GENOME RESEARCH
Volume 17 Issue 2 February 2007

Commentary and Review

Review Multiple sequence alignment: In pursuit of homologous DNA positions 127
Sudhir Kumar and Alan Filipski

Research

Letters Serum response factor binding sites differ in three human cell types 136
Sara J. Cooper, Nathan D. Trinklein, Loan Nguyen, and Richard M. Myers

Characterization and predictive discovery of evolutionarily conserved mammalian alternative promoters 145^OA
Daehyun Baek, Colleen Davis, Brent Ewing, David Gordon, and Phil Green

Widespread mRNA polyadenylation events in introns indicate dynamic interplay between polyadenylation and splicing 156
Bin Tian, Zhenhua Pan, and Ju Youn Lee

Comparative genomic analysis identifies an evolutionary shift of vomeronasal receptor gene repertoires in the vertebrate transition from water to land 166
Peng Shi and Jianzhi Zhang

Curated genome annotation of *Oryza sativa* ssp. *japonica* and comparative genome analysis with *Arabidopsis thaliana* 175^OA
The Rice Annotation Project

Highly efficient concerted evolution in the ribosomal DNA repeats: Total rDNA repeat variation revealed by whole-genome shotgun sequence data 184
Austen R.D. Ganley and Takehiko Kobayashi

Reductive evolution and niche adaptation inferred from the genome of *Mycobacterium ulcerans*, the causative agent of Buruli ulcer 192
Timothy P. Stinear, Torsten Seemann, Sacha Pidot, Wafa Frigui, Gilles Reysset, Thierry Garnier, Guillaume Meurice, David Simon, Christiane Bouchier, Laurence Ma, Magali Tichit, Jessica L. Porter, Janine Ryan, Paul D.R. Johnson, John K. Davies, Grant A. Jenkin, Pamela L.C. Small, Louis M. Jones, Fredj Tekaia, Françoise Laval, Mamadou Daffé, Julian Parkhill, and Stewart T. Cole

Methods and Resources

Methods Predicting tissue-specific enhancers in the human genome 201^OA
Len A. Pennacchio, Gabriela G. Loots, Marcelo A. Nobrega, and Ivan Ovcharenko

(continued)

A tale of two templates: Automatically resolving double traces has many applications, including efficient PCR-based elucidation of alternative splices 212
Aaron E. Tenney, Jia Qian Wu, Laura Langton, Paul Klueh, Ralph Quatrano, and Michael R. Brent

Evidence for large inversion polymorphisms in the human genome from HapMap data 219
Vikas Bansal, Ali Bashir, and Vineet Bafna

Improving gene annotation using peptide mass spectrometry 231
Stephen Tanner, Zhouxin Shen, Julio Ng, Liliana Florea, Roderic Guigó, Steven P. Briggs, and Vineet Bafna

Rapid and cost-effective polymorphism identification and genotyping using restriction site associated DNA (RAD) markers 240
Michael R. Miller, Joseph P. Dunham, Angel Amores, William A. Cresko, and Eric A. Johnson

Resources

Molecular refinement of gibbon genome rearrangements 249
Roberta Roberto, Oronzo Capozzi, Richard K. Wilson, Elaine R. Mardis, Mariana Lomiento, Eray Tuzun, Ze Cheng, Alan R. Mootnick, Nicoletta Archidiacono, Mariano Rocchi, and Evan E. Eichler

OAOpen Access paper.

Cover Deciphering of the genetic code of distant, tissue-specific enhancers in the human genome by the Enhancer Identification (EI) method. EI approach is based on the integration of multiple complementary computational approaches and genomic datasets that include (a) microarray multi-tissue gene expression data, (b) comparative genomics analysis of human and mouse genomes, and (c) analysis of patterns of transcription factor binding sites (TFBS). In summary, this advance in deciphering the so-called second code of the human genome promotes the ongoing foray into the mapping of human gene regulatory networks. (Cover illustration by Bang Wong, ClearScience, www.clearscience.info. [For details, see Pennacchio et al., pp. 201–211.])