Commentary and Review

Reviews

Synthetic biology projects in vitro
Anthony C. Forster and George M. Church

Research

Articles

Genome characteristics of facultatively symbiotic Frankia sp. strains reflect host range and host plant biogeography
Philippe Normand, Pascal Lapierre, Louis S. Tisa,
Johann Peter Gogarten, Nicole Alloisio, Emilie Bagnarol,
Carla A. Bassi, Alison M. Berry, Derek M. Bickhart, Nathalie Choisne,
Arnaud Couloux, Benoît Cournoyer, Stéphane Cruveiller,
Vincent Daubin, Nadia Demange, Maria Pilar Francino,
Eugene Goltsman, Ying Huang, Olga R. Kopp, Laurent Labarre,
Alla Lapidus, Celine Lavire, Joelle Marechal, Michele Martinez,
Juliana E. Mastronunzio, Beth C. Mullin, James Niemann,
Pierre Pujic, Tania Rawsley, Zoe Rouy, Chantal Schenowitz,
Anita Sellstedt, Fernando Tavares, Jeffrey P. Tomkins, David Vallenet,
Claudio Valverde, Luis G. Wall, Ying Wang, Claudine Medigue,
and David R. Benson

Letters

Human-specific insertions and deletions inferred from mammalian genome sequences
Feng-Chi Chen, Chueng-Jong Chen, Wen-Hsiung Li,
and Trees-Juen Chuang

Characterization of intron loss events in mammals
Jasmin Coulombe-Huntington and Jacek Majewski

Novel retrotransposon analysis reveals multiple mobility pathways dictated by hosts
Kenji Ichiyanaagi, Ryo Nakajima, Masaki Kajikawa,
and Norihiro Okada

Contrasting evolution of expression differences in the testis between species and subspecies of the house mouse
Christian Voolstra, Diethard Tautz, Patrick Farbrother,
Ludwig Eichinger, and Bettina Harr

Evolution of Chlamydia trachomatis diversity occurs by widespread interstrain recombination involving hotspots
João P. Gomes, William J. Bruno, Alexandra Nunes, Nicole Santos,
Carlos Florindo, Maria J. Borrego, and Deborah Dean

A bimodal pattern of relatedness between the Salmonella Paratyphi A and Typhi genomes: Convergence or divergence by homologous recombination?
Xavier Didelot, Mark Achtman, Julian Parkhill, Nicholas R. Thomson,
and Daniel Falush

(continued)
**Methods and Resources**

**Methods**

Gene discovery and annotation using LCM-454 transcriptome sequencing
Scott J. Emrich, W. Brad Barbazuk, Li Li, and Patrick S. Schnable

Genome-wide prediction of conserved and nonconserved enhancers by histone acetylation patterns
Tae-young Roh, Gang Wei, Catherine M. Farrell, and Keji Zhao

Localization of a long-range cis-regulatory element of IL13 by allelic transcript ratio mapping
Julian T. Forton, Irina A. Udalova, Susana Campino, Kirk A. Rockett, Jeremy Hull, and Dominic P. Kwiatkowski

A model-based approach to capture genetic variation for future association studies
Susana Eyheramendy, Jonathan Marchini, Gilean McVean, Simon Myers, and Peter Donnelly

Intra- and interpopulation genotype reconstruction from tagging SNPs

Large-scale production of SAGE libraries from microdissected tissues, flow-sorted cells, and cell lines
Jaswinder Khattra, Allen D. Delaney, Yongjun Zhao, Asim Siddiqui, Jennifer Asano, Helen McDonald, Pawan Pandoh, Noreen Dhalla, Anna-Iliasa Prabhu, Kevin Ma, Stephanie Lee, Adrian Ally, Angela Tam, Danne Sa, Sean Rogers, David Charest, Jeff Stott, Scott Zuyderduyn, Richard Varhol, Connie Eaves, Steven Jones, Robert Holt, Martin Hirst, Pamela A. Hoodless, and Marco A. Marra

**Resources**

Exploring genomic dark matter: A critical assessment of the performance of homology search methods on noncoding RNA
Eva K. Freyhult, Jonathan P. Bollback, and Paul P. Gardner

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**Cover**

Three-dimensional structures of 144 of the 151 macromolecules from *E. coli* predicted to enable self-replication in vitro from 31 small-molecule substrates: RNAs (orange), DNA template strands (teal), DNA–mRNA strands (aquamarine), and proteins (pink). Aminoacyl-tRNA synthetases, tRNAs, and release factors are organized in the middle according to the standard genetic code grid. RNA and protein modification enzymes are positioned near their substrates. The system is drawn to scale with one turn of the DNA being 3.4 nm. Two kilobase pairs of the 113-kbp DNA genome are shown and all mRNAs are omitted. Homology models, when employed, are very rough. This and other in vitro synthetic biology projects are reviewed in Forster and Church, pp. 1–6. (Cover illustration by George Church.)