

## Research

- Genome-wide map of regulatory interactions in the human genome** 1905<sup>OA</sup>  
Nastaran Heidari, Douglas H. Phanstiel, Chao He, Fabian Grubert, Fereshteh Jahanbani, Maya Kasowski, Michael Q. Zhang, and Michael P. Snyder
- Population and single-cell genomics reveal the *Aire* dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia** 1918<sup>OA</sup>  
Stephen N. Sansom, Noriko Shikama-Dorn, Saule Zhanybekova, Gretel Nusspaumer, Iain C. Macaulay, Mary E. Deadman, Andreas Heger, Chris P. Ponting, and Georg A. Holländer
- Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis** 1932<sup>OA</sup>  
Maxim Pimkin, Andrew V. Kossenkov, Tejaswini Mishra, Christopher S. Morrissey, Weisheng Wu, Cheryl A. Keller, Gerd A. Blobel, Dongwon Lee, Michael A. Beer, Ross C. Hardison, and Mitchell J. Weiss
- Dynamic shifts in occupancy by TALI are guided by GATA factors and drive large-scale reprogramming of gene expression during hematopoiesis** 1945<sup>OA</sup>  
Weisheng Wu, Christopher S. Morrissey, Cheryl A. Keller, Tejaswini Mishra, Maxim Pimkin, Gerd A. Blobel, Mitchell J. Weiss, and Ross C. Hardison
- Widespread contribution of transposable elements to the innovation of gene regulatory networks** 1963  
Vasavi Sundaram, Yong Cheng, Zhihai Ma, Daofeng Li, Xiaoyun Xing, Peter Edge, Michael P. Snyder, and Ting Wang
- Transposable element dynamics and PIWI regulation impacts lncRNA and gene expression diversity in *Drosophila* ovarian cell cultures** 1977  
Yuliya A. Sytnikova, Reazur Rahman, Gung-wei Chirn, Josef P. Clark, and Nelson C. Lau
- Molecular dissection of the genetic mechanisms that underlie expression conservation in orthologous yeast ribosomal promoters** 1991  
Danny Zeevi, Shai Lubliner, Maya Lotan-Pompan, Eran Hodis, Rita Vesterman, Adina Weinberger, and Eran Segal
- Heritable variation of mRNA decay rates in yeast** 2000  
Jennifer M. Andrie, Jon Wakefield, and Joshua M. Akey
- Accounting for biases in riboprofiling data indicates a major role for proline in stalling translation** 2011  
Carlo G. Artieri and Hunter B. Fraser

(continued)

## Methods

- DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly 2022<sup>OA</sup>  
Ilari Scheinin, Daoud Sie, Henrik Bengtsson, Mark A. van de Wiel, Adam B. Olshen, Hinke F. van Thuijl, Hendrik F. van Essen, Paul P. Eijk, François Rustenburg, Gerrit A. Meijer, Jaap C. Reijneveld, Pieter Wesseling, Daniel Pinkel, Donna G. Albertson, and Bauke Ylstra
- Tn5 transposase and tagmentation procedures for massively scaled sequencing projects 2033<sup>OA</sup>  
Simone Picelli, Åsa K. Björklund, Björn Reinius, Sven Sagasser, Gösta Winberg, and Rickard Sandberg
- In vitro, long-range sequence information for de novo genome assembly via transposase contiguity 2041  
Andrew Adey, Jacob O. Kitzman, Joshua N. Burton, Riza Daza, Akash Kumar, Lena Christiansen, Mostafa Ronaghi, Sasan Amini, Kevin L. Gunderson, Frank J. Steemers, and Jay Shendure
- A formal perturbation equation between genotype and phenotype determines the Evolutionary Action of protein-coding variations on fitness 2050<sup>OA</sup>  
Panagiotis Katsonis and Olivier Lichtarge
- Megabase-scale deletion using CRISPR/Cas9 to generate a fully haploid human cell line 2059  
Patrick Essletzbichler, Tomasz Konopka, Federica Santoro, Doris Chen, Bianca V. Gapp, Robert Kralovics, Thijn R. Brummelkamp, Sebastian M.B. Nijman, and Tilmann Bürckstümmer

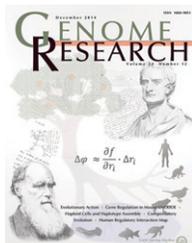
## Resources

- Single haplotype assembly of the human genome from a hydatidiform mole 2066  
Karyn Meltz Steinberg, Valerie A. Schneider, Tina A. Graves-Lindsay, Robert S. Fulton, Richa Agarwala, John Huddleston, Sergey A. Shiryev, Aleksandr Morgulis, Urvashi Surti, Wesley C. Warren, Deanna M. Church, Evan E. Eichler, and Richard K. Wilson
- Alignathon: a competitive assessment of whole-genome alignment methods 2077<sup>OA</sup>  
Dent Earl, Ngan Nguyen, Glenn Hickey, Robert S. Harris, Stephen Fitzgerald, Kathryn Beal, Igor Seledtsov, Vladimir Molodtsov, Brian J. Raney, Hiram Clawson, Jaebum Kim, Carsten Kemena, Jia-Ming Chang, Ionas Erb, Alexander Poliakov, Minmei Hou, Javier Herrero, William James Kent, Victor Solovyev, Aaron E. Darling, Jian Ma, Cedric Notredame, Michael Brudno, Inna Dubchak, David Haussler, and Benedict Paten

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<sup>OA</sup>Open Access paper



**Cover** Every mutation triggers an unknown cascade of molecular events, limiting our understanding of the fitness effect of genetic variations and thus, the impact of clinical sequencing. In this issue, a formal approach to this problem is presented. In the illustration, Sir Isaac Newton, an apple tree, and planetary orbits symbolize the laws of physics and math; Charles Darwin, the tree of life; and his original sketch and writings symbolize the laws of evolution. At the junction of the two trees, composed of nucleotide sequences, the Evolutionary Action equation unites these laws to express the genotype to phenotype relationship as a perturbation process. The terms of this equation can be evaluated and yield the fitness effect of genetic variations at the heart of evolution. (Cover illustration by Teng-Kuei Hsu. [For details, see Katsonis and Lichtarge, pp. 2050–2058.]