# EDITORS' CHOICE

edited by Gilbert Chin

CELL BIOLOGY

## Membrane Sorting

Endocytosis is the process by which cells take up materials such as nutrients, hormones, and growth factors from the outside milieu into membrane-bound intracellular compartments, known as endosomes. The receptors for these materials are then trucked to the degradative organelle of the cell, the lysosome, or recycled to the cell surface. In some systems, modification of membrane proteins by ubiquitin has been linked to uptake and endocytic traffic. Ubiquitin is added to target proteins by ubiquitin ligases and can be removed by the proteasome, which can either remove ubiquitin groups or degrade the entire protein.

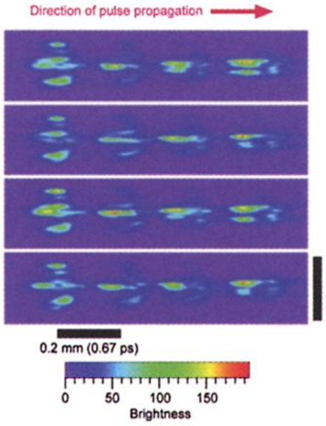
Longva *et al.* and Bishop *et al.* describe their independent analyses of factors controlling the trafficking of epidermal growth factor (EGF) and its receptor after internalization. After binding EGF, the EGF receptor becomes internalized. Prolonged administration of EGF causes some ubiquitination of the receptor and correlates with the recruitment of the ubiquitin ligase c-Cbl to the EGF-containing endosomes. The ubiquitination of the EGF receptor–containing endosomes appears to recruit a protein important in lysosomal targeting termed Vps28. When Vps28 antibodies were microinjected into cells, EGF degradation was retarded, and ubiquitin conjugates accumulated in the endosomes. These findings extend and confirm findings by van Kerkhof *et al.*, who have found that protea-some inhibitors blocked a late step in lysosomal transport of membrane proteins without affecting the trafficking of soluble proteins. — SMH

*J. Cell Biol.* **156**, 843 (2002);
*J. Cell Biol.*, in press;
*Mol. Biol. Cell* **12**, 2556 (2001).

APPLIED PHYSICS

## Keeping an Eye on the Pulse

Nonlinear effects can occur when intense laser pulses interact with matter and can distort the pulses as they propagate through a medium. However, keeping tabs on such fleeting events is not a trivial task. Fujimoto *et al.* present a technique with which they can visualize the propagation of intense femtosecond laser pulses propagating through air. They send four probe pulses through the intense pulse, and the resulting interaction causes a shift in the polarization of the probe pulses. By piecing together the polarization changes in the four probe pulses, the authors can create a still-frame picture of the distorting main pulse as it propagates. The distortion of the pulses varies from shot to shot, possibly because of fluctuations in the pulse power or turbulence in the pathway. Visualizing such distortions may help in the characterization of high-power lasers and may lead to a more accurate delivery of the power to the desired location. — ISO



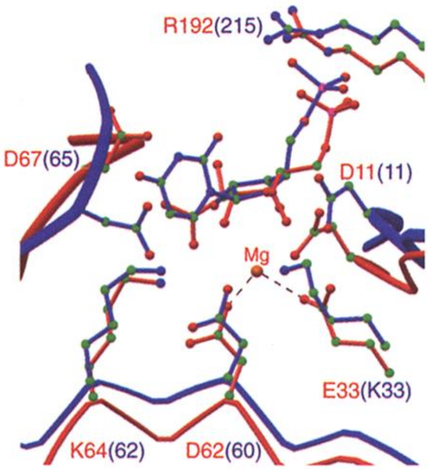
**Visualizing optical breakup.**

*Opt. Lett.* **27**, 309 (2002).

BIOCHEMISTRY

## Opportunistic Enzyme Evolution

Expanding one's biochemical repertoire might be supposed to have occurred by either of two complementary strategies. An enzyme could evolve to catalyze a new transformation of the same compound, gaining the next step in a nascent metabolic pathway, or the substrate-binding site might shift subtly, allowing the enzyme to retain aspects of the original chemistry. Wise *et al.* have compared the structure of 3-keto-L-gulonate 6-phosphate decarboxylase (KGPDC) to that of orotidine-5′-monophosphate decarboxylase (OMPDC). Although both enzymes catalyze decarboxylation, the mechanisms have no obvious features in common. In KGPDC, the reaction depends on magnesium, whereas in OMPDC the reaction is metal-independent (and a topic of continuing investigation regarding its catalytic proficiency).



**Superposition of the active sites, KGPDC (red) and OMPDC (blue), and substrates.**

Both enzymes display the $(\beta/\alpha)_8$-barrel fold, and sequence and structural homologies indicate that they are derived from a common ancestor. Amino acids strictly conserved in OMPDCs include an aspartate at the end of the first strand (D11), a lysine at the end of the second strand (K33), and an Asp-X-Lys-X-X-Asp (D60-D65) motif at the end of the third strand. All of these residues are conserved in KGPDC, apart from K33, which is replaced by glutamate. The magnesium ion in KGPDC stabilizes an enediol anion intermediate and is coordinated by carboxylates (D11, E33, and D62). In OMPDC, however, D60 acts to destabilize the substrate, and K33 hinders formation of a vinyl anion intermediate that would be too unstable to be kinetically competent. Thus, a conserved constellation of active site residues appears to have been commandeered opportunistically to implement a disparate mechanism on a dissimilar subtrate, suggesting that inferring function strictly on the basis of homology can be hazardous. — VV

*Biochemistry* 10.1021/bi012174e (2002).

CHEMISTRY

## It's Not Just Another Phase

Many aspects of the microscopic structure of water in its many phases remain incompletely understood. For example, the structure of the liquid water surface influences key properties, such as surface tension and the mobility of molecules across the liquid-gas interface, but it has been difficult to determine the surface hydrogen bond configurations of water molecules. Wilson *et al.* have used near-edge x-ray absorption fine structure measurements to

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CREDITS: (LEFT) WISE *ET AL.*, *BIOCHEMISTRY* 10.1021/BI012174E (2002); (RIGHT) FUJIMOTO *ET AL.*, *OPT. LETT.* 27, 309 (2002)

characterize the liquid surface of water jets in thermal equilibrium with local water vapor. Total ion–yield spectra, which reveal free OH bonds, were combined with simulations to identify a new interfacial species: acceptor-only water molecules that have two free OH bonds and are in dynamic equilibrium with the vapor. Condensation of these molecules is likely to occur through the initial formation of an acceptor hydrogen bond, in contrast to the condensation dynamics of amorphous ice, where vapor molecules are captured by forming donor and acceptor bonds.

Using a related technique, Myneni *et al.* have investigated the electronic structure of bulk liquid water, which differs substantially from that of the solid and of the vapor. Theoretical calculations indicate that this difference arises from a substantial fraction of water molecules with free OH bonds. On average, molecules have 2.4 to 2.8 hydrogen bonds, significantly less than the value of 3.5 found in previous molecular dynamics simulations.

Finally, although the bulk structure of ice is better understood than that of the liquid, the properties of the liquid layer that exists at the surface of ice near its melting point has been a topic of controversy. Bluhm *et al.* have developed an electron spectrometer that can operate in the presence of water vapor. Their results show that "premelting" occurs between –20° to 0° Celsius and that organic contaminants can strongly enhance the premelting of ice. — JU

*J. Phys. Condens. Matt.* **14**, L221; L213; L227 (2002).

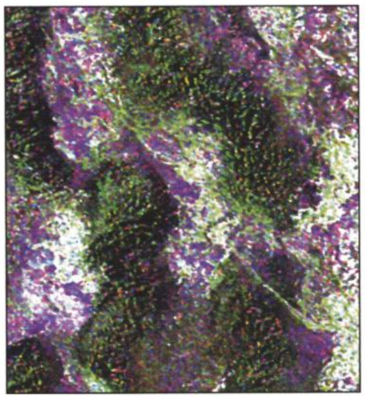
CLIMATOLOGY

## That's Not Dust, It's Data

Atmospheric mineral dust is an important agent of global climate change because of the many ways in which it can affect Earth's heat budget. Dust can act directly by inducing either radiative scattering or absorption and indirectly by causing cloud droplet condensation or influencing atmospheric $CO_2$ concentration (via deposition that results in the fertilization of oceanic primary productivity). Records extracted from ice cores in Greenland and Antarctica have shown that the concentration of atmospheric dust has varied by more than an order of magnitude across warm and cold intervals of glacial cycles.

In order to improve the temporal resolution of measurements of dust transport to Greenland, Bory *et al.* have obtained samples from snow pits and report on the mineralogical and Sr and Nd isotopic composition of dust deposited during the past decade. Present-day dust in north central Greenland originates primarily from the Taklamakan Desert in northwestern China, as is the case for dust that was deposited during the last glacial period and the Holocene. Moreover, the ability to measure seasonal variability in dust composition will help to correlate climate events in Asian dust source areas and in the North Atlantic and may provide more precise values of wind strength and regional aridity for input into atmospheric transport models. — HJS

*Earth Planet. Sci. Lett.*, in press.



**Radar image of a Silk Road settlement in the Taklamakan Desert.**

CREDIT: NASA

MOLECULAR BIOLOGY

## Manufacturing snRNPs

Spinal muscular atrophy is a genetic disease in which motor neurons in the spinal cord degenerate. The protein encoded by this gene is called survival of motor neurons (SMN) and is one component of the large multiprotein SMN complex. Diverse cellular processes rely on RNA-protein assemblies, and the SMN complex is involved in the orderly construction of the small nuclear ribonucleoprotein particles (snRNPs) involved in pre–messenger RNA splicing.

Yong *et al.* show that the SMN complex recognizes one of the four stem loops (SL1) of the U1 snRNA and that this region is necessary and sufficient for SMN complex interaction. A distinct region is responsible for gathering the Sm proteins, which form a heteroheptameric ring encircling the snRNA; together they comprise the core of the U1 snRNP. Some Sm proteins contain an Arg-Gly motif, and a separate complex, called the methylosome, uses the protein methyltransferase PRMT5 to N-methylate the arginine symmetrically, as shown by Freisen *et al.* and Meister *et al.* The resulting dimethylarginine is recognized by SMN, facilitating the supply of Sm proteins to the SMN complex. — GJC

*EMBO J.* **21**, 1188 (2002); *Mol. Cell. Biol.* **21**, 8289 (2001); *Curr. Biol.* **11**, 1990 (2001).