

Commentary and Review

- Commentary* Every genome sequence needs a good map 1925
 Harris A. Lewin, Denis M. Larkin, Joan Pontius, and Stephen J. O'Brien
- Perspective* Phylogenomics of primates and their ancestral populations 1929
 Adam Siepel

Research

- Letters* Population genomics in a disease targeted primary cell model 1942
 Elin Grundberg, Tony Kwan, Bing Ge, Kevin C.L. Lam, Vonda Koka, Andreas Kindmark, Hans Mallmin, Joana Dias, Dominique J. Verlaan, Manon Ouimet, Daniel Sinnett, Fernando Rivadeneira, Karol Estrada, Albert Hofman, Joyce M. van Meurs, André Uitterlinden, Patrick Beaulieu, Alexandru Graziani, Eef Harmsen, Östen Ljunggren, Claes Ohlsson, Dan Mellström, Magnus K. Karlsson, Olle Nilsson, and Tomi Pastinen
- Coexpression network based on natural variation in human gene expression reveals gene interactions and functions 1953
 Renuka R. Nayak, Michael Kearns, Richard S. Spielman, and Vivian G. Cheung
- Elucidation of the ELK1 target gene network reveals a role in the coordinate regulation of core components of the gene regulation machinery 1963^{OA}
 Joanna Boros, Ian J. Donaldson, Amanda O'Donnell, Zaneta A. Odrowaz, Leo Zeef, Mathieu Lupien, Clifford A. Meyer, X. Shirley Liu, Myles Brown, and Andrew D. Sharrocks
- The presence of RNA polymerase II, active or stalled, predicts epigenetic fate of promoter CpG islands 1974
 Hideyuki Takeshima, Satoshi Yamashita, Taichi Shimazu, Tohru Niwa, and Toshikazu Ushijima
- Exon-trapping mediated by the human retrotransposon SVA 1983
 Dustin C. Hancks, Adam D. Ewing, Jesse E. Chen, Katsushi Tokunaga, and Haig H. Kazazian Jr.
- 5'-Transducing SVA retrotransposon groups spread efficiently throughout the human genome 1992
 Annette Damert, Julija Raiz, Axel V. Horn, Johannes Löwer, Hui Wang, Jinchuan Xing, Mark A. Batzer, Roswitha Löwer, and Gerald G. Schumann

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Relative contribution of sequence and structure features to the mRNA binding of Argonaute/EIF2C-miRNA complexes and the degradation of miRNA targets	2009 ^{OA}
Jean Hausser, Markus Landthaler, Lukasz Jaskiewicz, Dimos Gaidatzis, and Mihaela Zavolan	
Complex selection on 5' splice sites in intron-rich organisms	2021 ^{OA}
Manuel Irimia, Scott William Roy, Daniel E. Neafsey, Josep F. Abril, Jordi Garcia-Fernandez, and Eugene V. Koonin	
Allele-specific DNA methylation in mouse strains is mainly determined by <i>cis</i> -acting sequences	2028
Elmar Schilling, Carol El Chartouni, and Michael Rehli	
Deeply conserved chordate noncoding sequences preserve genome synteny but do not drive gene duplicate retention	2036
Andrew L. Hufton, Susanne Mathia, Helene Braun, Udo Georgi, Hans Lehrach, Martin Vingron, Albert J. Poustka, and Georgia Panopoulou	
Profiling the repertoire of phenotypes influenced by environmental cues that occur during asexual reproduction	2052
Aviv Dombrovsky, Laury Arthaud, Terence N. Ledger, Sophie Tares, and Alain Robichon	
Repertoire and evolution of miRNA genes in four divergent nematode species	2064
Elzo de Wit, Sam E.V. Linsen, Edwin Cuppen, and Eugene Berezikov	

Methods and Resources

Methods

Rapid inexpensive genome-wide association using pooled whole blood	2075
Jamie E. Craig, Alex W. Hewitt, Amy E. McMellon, Anjali K. Henders, Lingjun Ma, Leanne Wallace, Shiwani Sharma, Kathryn P. Burdon, Peter M. Visscher, Grant W. Montgomery, and Stuart MacGregor	
Rapid identification of homologous recombinants and determination of gene copy number with reference/query pyrosequencing (RQPS)	2081
Zhenyi Liu, Anna C. Obenauf, Michael R. Speicher, and Raphael Kopan	
Distinguishing direct versus indirect transcription factor-DNA interactions	2090 ^{OA}
Raluca Gordân, Alexander J. Hartemink, and Martha L. Bulyk	
An ensemble model of competitive multi-factor binding of the genome	2101
Todd Wasson and Alexander J. Hartemink	
Automatic analysis of dividing cells in live cell movies to detect mitotic delays and correlate phenotypes in time	2113
Nathalie Harder, Felipe Mora-Bermúdez, William J. Godinez, Annelie Wünsche, Roland Eils, Jan Ellenberg, and Karl Rohr	

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Resources

- LookSeq: A browser-based viewer for deep sequencing data** 2125^{OA}
Heinrich Magnus Manske and Dominic P. Kwiatkowski
- mGene: Accurate SVM-based gene finding with an application to nematode genomes** 2133^{OA}
Gabriele Schweikert, Alexander Zien, Georg Zeller, Jonas Behr, Christoph Dieterich, Cheng Soon Ong, Petra Philips, Fabio De Bona, Lisa Hartmann, Anja Bohlen, Nina Krüger, Sören Sonnenburg, and Gunnar Rätsch
- Windshield splatter analysis with the Galaxy metagenomic pipeline** 2144^{OA}
Sergei Kosakovsky Pond, Samir Wadhawan, Francesca Chiaromonte, Guruprasad Ananda, Wen-Yu Chung, James Taylor, Anton Nekrutenko, and The Galaxy Team
- Singapore Genome Variation Project: A haplotype map of three Southeast Asian populations** 2154^{OA}
Yik-Ying Teo, Xueling Sim, Rick T.H. Ong, Adrian K.S. Tan, Jieming Chen, Erwin Tantoso, Kerrin S. Small, Chee-Seng Ku, Edmund J.D. Lee, Mark Seielstad, and Kee-Seng Chia

^{OA}Open Access paper.



Cover Genes interact in networks to orchestrate cellular processes. The illustration shows a gene coexpression network in humans. Since genes that are connected tend to be involved in similar processes, we can use gene coexpression networks to learn about the interactions and functions of genes, including those implicated in disease. (Cover illustration by Colleen McGarry and Renuka Nayak. [For details, see Nayak et al., pp. 1953–1962.])