

Commentary

- Decoding the human genome** 1599
Kelly A. Frazer

Perspectives

- What does our genome encode?** 1602
John A. Stamatoyannopoulos
- Toward mapping the biology of the genome** 1612
Stephen Chanock

Research

- Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs** 1616
Hagen Tilgner, David G. Knowles, Rory Johnson, Carrie A. Davis, Sudipto Chakraborty, Sarah Djebali, João Curado, Michael Snyder, Thomas R. Gingeras, and Roderic Guigó
- RNA editing in the human ENCODE RNA-seq data** 1626
Eddie Park, Brian Williams, Barbara J. Wold, and Ali Mortazavi
- Discovery of hundreds of mirtrons in mouse and human small RNA data** 1634
Erik Ladewig, Katsutomo Okamura, Alex S. Flynt, Jakub O. Westholm, and Eric C. Lai
- Long noncoding RNAs are rarely translated in two human cell lines** 1646
Balázs Bánfai, Hui Jia, Jainab Khatun, Emily Wood, Brian Risk, William E. Gundling Jr., Anshul Kundaje, Harsha P. Gunawardena, Yanbao Yu, Ling Xie, Krzysztof Krajewski, Brian D. Strahl, Xian Chen, Peter Bickel, Morgan C. Giddings, James B. Brown, and Leonard Lipovich
- Understanding transcriptional regulation by integrative analysis of transcription factor binding data** 1658
Chao Cheng, Roger Alexander, Renqiang Min, Jing Leng, Kevin Y. Yip, Joel Rozowsky, Koon-Kiu Yan, Xianjun Dong, Sarah Djebali, Yijun Ruan, Carrie A. Davis, Piero Carninci, Timo Lassman, Thomas R. Gingeras, Roderic Guigó, Ewan Birney, Zhiping Weng, Michael Snyder, and Mark Gerstein
- A highly integrated and complex PPARGC1A transcription factor binding network in HepG2 cells** 1668
Alexandra E. Charos, Brian D. Reed, Debasish Raha, Anna M. Szekely, Sherman M. Weissman, and Michael Snyder
- Widespread plasticity in CTCF occupancy linked to DNA methylation** 1680
Hao Wang, Matthew T. Maurano, Hongzhu Qu, Katherine E. Varley, Jason Gertz, Florencia Pauli, Kristen Lee, Theresa Canfield, Molly Weaver, Richard Sandstrom, Robert E. Thurman, Rajinder Kaul, Richard M. Myers, and John A. Stamatoyannopoulos

(continued)

Personal and population genomics of human regulatory variation	1689
Benjamin Vernot, Andrew B. Stergachis, Matthew T. Maurano, Jeff Vierstra, Shane Neph, Robert E. Thurman, John A. Stamatoyannopoulos, and Joshua M. Akey	
Methods	
Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome	1698
Cédric Howald, Andrea Tanzer, Jacqueline Chrast, Felix Kokocinski, Thomas Derrien, Nathalie Walters, Jose M. Gonzalez, Adam Frankish, Bronwen L. Aken, Thibaut Hourlier, Jan-Hinnerk Vogel, Simon White, Stephen Searle, Jennifer Harrow, Tim J. Hubbard, Roderic Guigó, and Alexandre Reymond	
Predicting cell-type-specific gene expression from regions of open chromatin	1711
Anirudh Natarajan, Galip Gürkan Yardımcı, Nathan C. Sheffield, Gregory E. Crawford, and Uwe Ohler	
Sequence and chromatin determinants of cell-type-specific transcription factor binding	1723
Aaron Arvey, Phaedra Agius, William Stafford Noble, and Christina Leslie	
Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements	1735
Anshul Kundaje, Sofia Kyriazopoulou-Panagiotopoulou, Max Libbrecht, Cheryl L. Smith, Debasish Raha, Elliott E. Winters, Steven M. Johnson, Michael Snyder, Serafim Batzoglou, and Arend Sidow	
Linking disease associations with regulatory information in the human genome	1748
Marc A. Schaub, Alan P. Boyle, Anshul Kundaje, Serafim Batzoglou, and Michael Snyder	
Resources	
GENCODE: The reference human genome annotation for The ENCODE Project	1760
Jennifer Harrow, Adam Frankish, Jose M. Gonzalez, Electra Tapanari, Mark Diekhans, Felix Kokocinski, Bronwen L. Aken, Daniel Barrell, Amonida Zadissa, Stephen Searle, If Barnes, Alexandra Bignell, Veronika Boychenko, Toby Hunt, Mike Kay, Gaurab Mukherjee, Jeena Rajan, Gloria Despacio-Reyes, Gary Saunders, Charles Steward, Rachel Harte, Michael Lin, Cédric Howald, Andrea Tanzer, Thomas Derrien, Jacqueline Chrast, Nathalie Walters, Suganthi Balasubramanian, Baikang Pei, Michael Tress, Jose Manuel Rodriguez, Işık Ezkurdia, Jeltje van Baren, Michael Brent, David Haussler, Manolis Kellis, Alfonso Valencia, Alexandre Reymond, Mark Gerstein, Roderic Guigó, and Tim J. Hubbard	
The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression	1775
Thomas Derrien, Rory Johnson, Giovanni Bussotti, Andrea Tanzer, Sarah Djebali, Hagen Tilgner, Gregory Guernec, David Martin, Angelika Merkel, David G. Knowles, Julien Lagarde, Lavanya Veeravalli, Xiaoan Ruan, Yijun Ruan, Timo Lassmann, Piero Carninci, James B. Brown, Leonard Lipovich, Jose M. Gonzalez, Mark Thomas, Carrie A. Davis, Ramin Shiekhattar, Thomas R. Gingeras, Tim J. Hubbard, Cedric Notredame, Jennifer Harrow, and Roderic Guigó	
Annotation of functional variation in personal genomes using RegulomeDB	1790
Alan P. Boyle, Eurie L. Hong, Manoj Hariharan, Yong Cheng, Marc A. Schaub, Maya Kasowski, Konrad J. Karczewski, Julie Park, Benjamin C. Hitz, Shuai Weng, J. Michael Cherry, and Michael Snyder	

(continued)

Jie Wang, Jiali Zhuang, Sowmya Iyer, XinYing Lin, Troy W. Whitfield, Melissa C. Greven, Brian G. Pierce, Xianjun Dong, Anshul Kundaje, Yong Cheng, Oliver J. Rando, Ewan Birney, Richard M. Myers, William S. Noble, Michael Snyder, and Zhiping Weng

ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia

Stephen G. Landt, Georgi K. Marinov, Anshul Kundaje, Pouya Kheradpour, Florencia Pauli, Serafim Batzoglou, Bradley E. Bernstein, Peter Bickel, James B. Brown, Philip Cayting, Yiwen Chen, Gilberto DeSalvo, Charles Epstein, Katherine I. Fisher-Aylor, Ghia Euskirchen, Mark Gerstein, Jason Gertz, Alexander J. Hartemink, Michael M. Hoffman, Vishwanath R. Iyer, Youngsook L. Jung, Subhradip Karmakar, Manolis Kellis, Peter V. Kharchenko, Qunhua Li, Tao Liu, X. Shirley Liu, Lijia Ma, Aleksandar Milosavljevic, Richard M. Myers, Peter J. Park, Michael J. Pazin, Marc D. Perry, Debasish Raha, Timothy E. Reddy, Joel Rozowsky, Noam Shores, Arend Sidow, Matthew Slattery, John A. Stamatoyannopoulos, Michael Y. Tolstorukov, Kevin P. White, Simon Xi, Peggy J. Farnham, Jason D. Lieb, Barbara J. Wold, and Michael Snyder

NOTE: All articles in this issue are freely available online and are distributed under a Creative Commons License (Attribution-NonCommercial 3.0 Unported License).

Cover *Genome Research* presents an ENCODE special issue highlighting novel analyses made possible within the production phase of The ENCODE Project. Near the *top center*, a mature mRNA in the cytosol (gray background) comprised of uninterrupted exons (colored blocks) is “attacked” by a (sun-like) ribosome. *Below*, in the nuclear fraction (on blue background at *bottom*), a nascent RNA in which many but not all introns have already been removed is still attached to RNA polymerase II (PolII) (Tilgner et al.). A lariat and a mirtron are close by (Ladewig et al.). Compared to this nuclear RNA, the cytosolic RNA contains a novel donor exon 4 represented by two additional light-blue codons (colored bars), a 3’ UTR exon (circle at black 3’ end), and an RNA editing event in the 3’ UTR (Howald et al.; Park et al.), highlighting the non-identical RNA populations of the nucleus and cytosol. At *bottom*, a DNA helix is bound by multiple transcription factors (TF, entirely red, yellow, or blue), nucleosomes (black with histone modifications), and kidney-shaped RNA-polymerases. (DNA, *left to right*) A TF-complex binding DNA upstream of a +1 nucleosome of a gene is surrounded by an asymmetric chromatin organization (differently spaced nucleosomes with different histone modifications) (Kundaje et al.); another +1 nucleosome with a combination of histone modifications is linked to transcription (note yellow-black PolII moving into the gene); cell-type-specific DNA harboring single-nucleotide polymorphisms (SNPs) and/or methylation (red, fluorescing circles) prevent a TF (CTCF here) from binding (Boyle et al.; H. Wang et al.). At the *extreme right* of the DNA molecule, a complex of only two TFs binds upstream of a gene of different function in a DNase-accessible region (Arvey et al.; J. Wang et al.) and this is predictive for expression (Natarajan et al.). At *bottom right*, above ENCODE, a lncRNA (black for noncoding) is represented as shorter than mRNAs, more lowly expressed, retained in the nucleus (Derrien et al.), and untranslated (Bánfai et al.). (Cover illustration in the style of Joan Miró by Luisa Lente at YOYO studio [<http://www.yoyo.es/>] with biological concepts by Hagen Tilgner. [For details, see above-referenced papers and related work, all in this issue at <http://genome.org/content/22/9.toc.>])

