Research

The landscape of genomic imprinting across diverse adult human tissues
Yael Baran, Meena Subramaniam, Anne Biton, Taru Tukiainen, Emily K. Tsang, Manuel A. Rivas, Matti Pirinen, Maria Gutierrez-Arcelus, Kevin S. Smith, Kim R. Kukurba, Rui Zhang, Celeste Eng, Dara G. Torgerson, Cydney Urbanek, the GTEx Consortium, Jin Billy Li, Jose R. Rodriguez-Santana, Esteban G. Burchard, Max A. Seibold, Daniel G. MacArthur, Stephen B. Montgomery, Noah A. Zeitlen, and Tuuli Lappalainen

Unbalanced translocations arise from diverse mutational mechanisms including chromothripsis
Brooke Weckselblatt, Karen E. Hermetz, and M. Katharine Rudd

Exome sequencing reveals pathogenic mutations in 91 strains of mice with Mendelian disorders

Characterization and dynamics of pericentromere-associated domains in mice
Patrick J. Wijchers, Geert Geeven, Michael Eyres, Atze J. Bergsma, Mark Janssen, Marjon Verstegen, Yun Zhu, Yori Schell, Carlo Vermeulen, Elzo de Wit, and Wouter de Laat

Using genome-wide measures of coancestry to maintain diversity and fitness in endangered and domestic pig populations
Mirte Bosse, Hendrik-Jan Megens, Ole Madsen, Richard P.M.A. Crooijmans, Oliver A. Ryder, Frédéric Austerlitz, Martien A.M. Groenen, and M. Angeles R. de Cara

Coordinated tissue-specific regulation of adjacent alternative 3′ splice sites in C. elegans
James Matthew Ragle, Sol Katzman, Taylor F. Akers, Sergio Barberan-Soler, and Alan M. Zahler

Unmasking alternative splicing inside protein-coding exons defines exitrons and their role in proteome plasticity
Yamile Marquez, Markus Höpfler, Zahra Ayatollahi, Andrea Barta, and Maria Kalyna

Core promoter sequence in yeast is a major determinant of expression level
Shai Lubliner, Ifat Regev, Maya Lotan-Pompan, Sarit Edelheit, Adina Weinberger, and Eran Segal

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Methods

Unraveling determinants of transcription factor binding outside the core binding site
Michal Levo, Einat Zalckvar, Eilon Sharon, Ana Carolina Dantas Machado, Yael Kalma, Maya Lotam-Pompan, Adina Weinberger, Zohar Yakhini, Remo Rohs, and Eran Segal

High-throughput gene targeting and phenotyping in zebrafish using CRISPR/Cas9
Gaurav K. Varshney, Wuhong Pei, Matthew C. LaFave, Jennifer Idol, Lisha Xu, Viviana Gallardo, Blake Carrington, Kevin Bishop, MaryPat Jones, Mingyu Li, Ursula Harper, Sunny C. Huang, Anupam Prakash, Wenbiao Chen, Raman Sood, Johan Ledin, and Shawn M. Burgess

CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes
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Using populations of human and microbial genomes for organism detection in metagenomes
Sasha K. Ames, Shea N. Gardner, Jose Manuel Marti, Tom R. Slezak, Maya B. Gokhale, and Jonathan E. Allen

The landscape of antisense gene expression in human cancers
O. Alejandro Balbin, Rohit Malik, Saravana M. Dhanasekaran, John R. Prensner, Xuhong Cao, Yi-Mi Wu, Dan Robinson, Rui Wang, Guoan Chen, David G. Beer, Alexey I. Nesvizhskii, and Arul M. Chinnaiyan

Cover
Alternative splicing is a key mechanism in controlling gene expression and is a major source of proteome complexity in eukaryotes. In this issue, a study describes an often overlooked facet of alternative splicing—exitron splicing. Exitrons (exonic introns) are internal parts of protein-coding exons that are alternatively spliced and thus contribute to proteome plasticity. The cover image is a kaleidoscopic view of the proteome, reflecting the diversity generated by alternative splicing. Radial shapes illustrate protein isoforms with variable domain compositions. The circles depict developmental stages and environmental conditions modulating alternative splicing outcomes. (Cover illustration by Maria Kalyna. [For details, see Marquez et al., pp. 995–1007.])

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