

<i>Letters</i>	Research	
	Ecological adaptation determines functional mammalian olfactory subgenomes	1
	Sara Hayden, Michaël Bekaert, Tess A. Crider, Stefano Mariani, William J. Murphy, and Emma C. Teeling	
	Extreme variability among mammalian VIR gene families	10
	Janet M. Young, Hillary F. Massa, Li Hsu, and Barbara J. Trask	
	A novel active endogenous retrovirus family contributes to genome variability in rat inbred strains	19
	Yongming Wang, František Liška, Claudia Gosele, Lucie Šedová, Vladimír Křen, Drahomíra Křenová, Zoltán Ivics, Norbert Hubner, and Zsuzsanna Izsvák	
	An integrative genomic analysis identifies <i>Bhmt2</i> as a diet-dependent genetic factor protecting against acetaminophen-induced liver toxicity	28
	Hong-Hsing Liu, Peng Lu, Yingying Guo, Erin Farrell, Xun Zhang, Ming Zheng, Betty Bosano, Zhaomei Zhang, John Allard, Guochun Liao, Siyu Fu, Jinzhi Chen, Kimberly Dolim, Ayako Kuroda, Jonathan Usuka, Janet Cheng, William Tao, Kevin Welch, Yanzhou Liu, Joseph Pease, Steve A. de Keczzer, Mohammad Masjedizadeh, Jing-Shan Hu, Paul Weller, Tim Garrow, and Gary Peltz	
	Genome-wide mapping of SMAD target genes reveals the role of BMP signaling in embryonic stem cell fate determination	36
	Teng Fei, Kai Xia, Zhongwei Li, Bing Zhou, Shanshan Zhu, Hua Chen, Jianping Zhang, Zhang Chen, Huasheng Xiao, Jing-Dong J. Han, and Ye-Guang Chen	
	Genome-wide mapping of alternative splicing in <i>Arabidopsis thaliana</i>	45
	Sergei A. Filichkin, Henry D. Priest, Scott A. Givan, Rongkun Shen, Douglas W. Bryant, Samuel E. Fox, Weng-Keen Wong, and Todd C. Mockler	
	A novel strategy of transcription regulation by intragenic nucleosome ordering	59
	Cédric Vaillant, Leonor Palmeira, Guillaume Chevereau, Benjamin Audit, Yves d'Aubenton-Carafa, Claude Thermes, and Alain Arneodo	

Methods and Resources

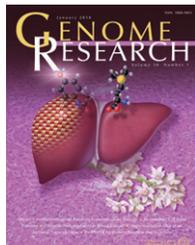
Methods

- Inferring tumor progression from genomic heterogeneity** 68^{OA}
Nicholas Navin, Alexander Krasnitz, Linda Rodgers, Kerry Cook, Jennifer Meth, Jude Kendall, Michael Riggs, Yvonne Eberling, Jennifer Troge, Vladimir Grubor, Dan Levy, Pär Lundin, Susanne Månér, Anders Zetterberg, James Hicks, and Michael Wigler
- Targeted chromosomal deletions in human cells using zinc finger nucleases** 81
Hyung Joo Lee, Eunji Kim, and Jin-Soo Kim
- High-resolution nucleosome mapping reveals transcription-dependent promoter packaging** 90^{OA}
Assaf Weiner, Amanda Hughes, Moran Yassour, Oliver J. Rando, and Nir Friedman
- Estimating population genetic parameters and comparing model goodness-of-fit using DNA sequences with error** 101^{OA}
Xiaoming Liu, Yun-Xin Fu, Taylor J. Maxwell, and Eric Boerwinkle
- Detection of nonneutral substitution rates on mammalian phylogenies** 110^{OA}
Katherine S. Pollard, Melissa J. Hubisz, Kate R. Rosenbloom, and Adam Siepel
- Reconstructing ancestral gene content by coevolution** 122
Tamir Tuller, Hadas Birin, Uri Gophna, Martin Kupiec, and Eytan Ruppin

Resources

- A single-base resolution map of an archaeal transcriptome** 133
Omri Wurtzel, Rajat Sapra, Feng Chen, Yiwon Zhu, Blake A. Simmons, and Rotem Sorek
- ProPhyLER: A curated online resource for protein function and structure based on evolutionary constraint analyses** 142
Jonathan Binkley, Kalpana Karra, Andrew Kirby, Midori Hosobuchi, Eric A. Stone, and Arend Sidow

^{OA}Open Access paper.



Cover Suspended over a liver and sectioned liver tissue background are the structural formulas for acetaminophen (*right*) and S-methylmethionine (SMM) (*over lobe filled with capsules*). SMM, a Chinese herbal medicine and dietary metabolite abundant in all flowering plants, is the substrate of BHMT2, an enzyme identified to confer protection against acetaminophen-induced liver injury *in vivo*. (Cover illustration by Myriam Kirkman-Oh, KO Studios, <http://www.kostudios.com>. [For details, see Liu et al., pp. 28–35.]