA precursors. In this issue, the nucleotide composition of the genome is shown to directly contribute to splicing efficiency in *Paramecium*. The artwork depicts the genome of the ciliated unicellular organism *Paramecium*, inspired by the cut-paper collages of Henri Matisse’s *Jazz* artbook. (Cover illustration by Eve Charmant, Instagram @evecharmant, eve.charmant@gmail.com. [For details, see Gnan et al., pp. 699–709.]