

Research

- Somatic retrotransposition in human cancer revealed by whole-genome and exome sequencing** 1053
Elena Helman, Michael S. Lawrence, Chip Stewart, Carrie Sougnez, Gad Getz, and Matthew Meyerson
- The effect of genotype and in utero environment on interindividual variation in neonate DNA methylomes** 1064^{OA}
Ai Ling Teh, Hong Pan, Li Chen, Mei-Lyn Ong, Shaillay Dogra, Johnny Wong, Julia L. MacIsaac, Sarah M. Mah, Lisa M. McEwen, Seang-Mei Saw, Keith M. Godfrey, Yap-Seng Chong, Kenneth Kwek, Chee-Keong Kwok, Shu-E. Soh, Mary F.F. Chong, Sheila Barton, Neerja Karnani, Clara Y. Cheong, Jan Paul Buschdorf, Walter Stünkel, Michael S. Kobor, Michael J. Meaney, Peter D. Gluckman, and Joanna D. Holbrook
- Comparative epigenomics in distantly related teleost species identifies conserved *cis*-regulatory nodes active during the vertebrate phylotypic period** 1075
Juan J. Tena, Cristina González-Aguilera, Ana Fernández-Miñán, Javier Vázquez-Marín, Helena Parra-Acero, Joe W. Cross, Peter W.J. Rigby, Jaime J. Carvajal, Joachim Wittbrodt, José L. Gómez-Skarmeta, and Juan R. Martínez-Morales
- Comparison of *D. melanogaster* and *C. elegans* developmental stages, tissues, and cells by modENCODE RNA-seq data** 1086^{OA}
Jingyi Jessica Li, Haiyan Huang, Peter J. Bickel, and Steven E. Brenner
- DNA replication and transcription programs respond to the same chromatin cues** 1102^{OA}
Yoav Lubelsky, Joseph A. Prinz, Leyna DeNapoli, Yulong Li, Jason A. Belsky, and David M. MacAlpine
- Evolution of H3K27me₃-marked chromatin is linked to gene expression evolution and to patterns of gene duplication and diversification** 1115^{OA}
Robert K. Arthur, Lijia Ma, Matthew Slattery, Rebecca F. Spokony, Alexander Ostapenko, Nicolas Nègre, and Kevin P. White
- The chromatin landscape of *Drosophila*: comparisons between species, sexes, and chromosomes** 1125
Emily J. Brown and Doris Bachtrog
- Extreme HOT regions are CpG-dense promoters in *C. elegans* and humans** 1138^{OA}
Ron A.-J. Chen, Przemyslaw Stempor, Thomas A. Down, Eva Zeiser, Sky K. Feuer, and Julie Ahringer
- Dissection of thousands of cell type-specific enhancers identifies dinucleotide repeat motifs as general enhancer features** 1147^{OA}
J. Omar Yáñez-Cuna, Cosmas D. Arnold, Gerald Stampfel, Łukasz M. Boryń, Daniel Gerlach, Martina Rath, and Alexander Stark

Methods

Quantifying ChIP-seq data: a spiking method providing an internal reference for sample-to-sample normalization

1157^{OA}

Nicolas Bonhoure, Gergana Bounova, David Bernasconi, Viviane Praz, Fabienne Lammers, Donatella Canella, Ian M. Willis, Winship Herr, Nouria Hernandez, Mauro Delorenzi, and The CycliX Consortium

LaSSO, a strategy for genome-wide mapping of intronic lariats and branch points using RNA-seq

1169^{OA}

Danny A. Bitton, Charalampos Rallis, Daniel C. Jeffares, Graeme C. Smith, Yuan Y.C. Chen, Sandra Codlin, Samuel Marguerat, and Jürg Bähler

Resources

A cloud-compatible bioinformatics pipeline for ultrarapid pathogen identification from next-generation sequencing of clinical samples

1180^{OA}

Samia N. Naccache, Scot Federman, Narayanan Veeraraghavan, Matei Zaharia, Deanna Lee, Erik Samayoa, Jerome Bouquet, Alexander L. Greninger, Ka-Cheung Luk, Barryett Enge, Debra A. Wadford, Sharon L. Messenger, Gillian L. Genrich, Kristen Pellegrino, Gilda Grard, Eric Leroy, Bradley S. Schneider, Joseph N. Fair, Miguel A. Martínez, Pavel Isa, John A. Crump, Joseph L. DeRisi, Taylor Sittler, John Hackett, Jr., Steve Miller, and Charles Y. Chiu

Natural variation in genome architecture among 205 *Drosophila melanogaster* Genetic Reference Panel lines

1193^{OA}

Wen Huang, Andreas Massouras, Yutaka Inoue, Jason Peiffer, Miquel Ràmia, Aaron M. Tarone, Lavanya Turlapati, Thomas Zichner, Dianhui Zhu, Richard F. Lyman, Michael M. Magwire, Kerstin Blankenburg, Mary Anna Carbone, Kyle Chang, Lisa L. Ellis, Sonia Fernandez, Yi Han, Gareth Highnam, Carl E. Hjelman, John R. Jack, Mehwish Javaid, Joy Jayaseelan, Divya Kalra, Sandy Lee, Lora Lewis, Mala Munidasa, Fiona Onger, Shohba Patel, Lora Perales, Agapito Perez, LingLing Pu, Stephanie M. Rollmann, Robert Ruth, Nehad Saada, Crystal Warner, Aneisa Williams, Yuan-Qing Wu, Akihiko Yamamoto, Yiqing Zhang, Yiming Zhu, Robert R.H. Anholt, Jan O. Korbel, David Mittelman, Donna M. Muzny, Richard A. Gibbs, Antonio Barbadilla, J. Spencer Johnston, Eric A. Stone, Stephen Richards, Bart Deplancke, and Trudy F.C. Mackay

Comparative validation of the *D. melanogaster* modENCODE transcriptome annotation

1209^{OA}

Zhen-Xia Chen, David Sturgill, Jiaxin Qu, Huaiyang Jiang, Soo Park, Nathan Boley, Ana Maria Suzuki, Anthony R. Fletcher, David C. Plachetzki, Peter C. FitzGerald, Carlo G. Artieri, Joel Atallah, Olga Barmina, James B. Brown, Kerstin P. Blankenburg, Emily Clough, Abhijit Dasgupta, Sai Gubbala, Yi Han, Joy C. Jayaseelan, Divya Kalra, Yoo-Ah Kim, Christie L. Kovar, Sandra L. Lee, Mingmei Li, James D. Malley, John H. Malone, Tittu Mathew, Nicolas R. Mattiuzzo, Mala Munidasa, Donna M. Muzny, Fiona Onger, Lora Perales, Teresa M. Przytycka, Ling-Ling Pu, Garrett Robinson, Rebecca L. Thornton, Nehad Saada, Steven E. Scherer, Harold E. Smith, Charles Vinson, Crystal B. Warner, Kim C. Worley, Yuan-Qing Wu, Xiaoyan Zou, Peter Cherbas, Manolis Kellis, Michael B. Eisen, Fabio Piano, Karin Kionte, David H. Fitch, Paul W. Sternberg, Asher D. Cutter, Michael O. Duff, Roger A. Hoskins, Brenton R. Graveley, Richard A. Gibbs, Peter J. Bickel, Artyom Kopp, Piero Carninci, Susan E. Celniker, Brian Oliver, and Stephen Richards

(continued)

Diverse patterns of genomic targeting by transcriptional regulators in *Drosophila melanogaster*

1224^{OA}

Matthew Slattery, Lijia Ma, Rebecca F. Spokony, Robert K. Arthur, Pouya Kheradpour, Anshul Kundaje, Nicolas Nègre, Alex Crofts, Ryan Ptashkin, Jennifer Zieba, Alexander Ostapenko, Sarah Suchy, Alec Victorsen, Nader Jameel, A. Jason Grundstad, Wenxuan Gao, Jennifer R. Moran, E. Jay Rehm, Robert L. Grossman, Manolis Kellis, and Kevin P. White

Diversity of miRNAs, siRNAs, and piRNAs across 25 *Drosophila* cell lines

1236^{OA}

Jiayu Wen, Jaaved Mohammed, Diane Bortolamiol-Becet, Harrison Tsai, Nicolas Robine, Jakub O. Westholm, Erik Ladewig, Qi Dai, Katsutomo Okamura, Alex S. Flynt, Dayu Zhang, Justen Andrews, Lucy Cherbas, Thomas C. Kaufman, Peter Cherbas, Adam Siepel, and Eric C. Lai

^{OA}Open Access paper



Cover Inspired by M.C. Escher's artistic tessellations, the model organisms *Drosophila melanogaster* and *Caenorhabditis elegans* morph into human, reminding us of their common biology that has for decades informed human studies. In this issue of *Genome Research*, the National Human Genome Research Institute model organism ENCyclopedia Of DNA Elements (modENCODE) Project provides a comparative analysis of transcription, chromatin, and gene regulation across the three metazoan species, revealing important similarities and differences in their genome function. (Cover illustration by Darryl Leja, NHGRI, NIH. [For details, see Li et al., pp. 1086–1101; Lubelsky et al., pp. 1102–1114; Arthur et al., pp. 1115–1124; Chen et al., pp. 1209–1223; Slattery et al., pp. 1224–1235; and Wen et al., pp. 1236–1250.]