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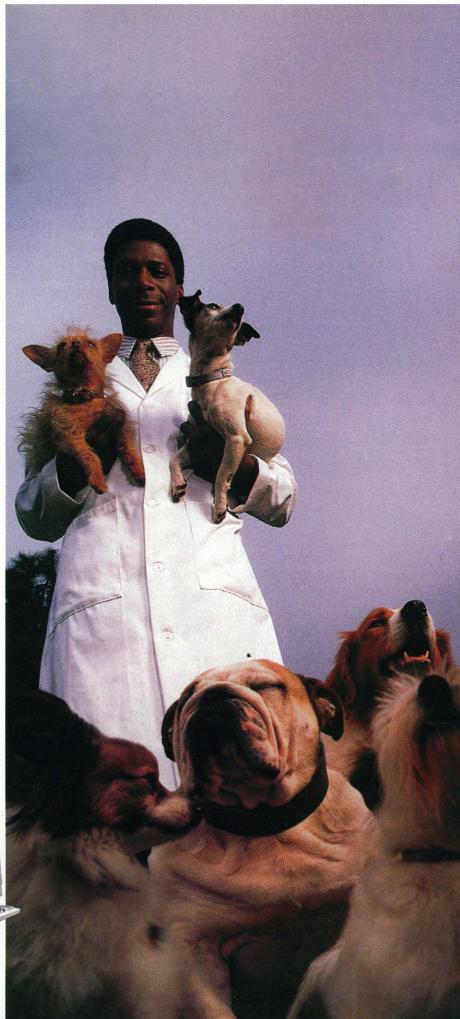
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NEWS & COMMENT







Making the right connections



1039 Plasma protein complex

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COVER

The Ulysses spacecraft superimposed on a soft x-ray image of the sun. The dark regions on the sun and the gaps in the sun's corona above the poles are coronal holes. The focus of the Ulysses mission is to explore the polar regions of the heliosphere. See the Reports in a special section beginning on page 1005 for results from Ulysses's pass over the sun's south pole. [Images: Courtesy of the European Space Agency]



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Γhis Week in Science

edited by DAVID LINDLEY

Cleaning up cars

Policies aimed at reducing automobile emissions may not always have the desired effect. Beaton et al. (p. 991) surveyed car emissions according to model age and maintenance histories, and show that poorly maintained new cars can be worse polluters than old cars lacking catalytic converters. And although electric cars are supposed to be clean, Lave et al. (p. 993) conclude that production and recycling associated with use of lead-acid batteries, for now the most cost-effective type, will generate up to 60 times the lead pollution of a car running on leaded gasoline.

Urease revealed

Urease from the jack bean plant was, in 1926, the first enzyme to be crystallized, and later became



the first identified nickel metalloenzyme. Jabri et al. (p. 998; see also Perspective by Lippard, p. 996) have now established the crystal structure of urease from Klebsiella aerogenes. The enzyme is a triangular trimer of T-shaped $\alpha\beta\gamma$ subunits, with the two nickel sites 3.5 angstroms apart on an $\alpha\beta$ barrel domain. The nickel atoms are each differently coordinated in a way that can explain their ligation to urea, which the enzyme hydrolyzes to carbon dioxide and ammonia. The barrel domain in urease closely resembles a corresponding structure in adenosine deaminase,

which has zinc instead of nickel atoms and catalyzes a mechanistically similar reaction.

Lack of tolerance

In response to moderately elevated temperatures, the protozoan Tetrahymena thermophila pauses to manufacture heat shock proteins before resuming growth and accumulates a ribosome-associated cytoplasmic RNA (G8). To investigate the function of G8 RNA, Fung et al. (p. 1036) inactivated the T. thermophila G8 genes. The G8deficient cells mounted an apparently normal heat shock response, but were unable to establish thermotolerance, an outcome of the heat shock response that enables cells to resist thermal killing. Although G8 RNA plays a role in maintaining a functional translational machinery at high temperatures, it is evidently not essential to all forms of heat tolerance.

Controlled excitement

Excitation of cardiac muscle cells leads to a precisely controlled contraction. The process relies on movement of Ca^{2+} into the cell through voltage-depen-

dent channels in the plasma membrane, which triggers release of intracellular stores of Ca²⁺ from the sarcoplasmic reticulum via its ryanodine receptors (RyRs). Such a system might seem prone to an all-ornone release of internal Ca²⁺, but López-López et al. (p. 1042) and Cannell et al. (p. 1045) present evidence that localized release of Ca²⁺ from RyRs is tightly coupled to entry of Ca²⁺ through single, closely opposed channels in the plasma membrane. This arrangement apparently allows for controlled amplification of the excitatory signal, permitting modulation of the strength of a contraction.

Nuclear importation

Proteins destined for a cell's nucleus are made in the cytosol and must be actively transported across proteinaceous pores in the nuclear envelope. Weis *et al.* (p. 1049) show that a protein found in the cytosol of human cells binds to nuclear localization sequences that act as signals for targeting to the nucleus, and promotes transport to the nuclear pores; there, another protein stimulates energy-dependent transfer across the nuclear envelope. The import

Looking up at the sun

Our understanding of the sun, the solar wind and magnetic field, and cosmic rays and dust has been largely based on data collected from Earth or from satellites near the ecliptic plane of the solar system. The goal of the Ulysses mission, which left the ecliptic after swinging around Jupiter in 1992, was to gather data from above the poles of the sun. Ten reports in this issue, beginning with an overview by Smith *et al.* (p. 1005), present results from the traverse of Ulysses to high latitudes and its passage over the solar south pole in 1994, near the time of solar minimum. Solar wind speed increased toward the south pole, reaching a constant 750 kilometers per second, and 26-day oscillations in the wind speed were evident only to about -50° latitude. Fluxes of cosmic rays varied little with latitude, in contrast to earlier predictions. receptor directly binds both of the known types of nuclear localization signals and is thus likely to be necessary for the import of most nuclear proteins.

Primitive processing

Ribosomal precursor RNA is processed in the nucleolus of eukaryotes by a ribonucleoprotein (RNP) particle that contains U3 RNA. Potter et al. (p. 1056) have studied the endonuclease involved in the processing of ribosomal RNA (rRNA) in the archaebacteria Sulfolobus acidocaldarius, and find that the rRNA processing activity contains a 159-nucleotide RNA with sequence and structural similarity to U3 small nucleolar RNA. Like RNA, this archaebacterial U3 may act in rRNA processing at sites that are analogous to those at which yeast U3 acts in yeast pre-rRNA, suggesting that the use of a U3containing RNP for rRNA processing predates the split of the archaea and eukaryotes.

Ancient apian alimentation

From bees preserved in amber 25 to 40 million years old, Cano and Borucki (p. 1060; see also news by Fischman, p. 977) have extracted a bacterial spore similar to those of Bacillus species that live symbiotically in the gut of modern bees, where they aid metabolic processes. Remarkably, the spore was revived and cultured. DNA analysis of the cultured bacteria, coupled with careful exclusion of contamination and consideration of the evolution of DNA sequences, indicates that the spore may indeed have been trapped in the amber when it formed.

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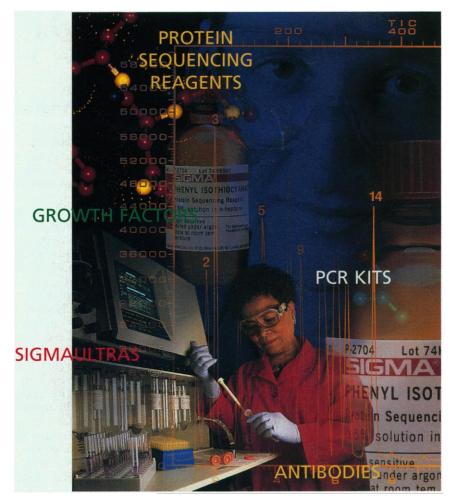
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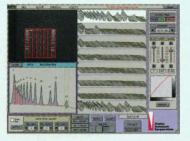
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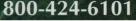
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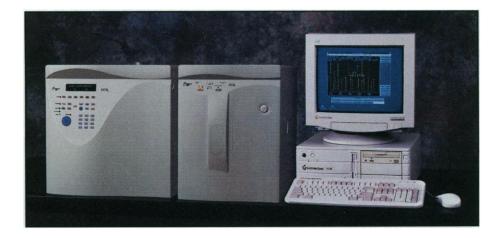
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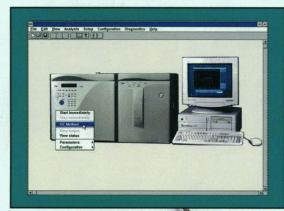
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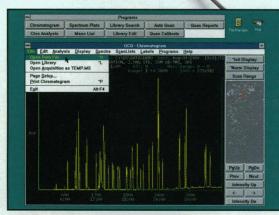
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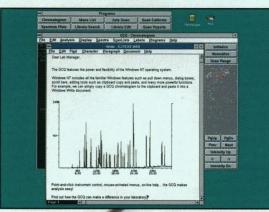




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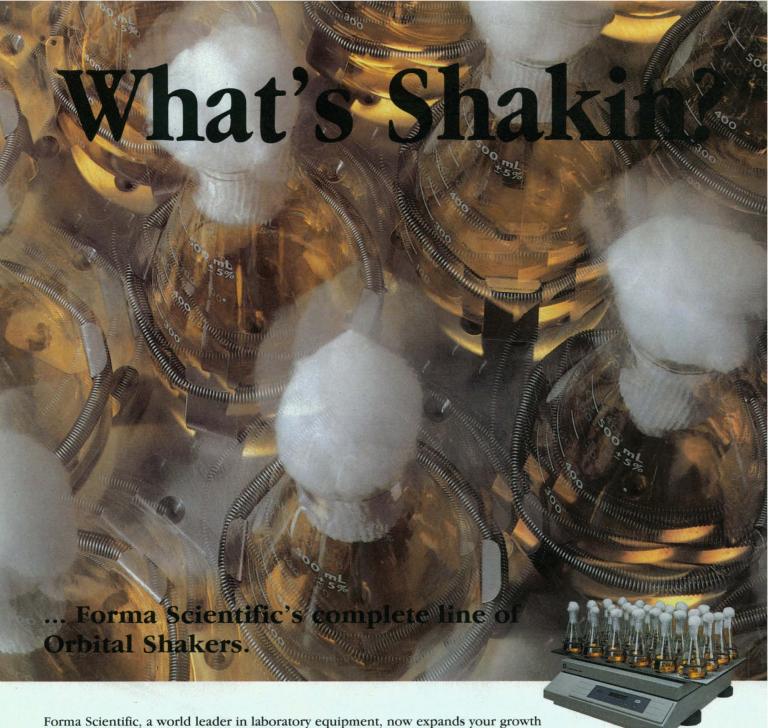


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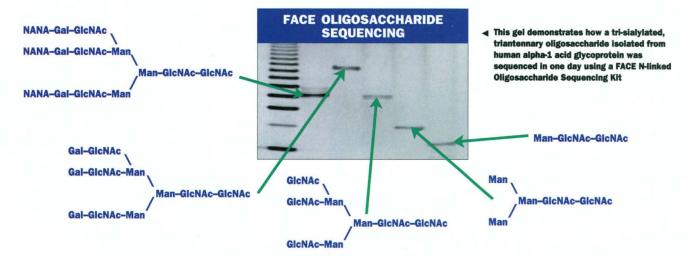
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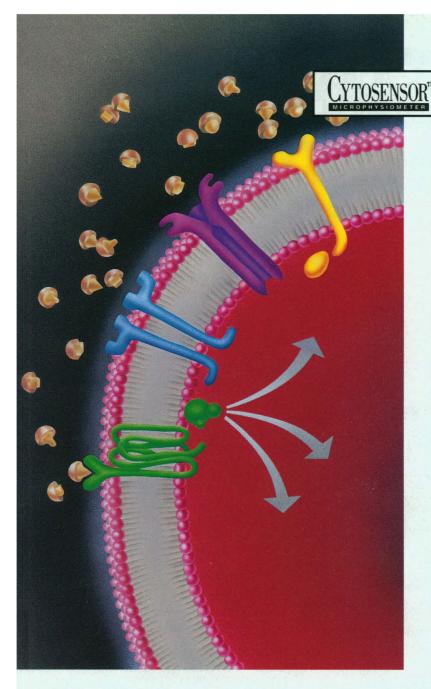
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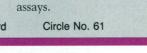
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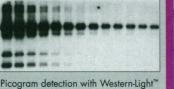
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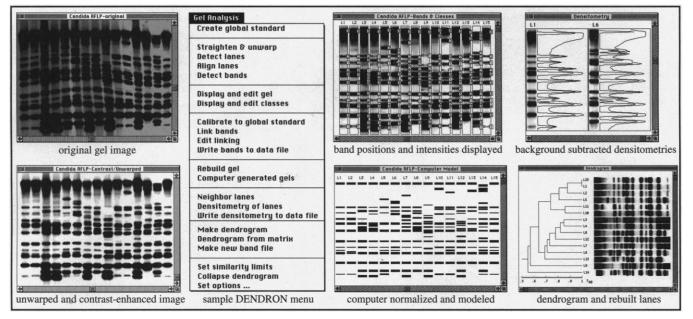
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Do you analyze gels?

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DENDRON[®]'s patented system corrects, processes and analyzes all forms of gels in order to compare banding patterns. It can analyze DNA fingerprint patterns, RFLP's, RAPD's, chromosome karyotyping gels, Southerns, Northerns, and Westerns. DENDRON[®] will analyze the gel images generated in a variety of gel documentation and gel imaging workstations. In the DENDRON[®] system, the gel image is scanned into a database and processed for contrast. If necessary, the digitized gel image is unwarped in order to rebuild an aligned image, as demonstrated below. Lanes and bands are automatically detected, band areas and intensities measured, and molecular weights determined. The process is extremely rapid. DENDRON[®] then computes similarity coefficients between every pair of lanes (strains) and generates matrices of similarity coefficients which are then used to construct dendrograms. When applied to DNA fingerprinting, DENDRON[®] can be used to compare any or all new strains with all previously analyzed strains.

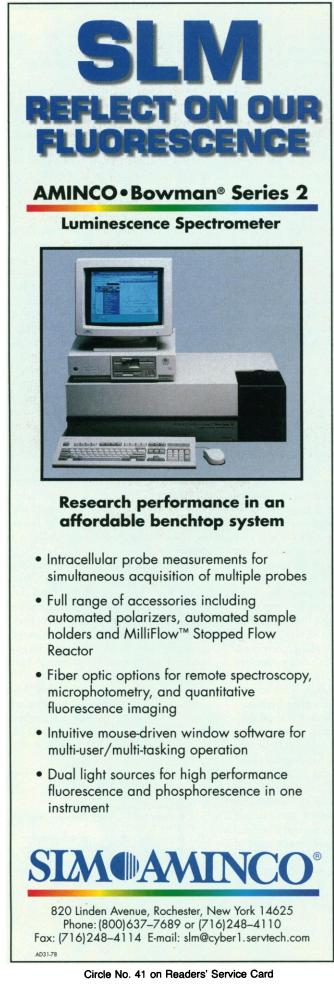


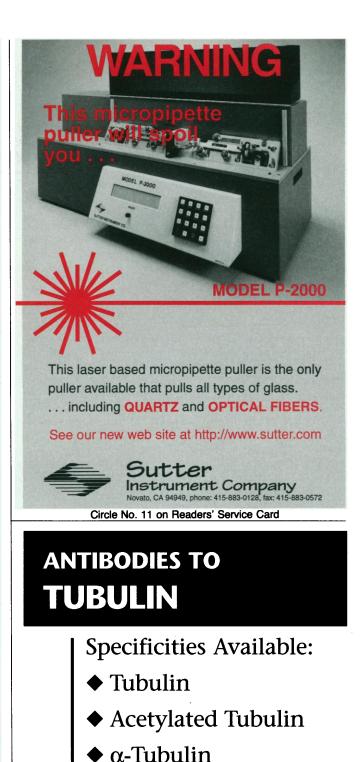
DENDRON® allows you to:

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- -Image process the entire gel or portions of the gel for background (see above)
- -Analyze warped or distorted gel images by removing all geometric distortions-i.e., smiles, frowns, other linear and non-linear distortions (see above)
- -Densitometrically scan the entire width of each lane for band intensities and positions (see above)
- -Automatically identify lanes and bands, and assign intensity classes and molecular weights to bands (see above)
- -Automatically subtract gel backgrounds in order to accurately assign intensity values to bands
- -Identify unique bands in different lanes
- -Normalize gel images nonlinearly to general standards to compare patterns on different gels
- -Compute similarity coefficients between every pair of lanes of interest on the same or different gels
- -Select from five formulas for calculating similarity coefficients
- -Generate matrices of similarity coefficients between every
- pair of up to 5000 patterns in a single grouping -Identify similar or identical strains in the same or different
- gels

- -Create dendrograms based upon similarity coefficients between any or all patterns in the same or different gels -Generate gel models (see above)
- -Display gel patterns horizontally next to their respective positions in a dendrogram (see above)
- -Test dendrogram stability mathematically
- -Normalize and neighbor any two or more lanes from the same or different gels for visual comparison
- -Create a database for cross-referencing and pattern selection from different gels based upon genotypic characteristics, phenotypic characteristics or patient characteristics
- -Export information to standard spreadsheet programs -Utilize additional features too numerous to describe here.
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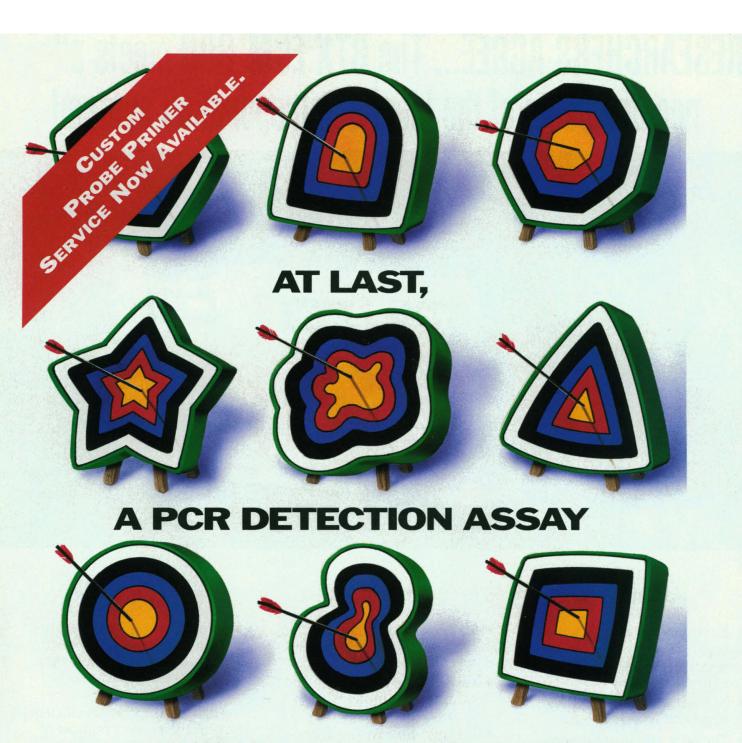
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