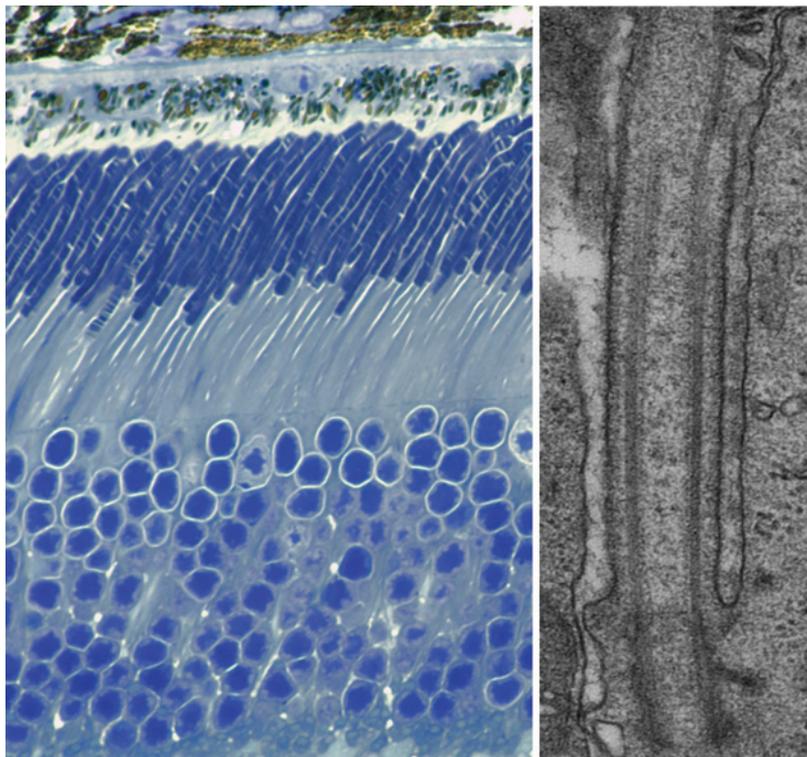


The Editorial Board of *Molecular Biology of the Cell* has highlighted the following articles from the December 1 and 15, 2010, and January 1 and 15, 2011, issues. From among the many fine articles in the journal, the Board selects for these Highlights articles that are of broad interest and significantly advance knowledge or provide new concepts or approaches that extend our understanding.



Light micrograph of the photoreceptor layer of a mouse retina (left) and an electron micrograph of the transition zone of the cilium of a mouse photoreceptor cell (right). (Image: Vanda Lopes and Conchi Lillo, University of California, Los Angeles, School of Medicine and University of California, San Diego, School of Medicine)

## **Microautophagy of the nucleus coincides with a vacuolar diffusion barrier at nuclear–vacuolar junctions**

Rosie Dawaliby and Andreas Mayer

Nuclear–vacuolar (NV) junctions are organelle contact sites in yeast. They exclude nuclear pores from the organelle interface. On the vacuolar side, a lipid-dependent process excludes specific membrane proteins, such as V-ATPase, from the contact site. This suggests that NV junctions establish selective diffusion barriers.

**Mol. Biol. Cell 21 (23): 4173–4183**

## **AS160 associates with the Na<sup>+</sup>,K<sup>+</sup>-ATPase and mediates the adenosine monophosphate–stimulated protein kinase–dependent regulation of sodium pump surface expression**

Daiane S. Alves, Glen A. Farr, Patricia Seo-Mayer, and Michael J. Caplan

The sodium pump interacts with AS160, a protein that regulates the trafficking of the GLUT4 glucose transporter. This interaction drives the internalization of the sodium pump from the cell surface, and this process is in turn controlled by the energy-sensing kinase adenosine monophosphate-stimulated protein kinase.

**Mol. Biol. Cell 21 (24): 4400–4408**

## **Finding the cell center by a balance of dynein and myosin pulling and microtubule pushing: a computational study**

Jie Zhu, Anton Burakov, Vladimir Rodionov, and Alex Mogilner

By comparing computer modeling predictions with observations, we conclude that strong dynein and weaker myosin-generated forces pull the microtubules inward, competing with microtubule plus-ends pushing the

microtubule aster outward. The balance of these forces positions the centrosome at the cell center.

**Mol. Biol. Cell 21 (24): 4418–4427**

## **NOA1 is an essential GTPase required for mitochondrial protein synthesis**

M. Kolanczyk, M. Pech, T. Zemojtel, H. Yamamoto, I. Mikula, M.-A. Calvaruso, M. van den Brand, R. Richter, B. Fischer, A. Ritz, N. Kossler, B. Thurisch, R. Spoerle, J. Smeitink, U. Kornak, D. Chan, M. Vingron, P. Martasek, R. N. Lightowers, L. Nijtmans, M. Schuelke, K. H. Nierhaus, and S. Mundlos

Nitric oxide associated-1 (NOA1) is an evolutionarily conserved guanosine triphosphate binding protein that localizes predominantly to mitochondria in mammalian cells. Here we determine NOA1 function through generation of knock-out mice and in vitro assays.

**Mol. Biol. Cell 22 (1), 1–11**

## **Cdase is a pan-ceramidase in *Drosophila***

C. Yuan, R. P. Rao, N. Jesmin, T. Bamba, K. Nagashima, A. Pascual, T. Preat, E. Fukusaki, U. Acharya, and J. K. Acharya

It is demonstrated that the Cdase gene encodes all measurable ceramidase function in *Drosophila*. BWA, an alkaline ceramidase homologue, does not exhibit ceramidase activity. *Bwa* genetically interacts with other ceramide-metabolizing enzymes by influencing the flux through the sphingolipid pathway.

**Mol. Biol. Cell 22 (1), 33–43**

### **Actin cables and the exocyst form two independent morphogenesis pathways in the fission yeast**

*F. O. Bendezú and S. G. Martin*

In fission yeast, long-range transport and vesicle tethering by the exocyst are individually dispensable but together essential for cell morphogenesis. Both pathways function downstream of Cdc42. The exocyst localizes to growing cell tips independently of the cytoskeleton and instead depends on PIP<sub>2</sub>.

**Mol. Biol. Cell 22 (1), 44–53**

### **A meiotic gene regulatory cascade driven by alternative fates for newly synthesized transcripts**

*N. Cremona, K. Potter, and J. A. Wise*

Analyses of 32 meiotic genes from fission yeast with respect to nascent transcription, RNA processing/accumulation, and effects of surveillance factor mutants reveal that the vast majority are “on” in proliferating cells and less than one-third show a transcriptional peak during meiosis, highlighting the important contribution of RNA-level regulation.

**Mol. Biol. Cell 22 (1), 66–77**

### **A Ral GAP complex links PI 3-kinase/Akt signaling to RalA activation in insulin action**

*X.-W. Chen, D. Leto, T. Xiong, G. Yu, A. Cheng, S. Decker, and A. R. Saltiel*

It is shown that RalA is regulated by a Ral GAP complex (RGC 1/2) in insulin action and links PI 3-kinase signaling to RalA activation. Akt phosphorylates the complex and inhibits its function, resulting in increased RalA activity and glucose uptake.

**Mol. Biol. Cell 22 (1), 141–152**

### **Requirement for Golgi-localized PI(4)P in fusion of COPII vesicles with Golgi compartments**

*A. Lorente-Rodríguez and C. Barlowe*

The role of specific membrane lipids in ER–Golgi transport is unclear. Using cell-free assays that measure stages in ER–Golgi transport, a variety of enzyme inhibitors, lipid-modifying enzymes, and lipid ligands were screened. The results indicate that PI(4)P is required for SNARE-dependent fusion of COPII vesicles with the Golgi complex.

**Mol. Biol. Cell 22 (2), 216–229**

### **Ubiquitin-dependent degradation of HDAC4, a new regulator of random cell motility**

*N. Cemotta, A. Clocchiatti, C. Florean, and C. Brancolini*

Histone deacetylase 4 (HDAC4) controls several cellular responses and is subjected to multiple levels of

regulation. Here it is shown that HDAC4 is under the regulation of the proteasome, in a growth factor- and GSK3 $\beta$ -dependent manner. Degradation of HDAC4 could contribute to the attenuation of random cell motility observed in cells in the G<sub>0</sub> phase of the cell cycle.

**Mol. Biol. Cell 22 (2), 278–289 ■**



*Model of the hexameric cleavage stimulation factor, which is involved in 3' end processing of vertebrate mRNAs. (Image: Nicole Kleinschmidt, University of Berne)*