

Research

- Tandem repeat variation in human and great ape populations and its impact on gene expression divergence** 1591
Tugce Bilgin Sonay, Tiago Carvalho, Mark D. Robinson, Maja P. Greminger, Michael Krützen, David Comas, Gareth Highnam, David Mittelman, Andrew Sharp, Tomàs Marques-Bonet, and Andreas Wagner
- GC skew defines distinct RNA polymerase pause sites in CpG island promoters** 1600
Wendy A. Kellner, Joshua S.K. Bell, and Paula M. Vertino
- Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans** 1610^{OA}
Can Cenik, Elif Sarinay Cenik, Gun W. Byeon, Fabian Grubert, Sophie I. Candille, Damek Spacek, Bilal Alsallakh, Hagen Tilgner, Carlos L. Araya, Hua Tang, Emiliano Ricci, and Michael P. Snyder
- DIS3 shapes the RNA polymerase II transcriptome in humans by degrading a variety of unwanted transcripts** 1622
Teresa Szczepińska, Katarzyna Kalisiak, Rafal Tomecki, Anna Labno, Lukasz S. Borowski, Tomasz M. Kulinski, Dorota Adamska, Joanna Kosinska, and Andrzej Dziembowski
- Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background** 1634^{OA}
Ingegerd Elvers, Jason Turner-Maier, Ross Swofford, Michele Koltoonian, Jeremy Johnson, Chip Stewart, Cheng-Zhong Zhang, Steven E. Schumacher, Rameen Beroukheim, Mara Rosenberg, Rachael Thomas, Evan Mauceli, Gad Getz, Federica Di Palma, Jaime F. Modiano, Matthew Breen, Kerstin Lindblad-Toh, and Jessica Alföldi
- Comparison against 186 canid whole-genome sequences reveals survival strategies of an ancient clonally transmissible canine tumor** 1646^{OA}
Brennan Decker, Brian W. Davis, Maud Rimbault, Adrienne H. Long, Eric Karlins, Vidhya Jagannathan, Rebecca Reiman, Heidi G. Parker, Cord Drögemüller, Jason J. Corneveaux, Erica S. Chapman, Jeffery M. Trent, Tosso Leeb, Matthew J. Huentelman, Robert K. Wayne, Danielle M. Karyadi, and Elaine A. Ostrander
- Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of *Ficedula* flycatchers** 1656^{OA}
Reto Burri, Alexander Nater, Takeshi Kawakami, Carina F. Mugal, Pall I. Olason, Linnea Smeds, Alexander Suh, Ludovic Dutoit, Stanislav Bureš, Laszlo Z. Garamszegi, Silje Hogner, Juan Moreno, Anna Qvarnström, Milan Ružić, Stein-Are Sæther, Glenn-Peter Sætre, Janos Török, and Hans Ellegren

(continued)

An extended family of novel vertebrate photopigments is widely expressed and displays a diversity of function	1666
Wayne I.L. Davies, T. Katherine Tamai, Lei Zheng, Josephine K. Fu, Jason Rihel, Russell G. Foster, David Whitmore, and Mark W. Hankins	
Cooperative target mRNA destabilization and translation inhibition by miR-58 microRNA family in <i>C. elegans</i>	1680
Deni Subasic, Anneke Brümmer, Yibo Wu, Sérgio Morgado Pinto, Jochen Imig, Martin Keller, Marko Jovanovic, Helen Louise Lightfoot, Sara Nasso, Sandra Goetze, Erich Brunner, Jonathan Hall, Ruedi Aebersold, Mihaela Zavolan, and Michael O. Hengartner	
Extensive cross-regulation of post-transcriptional regulatory networks in <i>Drosophila</i>	1692^{OA}
Marcus H. Stoiber, Sara Olson, Gemma E. May, Michael O. Duff, Jan Manent, Robert Obar, K.G. Guruharsha, Peter J. Bickel, Spyros Artavanis-Tsakonas, James B. Brown, Brenton R. Graveley, and Susan E. Celniker	
Zelda overcomes the high intrinsic nucleosome barrier at enhancers during <i>Drosophila</i> zygotic genome activation	1703^{OA}
Yujia Sun, Chung-Yi Nien, Kai Chen, Hsiao-Yun Liu, Jeff Johnston, Julia Zeitlinger, and Christine Rushlow	
Zelda is differentially required for chromatin accessibility, transcription factor binding, and gene expression in the early <i>Drosophila</i> embryo	1715
Katharine N. Schulz, Eliana R. Bondra, Arbel Moshe, Jacqueline E. Villalta, Jason D. Lieb, Tommy Kaplan, Daniel J. McKay, and Melissa M. Harrison	
DNA-guided establishment of nucleosome patterns within coding regions of a eukaryotic genome	1727
Leslie Y. Beh, Manuel M. Müller, Tom W. Muir, Noam Kaplan, and Laura F. Landweber	
Extensive de novo mutation rate variation between individuals and across the genome of <i>Chlamydomonas reinhardtii</i>	1739
Rob W. Ness, Andrew D. Morgan, Radhakrishnan B. Vasanthakrishnan, Nick Colegrave, and Peter D. Keightley	
Methods	
Oxford Nanopore sequencing, hybrid error correction, and de novo assembly of a eukaryotic genome	1750
Sara Goodwin, James Gurtowski, Scott Ethe-Sayers, Panchajanya Deshpande, Michael C. Schatz, and W. Richard McCombie	
Structured nucleosome fingerprints enable high-resolution mapping of chromatin architecture within regulatory regions	1757^{OA}
Alicia N. Schep, Jason D. Buenrostro, Sarah K. Denny, Katja Schwartz, Gavin Sherlock, and William J. Greenleaf	

(continued)

Resource

Regulation of alternative splicing in *Drosophila* by 56 RNA binding proteins

1771^{OA}

Angela N. Brooks, Michael O. Duff, Gemma May, Li Yang, Mohan Bolisetty, Jane Landolin, Ken Wan, Jeremy Sandler, Benjamin W. Booth, Susan E. Celniker, Brenton R. Graveley, and Steven E. Brenner

^{OA}Open Access paper



Cover A chimpanzee considers a DNA molecule exhibiting a repetitive sequence. (Cover illustration by Erick Galdamez, with biological concepts by Tiago Carvalho, and helpful comments from the rest of the members from the Comparative Genomics group from the Evolutionary Institute of Biology at Universitat Pompeu Fabra. [For details, see Bilgin Sonay et al., pp. 1591–1599.])