

Research

- Hominoid fission of chromosome 14/15 and the role of segmental duplications** 1763
Giuliana Giannuzzi, Michele Pazienza, John Huddleston, Francesca Antonacci, Maika Malig, Laura Vives, Evan E. Eichler, and Mario Ventura
- Bubble-seq analysis of the human genome reveals distinct chromatin-mediated mechanisms for regulating early- and late-firing origins** 1774
Larry D. Mesner, Veena Valsakumar, Marcin Cieřlik, Rebecca Pickin, Joyce L. Hamlin, and Stefan Bekiranov
- RNA–DNA differences in human mitochondria restore ancestral form of 16S ribosomal RNA** 1789
Dan Bar-Yaacov, Gal Avital, Liron Levin, Allison L. Richards, Naomi Hachen, Boris Rebolledo Jaramillo, Anton Nekrutenko, Raz Zarivach, and Dan Mishmar
- Oncogenic ETS fusions deregulate E2F3 target genes in Ewing sarcoma and prostate cancer** 1797^{OA}
Sven Bilke, Raphaela Schwentner, Fan Yang, Maximilian Kauer, Gunhild Jug, Robert L. Walker, Sean Davis, Yuelin J. Zhu, Marbin Pineda, Paul S. Meltzer, and Heinrich Kovar
- The evolution of evolvability in microRNA target sites in vertebrates** 1810
Jin Xu, Rui Zhang, Yang Shen, Guojing Liu, Xuemei Lu, and Chung-I Wu
- Genome-wide evidence for speciation with gene flow in *Heliconius* butterflies** 1817
Simon H. Martin, Kanchon K. Dasmahapatra, Nicola J. Nadeau, Camilo Salazar, James R. Walters, Fraser Simpson, Mark Blaxter, Andrea Manica, James Mallet, and Chris D. Jiggins
- High-throughput chromatin motion tracking in living yeast reveals the flexibility of the fiber throughout the genome** 1829
Houssam Hajjoul, Julien Mathon, Hubert Ranchon, Isabelle Goiffon, Julien Mozziconacci, Benjamin Albert, Pascal Carrivain, Jean-Marc Victor, Olivier Gadal, Kerstin Bystricky, and Aurélien Bancaud
- A systems level predictive model for global gene regulation of methanogenesis in a hydrogenotrophic methanogen** 1839^{OA}
Sung Ho Yoon, Serdar Turkarslan, David J. Reiss, Min Pan, June A. Burn, Kyle C. Costa, Thomas J. Lie, Joseph Slagel, Robert L. Moritz, Murray Hackett, John A. Leigh, and Nitin S. Baliga

Methods

- Estimating inbreeding coefficients from NGS data: Impact on genotype calling and allele frequency estimation** 1852
Filipe G. Vieira, Matteo Fumagalli, Anders Albrechtsen, and Rasmus Nielsen

(continued)

- Defining cell-type specificity at the transcriptional level in human disease** 1862
 Wenjun Ju, Casey S. Greene, Felix Eichinger, Viji Nair, Jeffrey B. Hodgkin, Markus Bitzer, Young-suk Lee, Qian Zhu, Masami Kehata, Min Li, Song Jiang, Maria Pia Rastaldi, Clemens D. Cohen, Olga G. Troyanskaya, and Matthias Kretzler
- Network properties derived from deep sequencing of human B-cell receptor repertoires delineate B-cell populations** 1874^{OA}
 Rachael J.M. Bashford-Rogers, Anne L. Palsler, Brian J. Huntly, Richard Rance, George S. Vassiliou, George A. Follows, and Paul Kellam
- Analysis and correction of crosstalk effects in pathway analysis** 1885
 Michele Donato, Zhonghui Xu, Alin Tomoiaga, James G. Granneman, Robert G. MacKenzie, Riyue Bao, Nandor Gabor Than, Peter H. Westfall, Roberto Romero, and Sorin Draghici
- Efficient identification of Y chromosome sequences in the human and *Drosophila* genomes** 1894
 Antonio Bernardo Carvalho and Andrew G. Clark
- Massively parallel synthetic promoter assays reveal the in vivo effects of binding site variants** 1908
 Ilaria Mogno, Jamie C. Kwasnieski, and Barak A. Cohen
- Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome** 1916
 Ulrich Omasits, Maxime Quebatte, Daniel J. Stekhoven, Claudia Fortes, Bernd Roschitzki, Mark D. Robinson, Christoph Dehio, and Christian H. Ahrens
- Resources**
- Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach** 1928
 Pablo Meyer, Geoffrey Siwo, Danny Zeevi, Eilon Sharon, Raquel Norel, DREAM6 Promoter Prediction Consortium, Eran Segal, and Gustavo Stolovitzky
- Dynamic regulation of the transcription initiation landscape at single nucleotide resolution during vertebrate embryogenesis** 1938
 Chirag Nepal, Yavor Hadzhiev, Christopher Previti, Vanja Haberle, Nan Li, Hazuki Takahashi, Ana Maria M. Suzuki, Ying Sheng, Rehab F. Abdelhamid, Santosh Anand, Jochen Gehrig, Altuna Akalin, Christel E.M. Kockx, Antoine A.J. van der Sloot, Wilfred F.J. van IJcken, Olivier Armant, Sepand Rastegar, Craig Watson, Uwe Strähle, Elia Stupka, Piero Carninci, Boris Lenhard, and Ferenc Müller
- Honey bee protein atlas at organ-level resolution** 1951
 Queenie W.T. Chan, Man Yi Chan, Michelle Logan, Yuan Fang, Heather Higo, and Leonard J. Foster

^{OA}Open Access paper



Cover Drawing illustrates the concept of crowdsourcing to solve the code that relates DNA sequences to promoter activities. Trucks represent the participants of the DREAM6 Gene Promoter Expression Prediction challenge, each contributing different sequence features that predict RNA expression. RNA expression levels are denoted by the different number of RNA molecules carried by the trucks. These contributions are integrated via the crane on top of a chromosome. The crane represents the “machine-learning” approach that transforms the DNA sequences brought by the participants (and present in the chromosome) into promoter activities (i.e., the crane transporting RNA into the trucks), hence closing the loop of knowledge. (Cover illustration by Ricardo Cid, <http://blacklabelrobot.com>. [For details, see Meyer et al., pp. 1928–1937.]