

Research

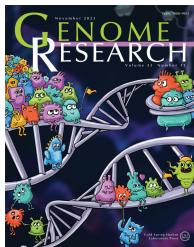
The human genome contains over a million autonomous exons	1865 ^{OA}
Nicholas Stepankiw, Ally W.H. Yang, and Timothy R. Hughes	
Characterization of human transcription factor function and patterns of gene regulation in HepG2 cells	1879 ^{OA}
Belle A. Moyers, E. Christopher Partridge, Mark Mackiewicz, Michael J. Betti, Roshan Darji, Sarah K. Meadows, Kimberly M. Newberry, Laurel A. Brandsmeier, Barbara J. Wold, Eric M. Mendenhall, and Richard M. Myers	
E4F1 and ZNF148 are transcriptional activators of the -57A > C and wild-type <i>TERT</i> promoter	1893 ^{OA}
Boon Haow Chua, Nurkaiyisah Zaal Anuar, Laure Ferry, Cecilia Domrane, Anna Wittek, Vineeth T. Mukundan, Sudhakar Jha, Falk Butter, Daniel G. Tenen, Pierre-Antoine Defossez, and Dennis Kappei	
Cellular age explains variation in age-related cell-to-cell transcriptome variability	1906
Ming Yang, Benjamin R. Harrison, and Daniel E.L. Promislow	
Transposon wave remodeled the epigenomic landscape in the rapid evolution of X-Chromosome dosage compensation	1917
David C.H. Metzger, Imogen Porter, Brendan Mobley, Benjamin A. Sandkam, Lydia J.M. Fong, Andrew P. Anderson, and Judith E. Mank	
miRNA-like secondary structures in maize (<i>Zea mays</i>) genes and transposable elements correlate with small RNAs, methylation, and expression	1932 ^{OA}
Galen T. Martin, Edwin Solares, Jeanelle Guadardo-Mendez, Aline Muyle, Alexandros Bousios, and Brandon S. Gaut	
Telomeric repeat evolution in the phylum Nematoda revealed by high-quality genome assemblies and subtelomere structures	1947 ^{OA}
Jiseon Lim, Wonjoo Kim, Jun Kim, and Junho Lee	
Genome-wide chromatin interaction profiling reveals a vital role of super-enhancers and rearrangements in host enhancer contacts during BmNPV infection	1958
Shudi Zhao, Yuedong Li, Guanping Chen, Xingyang Wang, Nan Chen, and Xiaofeng Wu	
Proteome-wide structural analysis quantifies structural conservation across distant species	1975
Shijie Zhang, Teng Zhang, and Yuan Fu	

(continued)

Methods

De novo reconstruction of satellite repeat units from sequence data Yujie Zhang, Justin Chu, Haoyu Cheng, and Heng Li	1994
Integrating SNVs and CNAs on a phylogenetic tree from single-cell DNA sequencing data Liting Zhang, Hank W. Bass, Jerome Irianto, and Xian Mallory	2002
Characterization of meiotic recombination intermediates through gene knockouts in founder hybrid mice Benjamin Davies, Gang Zhang, Daniela Moralli, Samy Alghadban, Daniel Biggs, Chris Preece, Peter Donnelly, and Anjali Gupta Hinch	2018 ^{OA}

^{OA}Open Access paper



Cover In this issue, Moyers et al. report on analyses of 680 transcription factors in the HepG2 cell line. Transcription factors are depicted as characters associated with DNA, regulating the expression of genes. Some carry flags, denoting tagged ChIP-seq experiments. Some associate with one another by holding hands where different regions of DNA loop together, interacting to achieve the connection between the two distal DNA strands. Some characters accumulate in large numbers, depicting High Occupancy Target (HOT) sites on the DNA. A repressive transcription factor character flexes its muscles to keep others away. Histone proteins are larger characters around which DNA wraps. (Cover illustration concept by Cathleen Shaw, cshaw@hudsonalpha.org. [For details, see Moyers et al., pp. 1879–1892.])