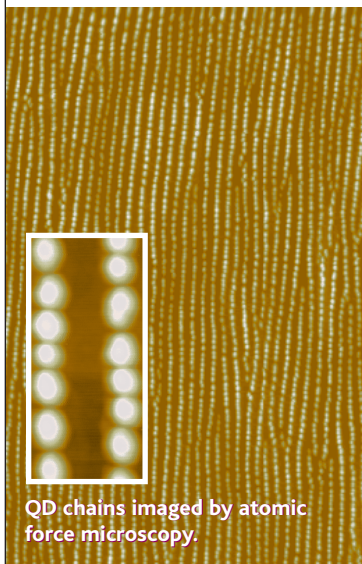


edited by Gilbert Chin



QD chains imaged by atomic force microscopy.

## APPLIED PHYSICS

### A String of Dots

The growth of self-assembled quantum dots (QDs) via a strain-driven mechanism has been shown to result in the formation of high-quality defect-free structures. However, this mode of fabrication yields an essentially random positioning of QDs on the substrate surface, and lithographic patterning is used to specify seeding and nucleation sites for QD growth.

Wang *et al.* show that the growth of QDs as self-assembled chains of several micrometers in length can be achieved simply by interrupting the growth sequence. Although the mechanism for the long-range alignment remains unclear, the ability to control the size, composition, and position of the dots within the deposition process should, nevertheless, provide the possibility of engineering some interesting device structures. — ISO

*Appl. Phys. Lett.* **84**, 1931 (2004).

## CLIMATE SCIENCE

### Way Back When

The El Niño–Southern Oscillation (ENSO) is the primary cause of modern interannual variability of tropical climate. Has ENSO always behaved as it does today? Some studies have indicated that its behavior may depend on the background climate state—particularly whether it is a glacial or warm interval—and that its strength, periodicity, and regularity can change. Unfortunately, annually resolved records are scarce.

Using a 350,000-year-old fossil coral from the southwestern tropical Pacific Ocean island of Vanuatu, Kilbourne *et al.* have measured Sr/Ca and oxygen isotopic anomalies, which are proxies for temperature and salinity changes, and compare them to those of a modern coral from the same location. Although annual sea surface temperature variations recorded in the corals were of the same amplitude, the seasonal salinity variations recorded by the fossil coral were smaller than those seen in the modern one. They also calculate that both the average sea surface temperature and salinity then were proba-

bly lower than today. They interpret these results as showing that ENSO or ENSO-like climate variations were in fact already present 350,000 years ago, although the South Pacific Convergence Zone did not migrate as far northward during austral winter then as it does today. — HJS

*Paleoceanography* **19**, 10.1029/2003PA000944 (2004).

## BIOCHEMISTRY

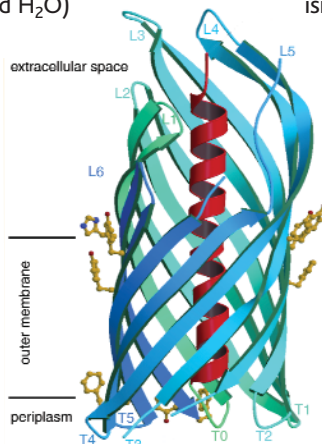
### Porin Proximity

Recent successes in membrane protein structure determination have advanced our understanding of how small hydrophilic entities (such as  $K^+$ , glycerol, and  $H_2O$ ) can be transported passively across hydrophobic biological membranes. How larger and less readily movable entities such as proteins are transported is still a bit fuzzy, although as usual, bacterial systems are likely to offer the first glimpses.

Oomen *et al.* describe the  $\beta$ -barrel structure of the C-terminal translocator domain of the autotransporter NaIP from *Neisseria meningitidis*; an  $\alpha$ -helical linker segment (which joins the N-terminal functional domain to the translocator) neatly fills the pore, which has an inner diameter of approximately 1 nm. Autotransporters encode and secrete virulence-related proteins (for example, a protease that attacks IgA molecules), and thus transit of the functional domain across the bacterial outer membrane via the  $\beta$  barrel would seem a plausible scenario.

Yet the answer isn't quite so simple.

Threading the functional domain, N-terminal end first, into and through the barrel would require both a targeting signal, which has not yet been identified, and an energy source analogous



The NaIP  $\beta$  barrel (blue) and  $\alpha$ -helical plug (red).

to the ribosome-powered translocation of proteins across the inner membrane. On the other hand, using the energy from folding to drive transport would mean pulling the C-terminal end of the functional domain through first (it is the C-terminal portion that folds first), but there isn't enough room in the pore for a helical hairpin, so the polypeptide would have to be dragged across in a fully unfolded and extended form. A third possibility, akin to the entry mechanism for colicin E3 proposed by Kurisu *et al.*, is that the translocator domain serves primarily to bring the functional domain close to an outer membrane porin, which serves as the actual protein transporter. — GJC

*EMBO J.* **10.1038/sj.emboj.7600148** (2004); *Nature Struct. Biol.* **10**, 948 (2003).

## CELL BIOLOGY

### Unloading Dock

The peroxisome is a membrane-bound organelle involved in lipid and drug metabolism. The protein constituents of the peroxisome are synthesized in the cytosol and must be imported into peroxisomes. One group of peroxisomal membrane proteins is known as the class I proteins, and their import into the peroxisome is facilitated by a chaperone protein, PEX19, which binds newly synthesized peroxisomal class I membrane proteins in the cytosol and ferries them to the peroxisome.

Fang *et al.* have identified a protein, PEX3, which plays an essential role in this process by acting as a docking factor on the peroxisomal membrane for PEX19-carried import substrates. In the absence of PEX3, class I peroxisomal membrane proteins cannot enter peroxisomes,

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