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FORTHCOMING PAPERS

Review

Alternative polyadenylation: New insights from global analyses

Yongsheng Shi

Letter to the Editor

Crystal structure of the primary piRNA biogenesis factor Zucchini reveals similarity to the bacterial PLD endonuclease Nuc

Franka Voigt, Michael Reuter, Anisa Kasaruho, Eike C. Schulz, Ramesh S. Pillai, and Orsolya Barabas

Reports

An RNAi screen identifies additional members of the *Drosophila* integrator complex and a requirement for cyclin C/Cdk8 in snRNA 3' end formation

Jiandong Chen, Nader Ezzeddine, Bernhard Waltenspiel, Todd R. Albrecht, William D. Warren, William F. Marzluff, and Eric J. Wagner

Activation of PKR by RNA misfolding: HDV ribozyme dimers activate PKR

Laurie A. Heinicke and Philip C. Bevilacqua

Articles

Twist-joints and double twist-joints in RNA structure

Yury I. Boutorine and Sergey V. Steinberg

Cotranscriptional splicing efficiency differs dramatically between *Drosophila* and mouse

Yevgenia L. Khodor, Jerome S. Menet, Michael Tolan, and Michael Rosbash

Inhibition of polyadenylation reduces inflammatory gene induction

Alexander Kondrashov, Hedda A. Meijer, Adeline Barthet-Barateig, Hannah N. Parker, Asma Khurshid, Sarah Tessier, Marie Sicard, Alan J. Knox, Linhua Pang, and Cornelia H. de Moor

Post-developmental microRNA expression is required for normal physiology, and regulates aging in parallel to Insulin/IGF-1 signaling in *C. elegans*

Nicolas J. Lehrbach, Cecilia Castro, Kenneth J. Murfitt, Cei Abreu-Goodger, Julian L. Griffin, and Eric A. Miska

RNase III-independent microRNA biogenesis in mammalian cells

Thomas Maurin, Demián Cazalla, Jr-Shiuan Yang, Diane Bortolamiol-Becet, and Eric C. Lai

Kinetic analysis of pre-ribosome structure in vivo

Agata Swiatkowska, Wiebke Wlotzka, Alex Tuck, J. David Barrass, Jean D. Beggs, and David Tollervey

Transcriptomic profiling of the oyster pathogen *Vibrio splendidus* opens a window on the evolutionary dynamics of the small RNA repertoire in the *Vibrio* genus

Claire Toffano-Nioche, An N. Nguyen, Claire Kuchly, Alban Ott, Daniel Gautheret, Philippe Bouloc, and Annick Jacq

Method

RNA-ID, a highly sensitive and robust method to identify *cis*-regulatory sequences using superfolder GFP and a fluorescence-based assay

Kimberly M. Dean and Elizabeth J. Grayhack