

## Research

- Experimental and pan-cancer genome analyses reveal widespread contribution of acrylamide exposure to carcinogenesis in humans** 521<sup>OA</sup>  
Maria Zhivagui, Alvin W.T. Ng, Maude Ardin, Mona I. Churchwell, Manuraj Pandey, Claire Renard, Stephanie Villar, Vincent Cahais, Alexis Robitaille, Liacine Bouaoun, Adriana Heguy, Kathryn Z. Guyton, Martha R. Stampfer, James McKay, Monica Hollstein, Magali Olivier, Steven G. Rozen, Frederick A. Beland, Michael Korenjak, and Jiri Zavadil
- Coexpression patterns define epigenetic regulators associated with neurological dysfunction** 532<sup>OA</sup>  
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- Cohesin occupancy and composition at enhancers and promoters are linked to DNA replication origin proximity in *Drosophila*** 602<sup>OA</sup>  
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Chromatin architecture reorganization during neuronal cell differentiation in *Drosophila* genome 613<sup>OA</sup>  
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Detection of vancomycin-resistant *Enterococcus faecium* hospital-adapted lineages in municipal wastewater treatment plants indicates widespread distribution and release into the environment 626<sup>OA</sup>  
Theodore Gouliouris, Kathy E. Raven, Danesh Moradigaravand, Catherine Ludden, Francesc Coll, Beth Blane, Plamena Naydenova, Carolyne Horner, Nicholas M. Brown, Jukka Corander, Direk Limmathurotsakul, Julian Parkhill, and Sharon J. Peacock

## Methods

Resolving the full spectrum of human genome variation using Linked-Reads 635<sup>OA</sup>  
Patrick Marks, Sarah Garcia, Alvaro Martinez Barrio, Kamila Belhocine, Jorge Bernate, Rajiv Bharadwaj, Keith Bjornson, Claudia Catalanotti, Josh Delaney, Adrian Fehr, Ian T. Fiddes, Brendan Galvin, Haynes Heaton, Jill Herschleb, Christopher Hindson, Esty Holt, Cassandra B. Jabara, Susanna Jett, Nikka Keivanfar, Sofia Kyriazopoulou-Panagiotopoulou, Monkol Lek, Bill Lin, Adam Lowe, Shazia Mahamdallie, Shamoni Maheshwari, Tony Makarewicz, Jamie Marshall, Francesca Meschi, Christopher J. O'Keefe, Heather Ordonez, Pranav Patel, Andrew Price, Ariel Royall, Elise Ruark, Sheila Seal, Michael Schnall-Levin, Preyas Shah, David Stafford, Stephen Williams, Indira Wu, Andrew Wei Xu, Nazneen Rahman, Daniel MacArthur, and Deanna M. Church

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Identification of human silencers by correlating cross-tissue epigenetic profiles and gene expression 657<sup>OA</sup>  
Di Huang, Hanna M. Petrykowska, Brendan F. Miller, Laura Elnitski, and Ivan Ovcharenko

Improved discovery of genetic interactions using CRISPRiSeq across multiple environments 668<sup>OA</sup>  
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Remodeling of epigenome and transcriptome landscapes with aging in mice reveals widespread induction of inflammatory responses 697<sup>OA</sup>  
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## Corrigenda

Corrigendum: H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells

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Agustín F. Fernández, Gustavo F. Bayón, Rocío G. Urduñigo, Estela G. Toraño, María G. García, Antonella Carella, Sandra Petrus-Reurer, Cecilia Ferrero, Pablo Martínez-Camblor, Isabel Cubillo, Javier García-Castro, Jesús Delgado-Calle, Flor M. Pérez-Campo, José A. Riancho, Clara Bueno, Pablo Menéndez, Anouk Mentink, Katia Mareschi, Fabian Claire, Corrado Fagnani, Emanuela Medda, Virgilia Toccaceli, Sonia Brescianini, Sebastián Moran, Manel Esteller, Alexandra Stolzing, Jan de Boer, Lorenza Nisticò, Maria A. Stazi, and Mario F. Fraga

Corrigendum: Initiation of mtDNA transcription is followed by pausing, and diverges across human cell types and during evolution

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Amit Blumberg, Edward J. Rice, Anshul Kundaje, Charles G. Danko, and Dan Mishmar

<sup>OA</sup>Open Access paper



**Cover** The changes in the 3D organization of chromatin after differentiation in *Drosophila* cell lines are illustrated. Topologically associating domains (TADs; represented by yellow pyramids) are associated with both divergent transcription at their borders (represented by taller ancient Egyptian men pointing to the direction of transcription) and active transcription by RNA polymerase II (represented by working men in white loincloths). In embryonic cells (top row), the TAD borders are separated by an architectural protein called BEAF-32 (represented by ibis birds). Upon differentiation in neuronal cells (middle row), BEAF-32 is reduced and replaced by CTCF (represented by Sphinx cats), leading to only a subset of TAD borders being maintained and the appearance of larger TADs (bottom row). (Cover artwork by Liudmila Mikheeva, lm17047@essex.ac.uk. [For details, see Chathoth et al., pp. 613–625.]