

| | | |
|--------------------|--|-----|
| | Commentary and Review | |
| <i>Commentary</i> | Confidence in comparative genomics Elliott H. Margulies | 199 |
| <i>Perspective</i> | Qualifying the relationship between sequence conservation and molecular function Gregory M. Cooper and Christopher D. Brown | 201 |
| | Research | |
| <i>Letters</i> | Quantitative systems-level determinants of human genes targeted by successful drugs Lixia Yao and Andrey Rzhetsky | 206 |
| | Alternative approach to a heavy weight problem Amir Goren, Eddo Kim, Maayan Amit, Ron Bochner, Galit Lev-Maor, Nadav Ahituv, and Gil Ast | 214 |
| | Gene number expansion and contraction in vertebrate genomes with respect to invertebrate genomes Anuphap Prachumwat and Wen-Hsiung Li | 221 |
| | Genome-wide analysis reveals regulatory role of G4 DNA in gene transcription Zhuo Du, Yiqiang Zhao, and Ning Li | 233 |
| | Comparative genomics beyond sequence-based alignments: RNA structures in the ENCODE regions Elfar Torarinsson, Zizhen Yao, Eric D. Wiklund, Jesper B. Bramsen, Claus Hansen, Jørgen Kjems, Niels Tommerup, Walter L. Ruzzo, and Jan Gorodkin | 242 |
| | Metrics of sequence constraint overlook regulatory sequences in an exhaustive analysis at <i>phox2b</i> David M. McGaughey, Ryan M. Vinton, Jimmy Huynh, Amr Al-Saif, Michael A. Beer, and Andrew S. McCallion | 252 |
| | Controlled exchange of chromosomal arms reveals principles driving telomere interactions in yeast Heiko Schober, Véronique Kalck, Miguel A. Vega-Palas, Griet Van Houwe, Daniel Sage, Michael Unser, Marc R. Gartenberg, and Susan M. Gasser | 261 |
| | <i>Wolbachia</i> genome integrated in an insect chromosome: Evolution and fate of laterally transferred endosymbiont genes Naruo Nikoh, Kohjiro Tanaka, Fukashi Shibata, Natsuko Kondo, Masahiro Hizume, Masakazu Shimada, and Takema Fukatsu | 272 |

(continued)

Genome-wide discovery and verification of novel structured RNAs in *Plasmodium falciparum* 281^{OA}

Tobias Mourier, Celine Carret, Sue Kyes, Zoe Christodoulou, Paul P. Gardner, Daniel C. Jeffares, Robert Pinches, Bart Barrell, Matt Berriman, Sam Griffiths-Jones, Alasdair Ivens, Chris Newbold, and Arnab Pain

A bacterial metapopulation adapts locally to phage predation despite global dispersal 293^{OA}

Victor Kunin, Shaomei He, Falk Warnecke, S. Brook Peterson, Hector Garcia Martin, Matthew Haynes, Natalia Ivanova, Linda L. Blackall, Mya Breitbart, Forest Rohwer, Katherine D. McMahon, and Philip Hugenholtz

Methods and Resources

Methods

Uncertainty in homology inferences: Assessing and improving genomic sequence alignment 298

Gerton Lunter, Andrea Rocco, Naila Mimouni, Andreas Heger, Alexandre Caldeira, and Jotun Hein

Generic eukaryotic core promoter prediction using structural features of DNA 310

Thomas Abeel, Yvan Saeys, Eric Bonnet, Pierre Rouzé, and Yves Van de Peer

Short read fragment assembly of bacterial genomes 324

Mark J. Chaisson and Pavel A. Pevzner

Resolving the structural features of genomic islands: A machine learning approach 331

Georgios S. Vernikos and Julian Parkhill

^{OA}Open Access paper



Cover Visual representation of two phenotype-related gene clusters within a large molecular network. These phenotype-associated genes are potential candidates for drug targeting. Each of the graph nodes corresponds to a gene; an edge between nodes depicts a functional relationship between the respective genes. The different colors of the network edges reflect the multitude of possible functional relationships between genes: There are hundreds of common molecular relation types. For example, one gene can transcriptionally regulate another; two genes can encode two proteins forming a complex; or one gene-encoded protein can phosphorylate, acylate, cleave, methylate, and glycosylate another protein. The red and the green areas represent two disease-related gene clusters. (Cover illustration by Andrey Rzhetsky. [For details, see Yao and Rzhetsky, pp. 206–213.])