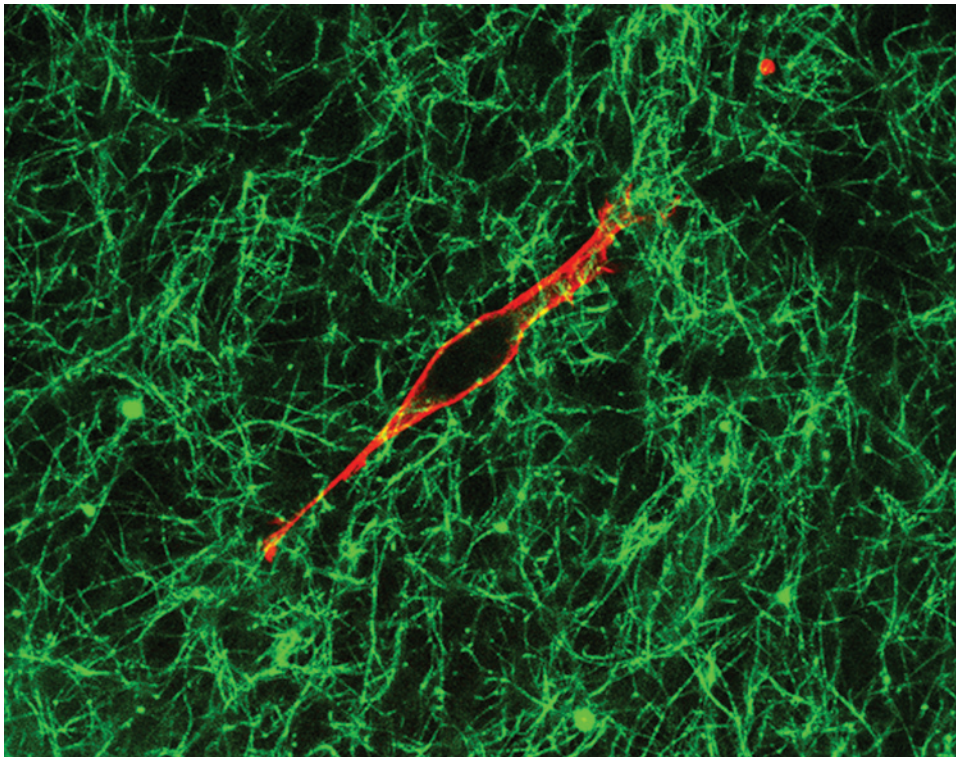
HIGHLIGHTS from *MBoC*

The Editorial Board of *Molecular Biology of the Cell* has highlighted the following articles from the February 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.



An MDA-MB-231 breast cancer cell devoid of paxillin expression invades a 3D collagen- and fibronectin-rich extracellular matrix. Such cells display a highly elongated hypermesenchymal morphology. (Image: Nicholas O. Deakin, *SUNY Upstate Medical University)*

The AAA-ATPase p97 is essential for outer mitochondrial membrane protein turnover
S. Xu, G. Peng, Y. Wang, S. Fang, and M. Karbowski

Recent studies have revealed a role for the Ub/proteasome system in the regulation and turnover of outer mitochondrial membrane (OMM)-associated proteins. The data presented show that an AAA-ATPase, p97, is required for the proteasomal degradation of Mcl1 and Mfn1, two unrelated OMM proteins, and establishes p97 as a novel and essential part of the OMM–protein degradation pathway.
Mol. Biol. Cell 22 (3), 291–300

Distinct roles for paxillin and Hic-5 in regulating breast cancer cell morphology, invasion, and metastasis
N. O. Deakin and C. E. Turner

This study reveals novel roles for the focal adhesion proteins paxillin and Hic-5 in regulating breast cancer invasion strategies and metastasis. Depletion of paxillin promotes a hypermesenchymal phenotype while dysregulating 3D adhesion dynamics. In contrast, RNAi of Hic-5 induces a hyperamoeboid phenotype with dysregulated RhoA/pMLC signaling.
Mol. Biol. Cell 22 (3), 327–341

Three sorting nexins drive the degradation of apoptotic cells in response to PtdIns(3)P signaling
N. Lu, Q. Shen, T. R. Mahoney, X. Liu, and Z. Zhou

LST-4/SNX9, SNX-1, and SNX-6 together drive the degradation of apoptotic cells, as PtdIns(3)P effectors, during *Caenorhabditis elegans* development. By inducing regional membrane curvature and maintaining RAB-7 GTPase on phagosomes, these three sorting nexins stimulate the fusion of endocytic organelles with phagosomes.
Mol. Biol. Cell 22 (3), 354–374

Histone and TK0471/TrmBL2 form a novel heterogeneous genome architecture in the hyperthermophilic archaeon *Thermococcus kodakarensis*
H. Maruyama, M. Shin, T. Oda, R. Matsumi, R. L. Ohniwa, T. Itoh, K. Shirahige, T. Imanaka, H. Atomi, S. H. Yoshimura, and K. Takeyasu

This study demonstrates that the chromosome of the hyperthermophilic archaeon *Thermococcus kodakarensis* is organized into a heterogeneous structure created with histone and a novel protein TK0471/TrmBL2. TK0471/TrmBL2 plays dual roles as a chromosomal protein and as a global transcriptional repressor, and it is conserved in some archaeal and bacterial species.
Mol. Biol. Cell 22 (3), 386–398

A novel acetylation of β-tubulin by San modulates microtubule polymerization via down-regulating tubulin incorporation
C.-W. Chu, F. Hou, J. Zhang, L. Phu, A. V. Loktev, D. S. Kirkpatrick, P. K. Jackson, Y. Zhao, and H. Zou

We report that San, an acetyltransferase required for sister chromatid cohesion, also acetylates β-tubulin at lysine 252. The acetylation happens only on free tubulin heterodimers, and it delays the incorporation of modified tubulins into microtubules in vivo.
Mol. Biol. Cell 22 (4), 448–456

The Dam1 ring binds to the E-hook of tubulin and diffuses along the microtubule
V. H. Ramey, H.-W. Wang, Y. Nakajima, A. Wong, J. Liu, D. Drubin, G. Barnes, and E. Nogales

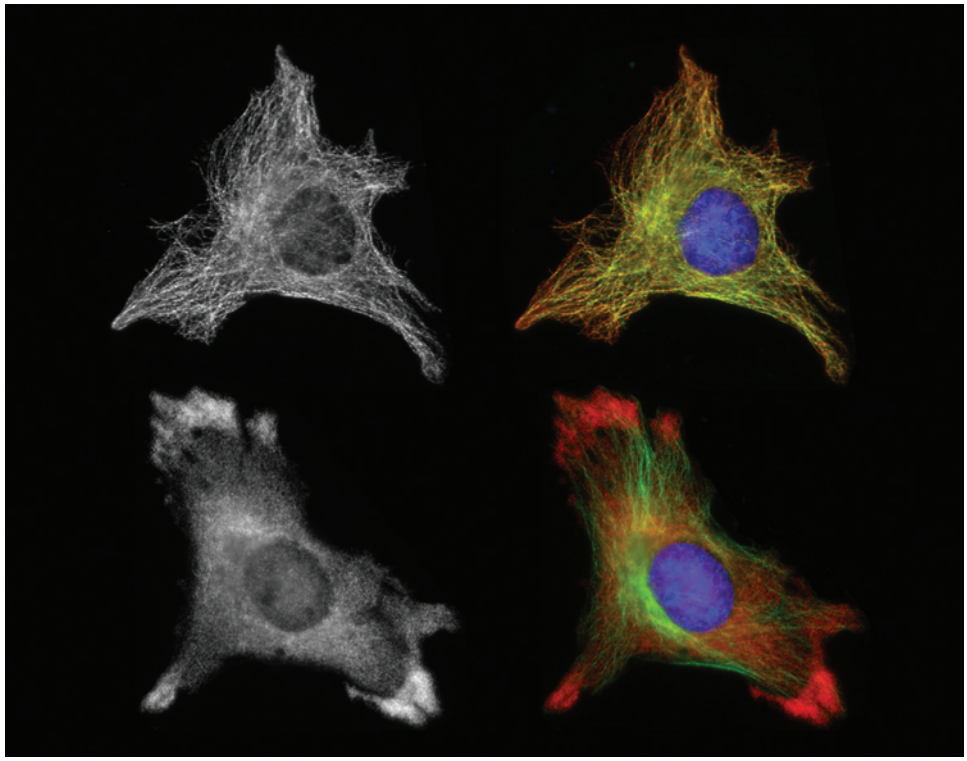
Several models of Dam1 complex function at the kinetochore have been proposed. Here we show that removal of the E-hooks of tubulin reduces Dam1 binding 40-fold. We also report the first structure of the Dam1 ring around microtubules and evidence that this ring freely diffuses on microtubules based on imaging individual rings.
Mol. Biol. Cell 22 (4), 457–466

Recruitment of dynein to late endosomes and lysosomes through light intermediate chains
S. C. Tan, J. Scherer, and R. B. Vallee

How cytoplasmic dynein is recruited to diverse organelles remains incompletely understood. Using subcellular localization of light intermediate chain (LIC) isoforms, along with RNAi, RILP, and dynactin dominant negatives, the LIC subunits are found to recruit dynein specifically to components of the late endocytic pathway through a dynactin-independent mechanism.
Mol. Biol. Cell 22 (4), 467–477

In vivo kinetics of U4/U6·U5 tri-snRNP formation in Cajal bodies
I. Novotný, M. Blažíková, D. Staněk, P. Herman, and J. Malinsky

A combination of mathematical modeling and live-cell measurements was applied to determine the dynamics of small nuclear ribonucleoprotein (snRNP) formation in Cajal bodies of living cells. Our results indicate that a substantial fraction of tri-snRNPs is formed in Cajal bodies in cells with many Cajal bodies per nucleus.
Mol. Biol. Cell 22 (4), 513–523 ■



In HeLa cells recovering from cold treatment, wild-type β-tubulin is incorporated into microtubules (upper panels), whereas the K252Q mutant β-tubulin, which mimics San-acetylated tubulin, remains in the cytosol (lower panels). (Image: Chih-Wen Chu, *University of Texas Southwestern Medical Center)*