Research

The mutational spectrum of non-CpG DNA varies with CpG content 875
Jean-Claude Walser and Anthony V. Furano

Allele-specific methylation is prevalent and is contributed by CpG-SNPs in the human genome 883
Robert Shoemaker, Jie Deng, Wei Wang, and Kun Zhang

Sequence features that drive human promoter function and tissue specificity 890
Jane M. Landolin, David S. Johnson, Nathan D. Trinklein, Shelly F. Aldred, Catherine Medina, Hennady Shulha, Zhiping Weng, and Richard M. Myers

Characterization of the RNA content of chromatin 899OA
Tanmoy Mondal, Markus Rasmussen, Gaurav Kumar Pandey, Anders Isaksson, and Chandrasekhar Kanduri

Complete mitochondrial genome phylogeographic analysis of killer whales (Orcinus orca) indicates multiple species 908
Phillip A. Morin, Frederick I. Archer, Andrew D. Foote, Julia Vilstrup, Eric E. Allen, Paul Wade, John Durban, Kim Parsons, Robert Pitman, Lewyn Li, Pascal Bouffard, Sandra C. Abel Nielsen, Morten Rasmussen, Eske Willerslev, M. Thomas P. Gilbert, and Timothy Harkins

Evolution of a genomic regulatory domain: The role of gene co-option and gene duplication in the Enhancer of split complex 917
Elizabeth J. Duncan and Peter K. Dearden

Genome-wide gene expression regulation as a function of genotype and age in C. elegans 929OA
Ana Vinuéla, L. Basten Snoek, Joost A.G. Riksen, and Jan E. Kammenga

Population genomic sequencing of Coccidioides fungi reveals recent hybridization and transposon control 938

(continued)
A global network of coexisting microbes from environmental and whole-genome sequence data
Samuel Chaffron, Hubert Rehrauer, Jakob Pernthaler, and Christian von Mering

Methods
Analysis of membrane proteins in metagenomics: Networks of correlated environmental features and protein families
Prianka V. Patel, Tara A. Gianoulis, Robert D. Bjornson, Kevin Y. Yip, Donald M. Engelman, and Mark B. Gerstein

Chromatin and sequence features that define the fine and gross structure of genomic methylation patterns
John R. Edwards, Anne H. O'Donnell, Robert A. Rollins, Heather E. Peckham, Clarence Lee, Maria H. Milekic, Benjamin Chanrion, Yutao Fu, Tao Su, Hanina Hibshoosh, Jay A. Gingrich, Fatemeh Haghighi, Robert Nutter, and Timothy H. Bestor

Rapid identification of heterozygous mutations in Drosophila melanogaster using genomic capture sequencing
Hui Wang, Abanti Chattopadhyay, Zhe Li, Bryce Daines, Yumei Li, Chunxu Gao, Richard Gibbs, Kun Zhang, and Rui Chen

Strand-specific deep sequencing of the transcriptome
Ana P. Vivancos, Marc Güell, Juliane C. Dohm, Luis Serrano, and Heinz Himmelbauer

OAOpen Access paper.

Cover Adapted image of sea surface temperature (NASA) showing environmental variation across the ocean through a color gradient. Sea surface temperature represents one of the 15 features used in a study correlating environmental variation with different types of membrane protein families in metagenomic sequence data from the Global Ocean Sampling Expedition. (Cover illustration by Prianka Patel and Tara Gianoulis. [For details, see Patel et al., pp. 960–971.])