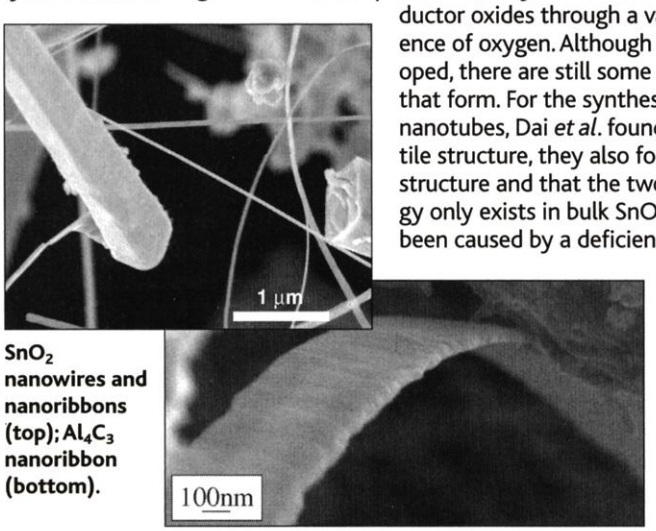
EDITORS' CHOICE

edited by Stella Hurtley

CHEMISTRY

Surprises in Nanoribbon Synthesis

In the world of nanoparticles, nanoribbons are a newcomer to the variety of shapes that have been synthesized. Starting from molecular precursors, they have been fabricated from a variety of semiconductor oxides through a vapor deposition process in the presence of oxygen. Although this technique is now well developed, there are still some occasional surprises in the products that form. For the synthesis of tin oxide (SnO_2) nanowires and nanotubes, Dai *et al.* found that in addition to the normal rutile structure, they also formed an orthorhombic superlattice structure and that the two could coexist. This latter morphology only exists in bulk SnO_2 at high pressures, and it may have been caused by a deficiency in oxygen during the wire growth.



SnO_2 nanowires and nanoribbons (top); Al_4C_3 nanoribbon (bottom).

Extending the synthesis of these objects to non-oxide systems, Zhang *et al.* found that with the addition of lithium, they could form aluminum carbide nanowires and nanoribbons. While attempting to make a metal aluminum carbide solid, some of the lithium reacted to form gaseous CLi_x molecules, which subsequently reacted to form Al_4C_3. This serendipitous observation indicates that it may be possible to use Li as a catalyst to form other carbide and nitride nanowires and nanoribbons from materials that do not naturally have molecular precursors. — MSL

J. Phys. Chem. B 10.1021/jp013214r; *Nano Lett.* 10.1021/nl015656k.

BIOCHEMISTRY

Into the Membrane

C2 domains are membrane-docking modules found in many signal transduction and vesicle-trafficking proteins. In many cases, calcium binding regulates membrane association.

Murray and Honig used finite-difference Poisson-Boltzmann calculations to describe the electrostatic interactions of C2 domains of known structure with phospholipid membranes. Nonspecific electrostatic interactions were important for association with both negatively charged and neutral membranes. Calcium provided positive charge that attracted negatively charged membranes and reduced the desolvation penalty associated with membrane binding. Desolvation effects were particularly important in penetration of neutral membranes that in turn facilitate hydrophobic interactions. Calcium-independent C2 domains had similar electrostatic profiles. Quantitative estimates of the effect of experimental variables such as lipid composition, ionic strength, and mutations support a general role for these nonspecific electrostatic interactions. — VV

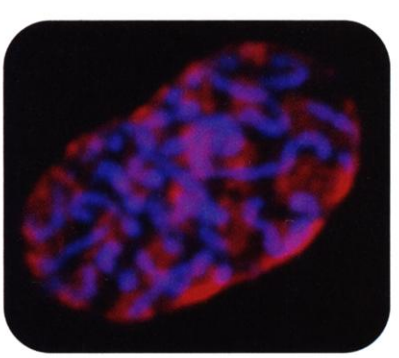
Mol. Cell **9**, 145 (2002).

CELL BIOLOGY

That's Torn It

At the beginning of mitosis, the cell's nucleus breaks down, releasing the condensed chromosomes to be arranged on the mitotic spindle for partitioning to daughter cells. Basic morphological evidence of this process is well established.

Now Beaudouin *et al.* have examined the process of nuclear envelope breakdown in real time in living cells, and Salina *et al.* examined the same process in synchronized cell cultures entering mitosis. They both observed the catastrophic "tearing" of the nuclear envelope at the onset of mitosis. This tearing process appears to be actively mediated by microtubules with the help of the molecular motor dynein. If microtubules are disrupted just before mitosis, envelope breakdown is inhibited. Dynein concentrates on the nuclear envelope before its breakdown, and interfering with dynein activity inhibits nuclear envelope breakdown. Fragments of nuclear envelope that remain attached to condensed chromosomes move toward the centrosomes along microtubules. Together the papers suggest a mechanical process by which biochemical processes involved in the breakdown of the nuclear envelope are enhanced to facilitate progression through mitosis. — SMH



Tears in the nuclear envelope (red); condensed chromosomes (blue).

Cell **108**, 83; 97 (2002).

CLIMATOLOGY

Putting a Lid on CO_2?

The concentration of atmospheric CO_2 increased during the last deglaciation from about 190 parts per million (ppm) 17,000 years ago to about 265 ppm 11,000 years ago. A variety of hypotheses have tried to explain this observation, but none can account for the entire observed difference. One recent proposal [B. B. Stephens, R. F. Keeling, *Nature* **404**, 171 (2000)] suggested that wintertime expansion and compaction of sea ice around Antarctica during the last glacial period may have inhibited the outgassing of CO_2 from the ocean around the time of the Last Glacial Maximum.

Morales and Rahmsdorf present results from a coupled sea ice–upper ocean model, which show that ice-area fractions large enough to cause the observed difference might not have prevailed even under extreme glacial conditions. This mechanism could only account for 15 to 50% of the

CONTINUED ON PAGE 769

total glacial CO_2 depression. Thus, Antarctic sea ice expansion needs to be considered in conjunction with other mechanisms to solve the persistent puzzle of why atmospheric CO_2 levels were so low during glacial episodes. — HJS

Geophys. Res. Lett. 10.1029/2001GL013240.

IMMUNOLOGY

Making a Mark on Memory

B cells generate distinct classes of antibody, which execute specific functions in different types of immune response. Changes in these secreted antibody [immunoglobulin (Ig)] isotypes are matched by the membrane-bound versions of the same antibodies, which form B cell receptors. In secondary (memory) responses to antigen, early IgM antibodies are replaced by IgG antibodies, which dominate in memory B cell pools.

Martin and Goodnow now show that a component in the membrane-associated tail of the IgG protein directly affects secondary B cell responses. Replacing the tail of IgM with that of IgG led to increased antibody production in antigen-specific Ig-transgenic mice. These elevated levels of antibody resulted from an increase in the number of antibody-secreting cells in areas of lymphoid tissue that normally host secondary B cell responses. Increases were due to increased survival of B cells after activation, rather than increased cell division. Thus, the membrane tail of the IgG protein confers specific cell survival signals that may contribute to IgG dominance in B cell memory. — SJS

Nature Immunol. 10.1038/ni752.

HYDROLOGY

Going with Less of the Flow

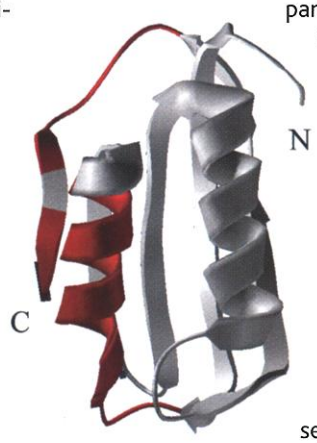
Long-term records of river flow are essential, for example, to assess whether human activities are affecting flood frequency or severity or for allocating water. Freshwater input into the oceans also has important implications for assessing climate change and for coastal ecosystems. Stream-gauge data in fact indicate that the flow of streams and rivers globally has declined worldwide during the past several decades. However, within the United States alone, the number of gauging stations has declined by nearly 14% since the 1960s, which may make it difficult to assess the larger impacts of changes in river flow. Shiklomanov *et al.* focus on the implications of monitoring drainage into the Arctic Ocean, where large numbers of gauges have been recently closed in Alaska, Ontario, and the former Soviet Union. Although several gauges providing long-term records are still operational, the authors conclude that the closures pose a threat to the understanding of Arctic and global environmental change. — BH

Eos **83**, 13 (2002).

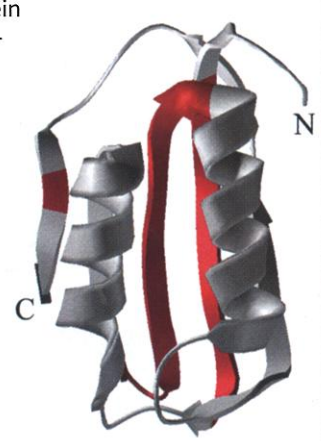
BIOCHEMISTRY

Mutate and Aggregate

In fully folded proteins, hydrophobic amino acids are hidden in the protein core. But when a protein is unfolded or partially folded, these residues render it prone to aggregation.



Chiti *et al.* now provide much-needed insights into the molecular basis of aggregate formation. They introduced point mutations in the protein acylphosphatase (AcP) and determined the relative aggregation rates of the mutants. Mutations in two particular regions of the protein, which possess high hydrophobicity and propensity to form β-sheet structure, led to increased rates of aggregate formation. Mutational "hot spots" in protein misfolding diseases may thus result from changes in the aggregation behavior.



Red areas important for aggregation (top) or folding (bottom) in acylphosphatase.

The regions determining the aggregation rate are distinct from those that determine protein folding. Only a small number of residues is involved in setting the scene for aggregation, raising the hope that aggregation is governed by relatively simple principles. — JU

Nature Struct. Biol. 10.1038/nsb752.

CREDIT: CHITI *ET AL.*, *NATURE STRUCT. BIOL.* 10.1038/NSB752