

Articles

Research

Allele-specific gene expression patterns in primary leukemic cells reveal regulation of gene expression by CpG site methylation

1^{OA}

Lili Milani, Anders Lundmark, Jessica Nordlund, Anna Kiialainen, Trond Flaegstad, Gudmundur Jonmundsson, Jukka Kanerva, Kjeld Schmiegelow, Kevin L. Gunderson, Gudmar Lönnérholm, and Ann-Christine Syvänen

Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of *Pseudomonas aeruginosa*

12^{OA}

Craig Winstanley, Morgan G.I. Langille, Joanne L. Fothergill, Irena Kukavica-Ibrulj, Catherine Paradis-Bleau, François Sanschagrin, Nicholas R. Thomson, Geoff L. Winsor, Michael A. Quail, Nicola Lennard, Alexandra Bignell, Louise Clarke, Kathy Seeger, David Saunders, David Harris, Julian Parkhill, Robert E.W. Hancock, Fiona S.L. Brinkman, and Roger C. Levesque

Letters

Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains

24^{OA}

Suresh Cuddapah, Raja Jothi, Dustin E. Schones, Tae-Young Roh, Kairong Cui, and Keji Zhao

Comparative sequence analysis of primate subtelomeres originating from a chromosome fission event

33

M. Katharine Rudd, RaeLynn M. Endicott, Cynthia Friedman, Megan Walker, Janet M. Young, Kazutoyo Osoegawa, NISC Comparative Sequencing Program, Pieter J. de Jong, Eric D. Green, and Barbara J. Trask

Identification of miniature inverted-repeat transposable elements (MITEs) and biogenesis of their siRNAs in the Solanaceae: New functional implications for MITEs

42

Hanhui Kuang, Chellappan Padmanabhan, Feng Li, Ayako Kamei, Pudota B. Bhaskar, Shu Ouyang, Jiming Jiang, C. Robin Buell, and Barbara Baker

(continued)

	Novel long non-protein coding RNAs involved in <i>Arabidopsis</i> differentiation and stress responses	57
	Besma Ben Amor, Sonia Wirth, Francisco Merchan, Philippe Laporte, Yves d'Aubenton-Carafa, Judith Hirsch, Alexis Maizel, Allison Mallory, Antoine Lucas, Jean Marc Deragon, Herve Vaucheret, Claude Thermes, and Martin Crespi	
	Genome-wide identification and analysis of small RNAs originated from natural antisense transcripts in <i>Oryza sativa</i>	70
	Xuefeng Zhou, Ramanjulu Sunkar, Hailing Jin, Jian-Kang Zhu, and Weixiong Zhang	
	Principles of transcriptional regulation and evolution of the metabolic system in <i>E. coli</i>	79
	Aswin S.N. Seshasayee, Gillian M. Fraser, M. Madan Babu, and Nicholas M. Luscombe	
	Methods and Resources	
<i>Methods</i>	Most mammalian mRNAs are conserved targets of microRNAs	92^{OA}
	Robin C. Friedman, Kyle Kai-How Farh, Christopher B. Burge, and David P. Bartel	
	MSB: A mean-shift-based approach for the analysis of structural variation in the genome	106
	Lu-yong Wang, Alexej Abyzov, Jan O. Korbel, Michael Snyder, and Mark Gerstein	
	Targeted screening of <i>cis</i>-regulatory variation in human haplotypes	118
	Dominique J. Verlaan, Bing Ge, Elin Grundberg, Rose Hoberman, Kevin C.L. Lam, Vonda Koka, Joana Dias, Scott Gurd, Nicolas W. Martin, Hans Mallmin, Olof Nilsson, Eef Harmsen, Ken Dewar, Tony Kwan, and Tomi Pastinen	
	Ortho-proteogenomics: Multiple proteomes investigation through orthology and a new MS-based protocol	128
	Sébastien Gallien, Emmanuel Perrodou, Christine Carapito, Caroline Deshayes, Jean-Marc Reyrat, Alain Van Dorsselaer, Olivier Poch, Christine Schaeffer, and Odile Lecompte	
<i>Resources</i>	Fast and flexible simulation of DNA sequence data	136
	Gary K. Chen, Paul Marjoram, and Jeffrey D. Wall	
	genBlastA: Enabling BLAST to identify homologous gene sequences	143
	Rong She, Jeffrey S.-C. Chu, Ke Wang, Jian Pei, and Nansheng Chen	

(continued)

A resource for the simultaneous high-resolution mapping of multiple quantitative trait loci in rats: The NIH heterogeneous stock

150

Martina Johannesson, Regina Lopez-Aumatell, Pernilla Stridh, Margarita Diez, Jonatan Tuncel, Gloria Blázquez, Esther Martinez-Membrives, Toni Cañete, Elia Vicens-Costa, Delyth Graham, Richard R. Copley, Polinka Hernandez-Pliego, Amennai D. Beyeen, Johan Öckinger, Cristina Fernández-Santamaría, Percio S. Gulko, Max Brenner, Adolf Tobeña, Marc Guitart-Masip, Lydia Giménez-Llort, Anna Dominiczak, Rikard Holmdahl, Dominique Gauguier, Tomas Olsson, Richard Mott, William Valdar, Eva E. Redei, Alberto Fernández-Teruel, and Jonathan Flint

Dissecting the effects of mtDNA variations on complex traits using mouse conplastic strains

159

Xinhua Yu, Ulrike Gimsa, Lena Wester-Rosenlöf, Ellen Kanitz, Winfried Otten, Manfred Kunz, and Saleh M. Ibrahim

^{OA}Open Access paper.



Cover Selected vertebrate animals with complete genome sequences are shown as a collage of seeds. In this issue, 23 vertebrate genomes are compared in order to identify and quantify conserved microRNA targeting, which is mediated by matches to “seed” regions at the 5’ ends of microRNAs. In all, 60% of genes are conserved targets of broadly-conserved vertebrate microRNAs. (Illustration by Robin Friedman and Shannon McArdel. [For details, see Friedman et al., pp. 92–105.])