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Research

Genome-wide map of regulatory interactions in the human genome 1905 OA
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 OA
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 OA
Maxim Pimkin, Andrew V. Kossenkov, Tejaswini Mishra, Christapher 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 TAL1 are guided by GATA factors and drive large-scale reprogramming of gene expression during hematopoiesis 1945 OA
Weisheng Wu, Christapher 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[OA]
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[OA]
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[OA]
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[OA]
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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[OA]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.])