

Research

- Plasticity in patterns of histone modifications and chromosomal proteins in *Drosophila* heterochromatin 147
Nicole C. Riddle, Aki Minoda, Peter V. Kharchenko, Artyom A. Alekseyenko, Yuri B. Schwartz, Michael Y. Tolstorukov, Andrey A. Gorchakov, Jacob D. Jaffe, Cameron Kennedy, Daniela Linder-Basso, Sally E. Peach, Gregory Shanower, Haiyan Zheng, Mitzi I. Kuroda, Vincenzo Pirrotta, Peter J. Park, Sarah C.R. Elgin, and Gary H. Karpen
- Chromatin signatures of the *Drosophila* replication program 164^{OA}
Matthew L. Eaton, Joseph A. Prinz, Heather K. MacAlpine, George Tretyakov, Peter V. Kharchenko, and David M. MacAlpine
- Developmental control of the DNA replication and transcription programs 175^{OA}
Jared Nordman, Sharon Li, Thomas Eng, David MacAlpine, and Terry L. Orr-Weaver
- Genome-wide analysis of promoter architecture in *Drosophila melanogaster* 182^{OA}
Roger A. Hoskins, Jane M. Landolin, James B. Brown, Jeremy E. Sandler, Hazuki Takahashi, Timo Lassmann, Charles Yu, Benjamin W. Booth, Dayu Zhang, Kenneth H. Wan, Li Yang, Nathan Boley, Justen Andrews, Thomas C. Kaufman, Brenton R. Graveley, Peter J. Bickel, Piero Carninci, Joseph W. Carlson, and Susan E. Celniker
- Conservation of an RNA regulatory map between *Drosophila* and mammals 193^{OA}
Angela N. Brooks, Li Yang, Michael O. Duff, Kasper D. Hansen, Jung W. Park, Sandrine Dudoit, Steven E. Brenner, and Brenton R. Graveley
- Deep annotation of *Drosophila melanogaster* microRNAs yields insights into their processing, modification, and emergence 203^{OA}
Eugene Berezikov, Nicolas Robine, Anastasia Samsonova, Jakub O. Westholm, Ammar Naqvi, Jui-Hung Hung, Katsutomo Okamura, Qi Dai, Diane Bortolamiol-Becet, Raquel Martin, Yongjun Zhao, Phillip D. Zamore, Gregory J. Hannon, Marco A. Marra, Zhiping Weng, Norbert Perrimon, and Eric C. Lai
- Polycomb preferentially targets stalled promoters of coding and noncoding transcripts 216^{OA}
Daniel Enderle, Christian Beisel, Michael B. Stadler, Moritz Gerstung, Prashanth Athri, and Renato Paro
- Broad chromosomal domains of histone modification patterns in *C. elegans* 227^{OA}
Tao Liu, Andreas Rechtsteiner, Thea A. Egelhofer, Anne Vielle, Isabel Latorre, Ming-Sin Cheung, Sevinc Ercan, Kohta Ikegami, Morten Jensen, Paulina Kolasinska-Zwierz, Heidi Rosenbaum, Hyunjin Shin, Scott Taing, Teruaki Takasaki, A. Leonardo Iniguez, Arshad Desai, Abby F. Dernburg, Hiroshi Kimura, Jason D. Lieb, Julie Ahringer, Susan Strome, and X. Shirley Liu

(continued)

High nucleosome occupancy is encoded at X-linked gene promoters in <i>C. elegans</i> Sevinç Ercan, Yaniv Lubling, Eran Segal, and Jason D. Lieb	237
Diverse transcription factor binding features revealed by genome-wide ChIP-seq in <i>C. elegans</i> Wei Niu, Zhi John Lu, Mei Zhong, Mihail Sarov, John I. Murray, Cathleen M. Brdlik, Judith Janette, Chao Chen, Pedro Alves, Elicia Preston, Cindie Slightham, Lixia Jiang, Anthony A. Hyman, Stuart K. Kim, Robert H. Waterston, Mark Gerstein, Michael Snyder, and Valerie Reinke	245
A global analysis of <i>C. elegans</i> trans-splicing Mary Ann Allen, LaDeana W. Hillier, Robert H. Waterston, and Thomas Blumenthal	255
 Methods	
Multimodal RNA-seq using single-strand, double-strand, and CircLigase-based capture yields a refined and extended description of the <i>C. elegans</i> transcriptome Ayelet T. Lamm, Michael R. Stadler, Huibin Zhang, Jonathan I. Gent, and Andrew Z. Fire	265
Prediction and characterization of noncoding RNAs in <i>C. elegans</i> by integrating conservation, secondary structure, and high throughput sequencing and array data Zhi John Lu, Kevin Y. Yip, Guilin Wang, Chong Shou, LaDeana W. Hillier, Ekta Khurana, Ashish Agarwal, Raymond Auerbach, Joel Rozowsky, Chao Cheng, Masaomi Kato, David M. Miller, Frank Slack, Michael Snyder, Robert H. Waterston, Valerie Reinke, and Mark B. Gerstein	276 ^{OA}
Computational and experimental identification of mirtrons in <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> Wei-Jen Chung, Phaedra Agius, Jakub O. Westholm, Michael Chen, Katsutomo Okamura, Nicolas Robine, Christina S. Leslie, and Eric C. Lai	286 ^{OA}
 Resources	
The transcriptional diversity of 25 <i>Drosophila</i> cell lines Lucy Cherbas, Aarron Willingham, Dayu Zhang, Li Yang, Yi Zou, Brian D. Eads, Joseph W. Carlson, Jane M. Landolin, Philipp Kapranov, Jacqueline Dumais, Anastasia Samsonova, Jeong-Hyeon Choi, Johnny Roberts, Carrie A. Davis, Haixu Tang, Marijke J. van Baren, Srinka Ghosh, Alexander Dobin, Kim Bell, Wei Lin, Laura Langton, Michael O. Duff, Aaron E. Tenney, Chris Zaleski, Michael R. Brent, Roger A. Hoskins, Thomas C. Kaufman, Justen Andrews, Brenton R. Graveley, Norbert Perrimon, Susan E. Celniker, Thomas R. Gingeras, and Peter Cherbas	301 ^{OA}
The <i>Drosophila melanogaster</i> transcriptome by paired-end RNA sequencing Bryce Daines, Hui Wang, Ligu Wang, Yumei Li, Yi Han, David Emmert, William Gelbart, Xia Wang, Wei Li, Richard Gibbs, and Rui Chen	315
A spatial and temporal map of <i>C. elegans</i> gene expression W. Clay Spencer, Georg Zeller, Joseph D. Watson, Stefan R. Henz, Kathie L. Watkins, Rebecca D. McWhirter, Sarah Petersen, Vipin T. Sreedharan, Christian Widmer, Jeanyoung Jo, Valerie Reinke, Lisa Petrella, Susan Strome, Stephen E. Von Stetina, Menachem Katz, Shai Shaham, Gunnar Rätsch, and David M. Miller III	325 ^{OA}

(continued)

Arun K. Ramani, John A. Calarco, Qun Pan, Sepand Mavandadi, Ying Wang,
Andrew C. Nelson, Leo J. Lee, Quaid Morris, Benjamin J. Blencowe, Mei Zhen,
and Andrew G. Fraser

^{OA}Open Access paper.



Cover A repeating pattern of *Drosophila melanogaster* (common fruit flies) and *Caenorhabditis elegans* (roundworms) is shown. Both organisms are targets of the National Human Genome Research Institute model organism ENCyclopedia Of DNA Elements (modENCODE) project, which seeks to identify the functional elements across the genomes of these two widely used experimental organisms. The patterns coloring the worms and flies represent the multiple data types and analyses reported in this special issue of *Genome Research*. (Cover illustration by Adrienne Waterston [<http://aquadesign.us>], adapted from an illustration by Michael Leykin [<http://www.leykin.com>], with original concept contributions from Peter Kharchenko and Gary H. Karpen.)