

Review

- What fraction of the human genome is functional? 1769^{OA}
Chris P. Ponting and Ross C. Hardison

Research

- Widespread signatures of recent selection linked to nucleosome positioning in the human lineage 1777
James G.D. Prendergast and Colin A.M. Semple
- Post-transcriptional exon shuffling events in humans can be evolutionarily conserved and abundant 1788^{OA}
Haya H. Al-Balool, David Weber, Yilei Liu, Mark Wade, Kamlesh Guleria, Pitsien Lang Ping Nam, Jake Clayton, William Rowe, Jonathan Coxhead, Julie Irving, David J. Elliott, Andrew G. Hall, Mauro Santibanez-Koref, and Michael S. Jackson
- Coevolution of retroelements and tandem zinc finger genes 1800
James H. Thomas and Sean Schneider
- Extensive variation and low heritability of DNA methylation identified in a twin study 1813
Kristina Gervin, Martin Hammerø, Hanne E. Akselsen, Rune Moe, Heidi Nygård, Ingunn Brandt, Håkon K. Gjessing, Jennifer R. Harris, Dag E. Undlien, and Robert Lyle
- Genome-wide depletion of replication initiation events in highly transcribed regions 1822
Melvenia M. Martin, Michael Ryan, RyangGuk Kim, Anna L. Zakas, Haiqing Fu, Chii Mei Lin, William C. Reinhold, Sean R. Davis, Sven Bilke, Hongfang Liu, James H. Doroshov, Mark A. Reimers, Manuel S. Valenzuela, Yves Pommier, Paul S. Meltzer, and Mirit I. Aladjem
- Late-replicating heterochromatin is characterized by decreased cytosine methylation in the human genome 1833
Masako Suzuki, Mayumi Oda, María-Paz Ramos, Marién Pascual, Kevin Lau, Edyta Stasiek, Frederick Agyiri, Reid F. Thompson, Jacob L. Glass, Qiang Jing, Richard Sandstrom, Melissa J. Fazzari, R. Scott Hansen, John A. Stamatoyannopoulos, Andrew S. McLellan, and John M. Greally
- Comparative methylomics reveals gene-body H3K36me3 in *Drosophila* predicts DNA methylation and CpG landscapes in other invertebrates 1841
Lisa Nanty, Guillermo Carbajosa, Graham A. Heap, Francis Ratnieks, David A. van Heel, Thomas A. Down, and Vardhman K. Rakyen
- Evolutionary divergence of intrinsic and *trans*-regulated nucleosome positioning sequences reveals plastic rules for chromatin organization 1851^{OA}
Alex Tsankov, Yoshimi Yanagisawa, Nicholas Rhind, Aviv Regev, and Oliver J. Rando

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Variety of genomic DNA patterns for nucleosome positioning Ilya Ioshikhes, Sergey Hosid, and B. Franklin Pugh	1863
A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry Raghothama Chaerkady, Dhanashree S. Kelkar, Babylakshmi Muthusamy, Kumaran Kandasamy, Sutopa B. Dwivedi, Nandini A. Sahasrabuddhe, Min-Sik Kim, Santosh Renuse, Sneha M. Pinto, Rakesh Sharma, Harsh Pawar, Nirujogi Raja Sekhar, Ajeet Kumar Mohanty, Derese Getnet, Yi Yang, Jun Zhong, Aditya P. Dash, Robert M. MacCallum, Bernard Delanghe, Godfree Mlambo, Ashwani Kumar, T.S. Keshava Prasad, Mobolaji Okulate, Nirbhay Kumar, and Akhilesh Pandey	1872
Phylogeny-wide analysis of social amoeba genomes highlights ancient origins for complex intercellular communication Andrew J. Heidel, Hajara M. Lawal, Marius Felder, Christina Schilde, Nicholas R. Helps, Budi Tunggal, Francisco Rivero, Uwe John, Michael Schleicher, Ludwig Eichinger, Matthias Platzer, Angelika A. Noegel, Pauline Schaap, and Gernot Glöckner	1882 ^{OA}
Parallel evolution of transcriptome architecture during genome reorganization Sung Ho Yoon, David J. Reiss, J. Christopher Bare, Dan Tenenbaum, Min Pan, Joseph Slagel, Robert L. Moritz, Sujung Lim, Murray Hackett, Angeli Lal Menon, Michael W.W. Adams, Adam Barnebey, Steven M. Yannone, John A. Leigh, and Nitin S. Baliga	1892
Methods	
Digital gene expression for non-model organisms Lewis Z. Hong, Jun Li, Anne Schmidt-Küntzel, Wesley C. Warren, and Gregory S. Barsh	1905
Locating protein-coding sequences under selection for additional, overlapping functions in 29 mammalian genomes Michael F. Lin, Pouya Kheradpour, Stefan Washietl, Brian J. Parker, Jakob S. Pedersen, and Manolis Kellis	1916 ^{OA}
New families of human regulatory RNA structures identified by comparative analysis of vertebrate genomes Brian J. Parker, Ida Moltke, Adam Roth, Stefan Washietl, Jiayu Wen, Manolis Kellis, Ronald Breaker, and Jakob Skou Pedersen	1929
Noncoding RNA gene silencing through genomic integration of RNA destabilizing elements using zinc finger nucleases Tony Gutschner, Marion Baas, and Sven Diederichs	1944
Phenotypic profiling of the human genome reveals gene products involved in plasma membrane targeting of SRC kinases Julia Ritzerfeld, Steffen Remmele, Tao Wang, Koen Temmerman, Britta Brügger, Sabine Wegehingel, Stella Tournaviti, Jeroen R.P.M. Strating, Felix T. Wieland, Beate Neumann, Jan Ellenberg, Chris Lawerenz, Jürgen Hesser, Holger Erfle, Rainer Pepperkok, and Walter Nickel	1955
Resources	
Genome-scale phylogenetic function annotation of large and diverse protein families Barbara E. Engelhardt, Michael I. Jordan, John R. Srouji, and Steven E. Brenner	1969 ^{OA}

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The Proteome Folding Project: Proteome-scale prediction of structure and function

1981^{OA}

Kevin Drew, Patrick Winters, Glenn L. Butterfoss, Viktors Berstis, Keith Uplinger,
Jonathan Armstrong, Michael Riffle, Erik Schweighofer, Bill Bovermann, David R. Goodlett,
Trisha N. Davis, Dennis Shasha, Lars Malmström, and Richard Bonneau

^{OA}Open Access paper.



Cover Closeup of African cheetah skin. Cheetah spots, zebra stripes, and similar periodic mammalian color patterns are an unsolved mystery. What molecular mechanisms underlie these patterns, and how has their diversity been shaped by evolution? Advances in sequencing technology and bioinformatics allow genome-scale gene expression information from non-model organisms. In this issue, EcoP15I-tagged Digital Gene Expression (EDGE) is applied to skin biopsy samples from a cheetah, identifying genes likely to control differences in the color of spotted versus non-spotted regions. (Photo: Anke van Wyk © 2007/Bigstock.com. [For details, see Hong et al., pp. 1905–1915.]