19 May 2000

Science

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Io
up close

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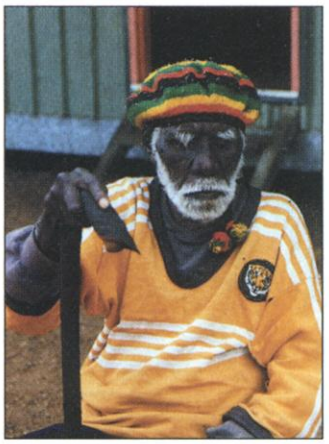
COVER Color mosaic of Culann Patera, an active volcano on Jupiter's moon Io, taken by NASA's Galileo spacecraft on 26 November 1999. A central caldera (green) feeds radial lava flows, including dark active flows (bottom left). Diffuse red material condenses from sulfur-rich gas erupting from the volcano. The scene width is 227 kilometers, at a scale of 200 meters per pixel; north is to the left. A collection of reports on Io begins on p. 1193. [Image processing: C. Phillips, University of Arizona, Tucson]



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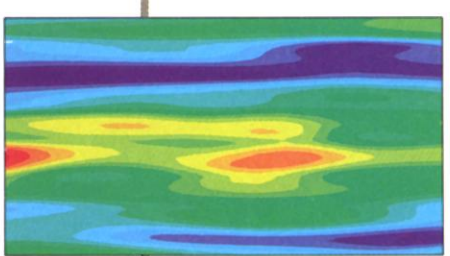

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Taming turbulence

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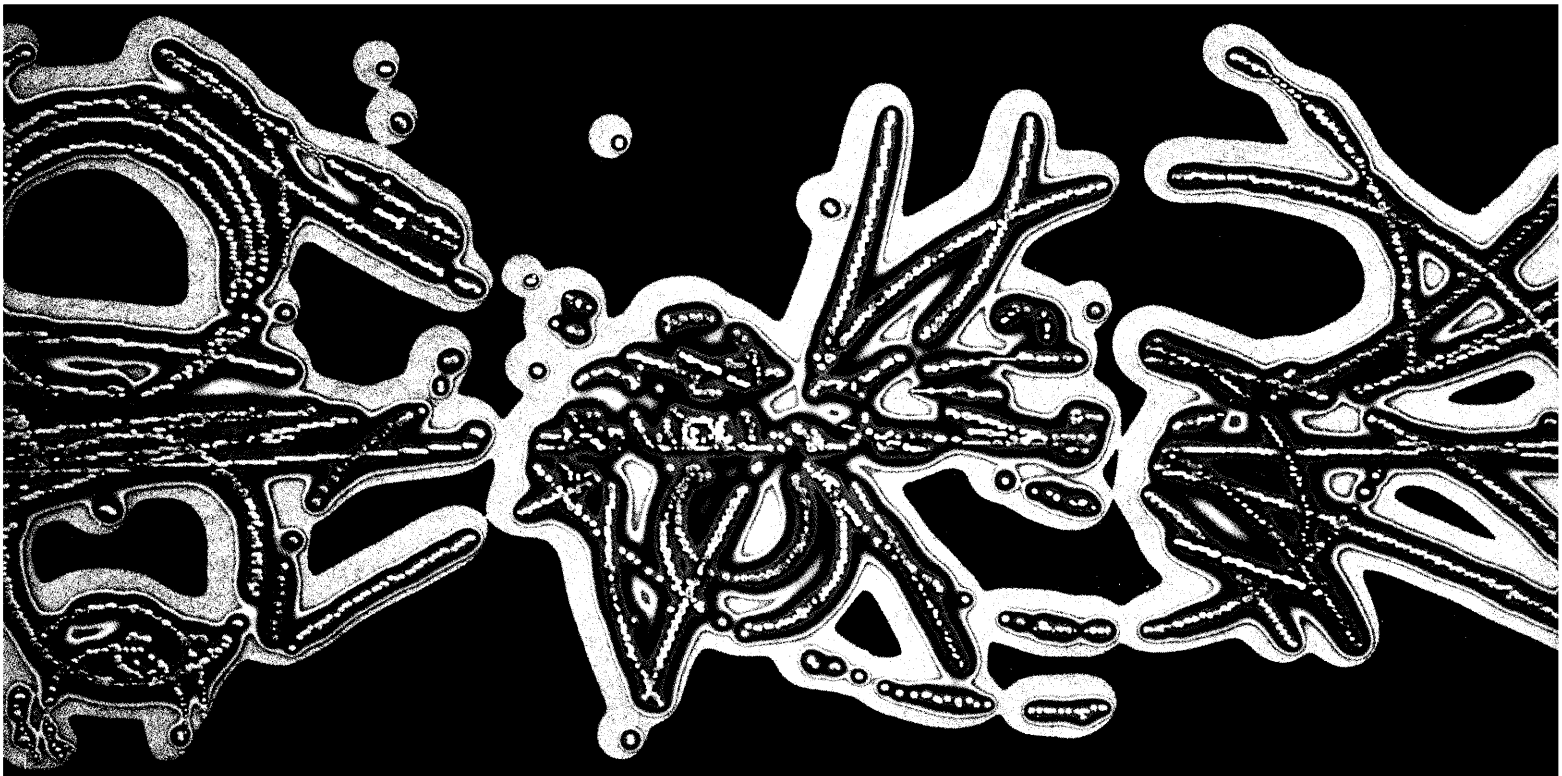

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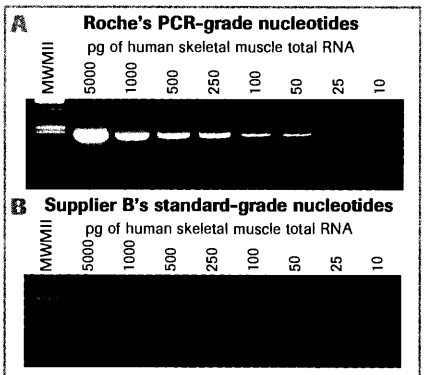

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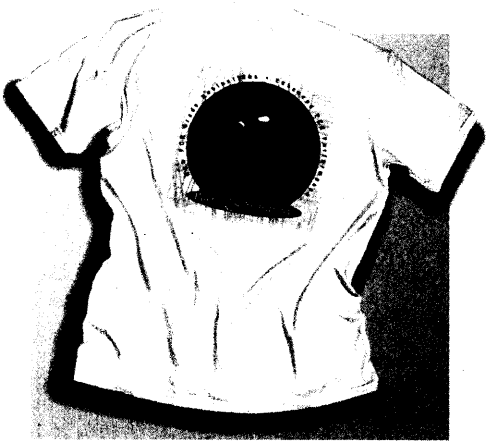

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UP FROM THE DEEP

Deep samples from the mantle provide direct evidence of mantle composition and processes. Most samples are diamonds and rock fragments known as xenoliths brought up in volcanic eruptions, or recovered along subduction zones, from depths of less than 150 kilometers (km). The deepest samples, perhaps even extending into the lower mantle (depths of 660 km or more), have been represented by diamonds and diamond inclusions or altered xenoliths. Collerson *et al.* (p. 1215) discuss evidence which suggests that xenoliths may have been brought to the surface from depths greater than 470 km on the island of Malaita, Southwest Pacific. The mineral assemblage in these xenoliths contain majorite (a phase thought to be present in the transition zone between the lower and upper mantle), diamond, and other phases.

IO POSES FOR A CLOSE-UP

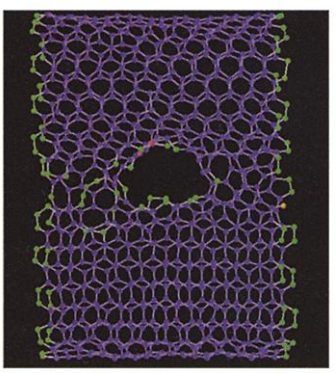
At the end of 1999 and the beginning of 2000, the Galileo spacecraft completed three close fly-bys of Io. Five reports describe high-resolution observations from this mission, as well as some made with the Hubble Space Telescope (HST), and provide new insight into the volcanic processes that continue to shape Io (see the cover). McEwen *et al.* (p. 1193) present images at a resolution of 5 to 500 meters per pixel of active lava lakes, an erupting curtain of lava and oddly shaped mountains influenced mainly by gravitational collapse rather than volcanism. They conclude that the active volcanism is related to fluid silicate magmas rather than sluggish sulfur magmas, although some of the bright flows might be sulfur-rich. Photopolarimeter-radiometer data presented by Spencer *et al.* (p. 1198) and near-infrared mapping by Lopes-Gautier *et al.* (p. 1201) suggest that the caldera floors are relatively cool and that the reddish-deposits surrounding active volcanoes represent dustings of exotic sulfur deposits (more polymerized species such as S_3 and S_4). The HST observations of Spencer *et al.* (p. 1208) provide evidence for gaseous S_2 in the plume of Pele. Estimates of the SO_2/S_2 ratio indicate that the silicate magmas may be buffered by an oxygen fugacity similar to conditions on Earth. Finally, Kieffer *et al.* (p. 1204) model the movement of Prometheus' plume, which has moved between 75 to 95 kilometers in 20 years. They suggest that lava flows moving over a sulfur-rich snowfield causes enhanced vaporization of the sulfur species.

A HAIRPIN TURN FOR DNA COMPUTING

Computation is possible with DNA sequences because certain logical operations can be represented by the success or failure of particular hybridization events within a large pool of molecules. As the problems become more complex (for example, performing larger searches), the number of DNA molecules needed and time for hybridization increases rapidly and appears to limit the practicality of this approach. Sakamoto *et al.* (p. 1223; see the news story by Cho) suggest an alternative implementation that may prove more efficient. Sequences are encoded within single-stranded DNA molecules such that incorrect solutions create "hairpins," or internal double-stranded regions. Digestion of hairpin DNAs or amplification of normal strands yielded the correct solution to a nontrivial search problem.

ZIPPING UP NANOTUBES

Theoretcial studies suggest that two single-walled nanotubes can coalesce to form a single nanotube with a wider diameter, but direct experimental evidence for such a process has been lacking. Terrones *et al.* (p. 1226) have now captured the coalescence process using high-resolution transmission electron microscopy. They also investigate coalescence through molecular dynamics and Monte Carlo simulations and suggest that a zipper-like mechanism triggered by vacancies in adjacent tubes is responsible for the large-scale reorganization that ultimately leads to the formation of a wider nanotube.



SMOOTHING OUT TURBULENCE

Turbulence invariably hinders movement of an object through a fluid. Typically, streaks and eddies are generated near a boundary. Du and Karniadakis (p. 1230), using both models and an experimental system, demonstrate a way to suppress such eddies through generation of a traveling wave oriented transverse to the main flow. In practice, they show that eddy suppression can be accomplished with arrays of vibrating electromagnetic tiles or other smart skins on a surface.

SURVIVING WITHOUT SEX

Sexual reproduction and genetic exchange are thought to be essential to long-term evolutionary success, yet there have long been puzzling hints that a small number of organisms persist without any exchange at all. The bdelloid rotifers, small translucent bag-like animals that inhabit freshwater, are all females that reproduce parthenogenetically; males have never been seen. Any suspicions that these organisms might indulge in sex at barely detectable levels have now been laid to rest. Mark Welch and Meselson (p. 1211; see the Perspective by Judson and Normark) analyzed DNA sequence data from representative rotifer species and find a wide divergence between allelic sequences within single individuals of the asexual species. The level of divergence is consistent with the view that the bdelloids have abstained from sex for many millions of years. With this result, the mystery of sexual reproduction is deepened.

CLASS-CONSCIOUS TBPS

Despite years of intense research, there are many unanswered questions about the protein machinery that ensures accurate transcription of genes in the eukaryotic cell. One of these questions centers on whether a key component of this machinery, called TBP (TATA-binding protein), always requires the assistance of proteins called TAFs (TBP-associated factors) in order to activate transcription. Two reports provide evidence from chromatin immune precipitation studies in yeast cells that TAFs are required for transcription of some, but not all, genes. Kuras *et al.* (p. 1244) show that TBP exists in two distinct transcriptionally active forms, one associated with TAFs and one free of TAFs, and that these two forms display promoter-selective binding. Li *et al.* (p. 1242) de-

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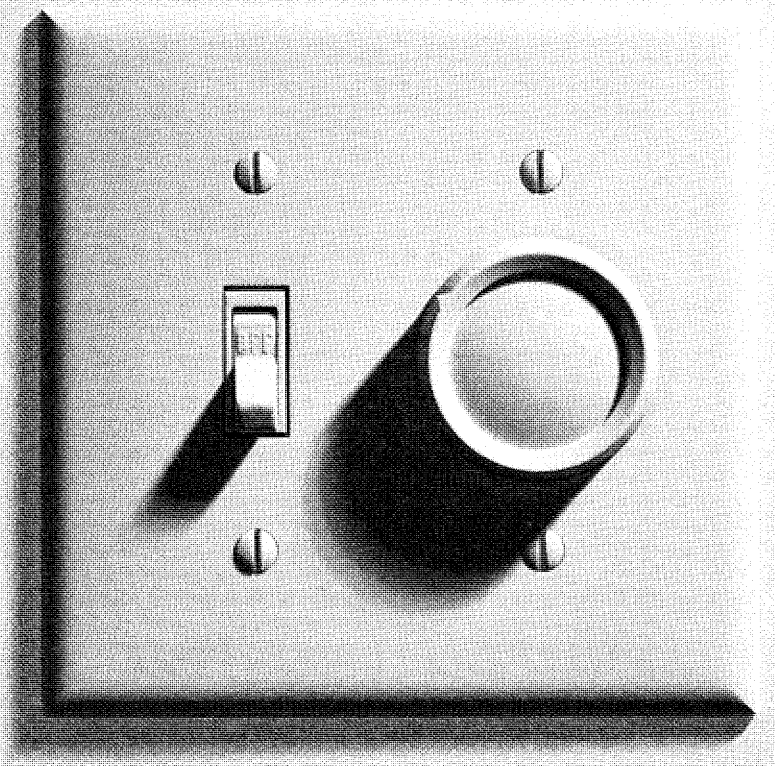

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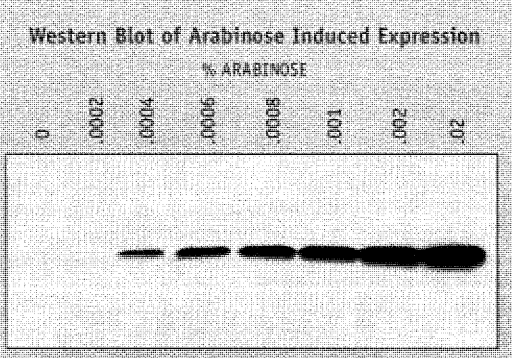

Arabinose induction of *E. coli* transformed with pBAD/His/Suprc-GFP

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THIS WEEK IN *SCIENCE*

CONTINUED FROM PAGE 1133

scribe two distinct classes of gene promoters, one that recruits TBP in the absence of TAFs and another that recruits both TBP and TAFs. These results challenge conventional views on how TBP is assembled at eukaryotic gene promoters.

STAYING A STEP AHEAD

Patients with cystic fibrosis (CF) produce a thickened form of mucus that stagnates in their lungs, which makes them highly susceptible to chronic colonization by the ubiquitous bacterium *Pseudomonas aeruginosa*. In vitro studies have previously shown that *P. aeruginosa* is highly adaptable under changing conditions. Oliver *et al.* (p. 1251; see the Perspective by Rainey and Moxon) have shown that naturally occurring isolates of the bacterium from CF patients not only show an extremely high frequency of "mutator" phenotypes but that the mutators also display high levels of antibiotic resistance. Unusually, mutators do not revert to wild type, but appear to become fixed in the population and persist in CF, probably because of the constant selection pressure from the antibiotic armamentarium given to these patients. The news that *P. aeruginosa* can accelerate its evolution under naturally occurring circumstances presents a significant challenge both to clinical scientists and to evolutionary biologists.

SYNAPTIC MODIFICATIONS

In the hippocampus, pyramidal neurons receive multiple excitatory stimuli through thousands of synapses. Accumulation of translation machinery in postsynaptic cells has been observed following stimulation, but the function has remained elusive. Huber *et al.* (p. 1254) examined the role of localized protein synthesis in generating changes in synaptic strength with stimulation. They found that protein synthesis in the postsynaptic cells modified synaptic transmission within minutes to create long-term depression of the synaptic contact. The finding has implications for the cellular mechanisms of information storage and memory.

SCRAPIE STRATEGY

Scrapie is carried by an abnormally folded, infective form of the prion protein, which then directly induces the abnormal form in previously normal prion protein molecules to cause disease in sheep, mice, and other animals. When animals are infected, the abnormal prions replicate in the spleen and then move into the central nervous system, a process that requires an intact immune system. Montrasio *et al.* (p. 1257) have now shown that dendritic cells are the key cellular element necessary for prion replication and neuroinvasion. They eliminated follicular dendritic cells, an antigen-presenting cell in the spleen by injecting a soluble lymphotoxin-β receptor that inhibited formation of functional dendritic cells. The similarity between the clinical course of scrapie and vCJD (the new variant of Jacob-Creutzfeld Disease seen in humans and possibly derived from bovine spongiform encephalopathy) suggests that interfering with the lymphotoxin-β receptor system may also delay the progress of the human disease.

TECHNICAL COMMENT SUMMARIES

Diversity of Human αβ T Cell Receptors

The full text of these comments can be seen at www.sciencemag.org/cgi/content/full/288/5469/1135a

Arstila *et al.* (Reports, 29 Oct., p. 958) estimated the lower limit of diversity of the human T cell receptor (TCR) repertoire at 2.5×10^7 different TCRs. The upper limit, they maintained, hinges on "the number of different α chains that each of the 10^6 β chains can pair with"—an average, they suggested, of 100 different α chains for each β chain. Noting that this implies an upper limit of some 10^8 different αβ combinations, Keşmir *et al.* comment that the actual upper bound could be considerably higher, as the same β chain may appear repeatedly and, each time, garner an alternative set of 100 different α chains. Thus, Keşmir *et al.* calculate, the upper bound for TCR diversity could be as high as 10^{11}, a figure that "would allow almost every T cell in the naïve repertoire to have a unique TCR." Arstila *et al.* respond that the alternative calculation of Keşmir *et al.* may rest on incorrect assumptions regarding the total turnover of naïve T cells, and may be less compatible than the Arstila *et al.* model with data regarding cell cycle length and the frequency of antigen-specific T cell precursors. "The phenomenon that Keşmir *et al.* postulate," they conclude, "although in principle possible, has little impact on the total diversity."

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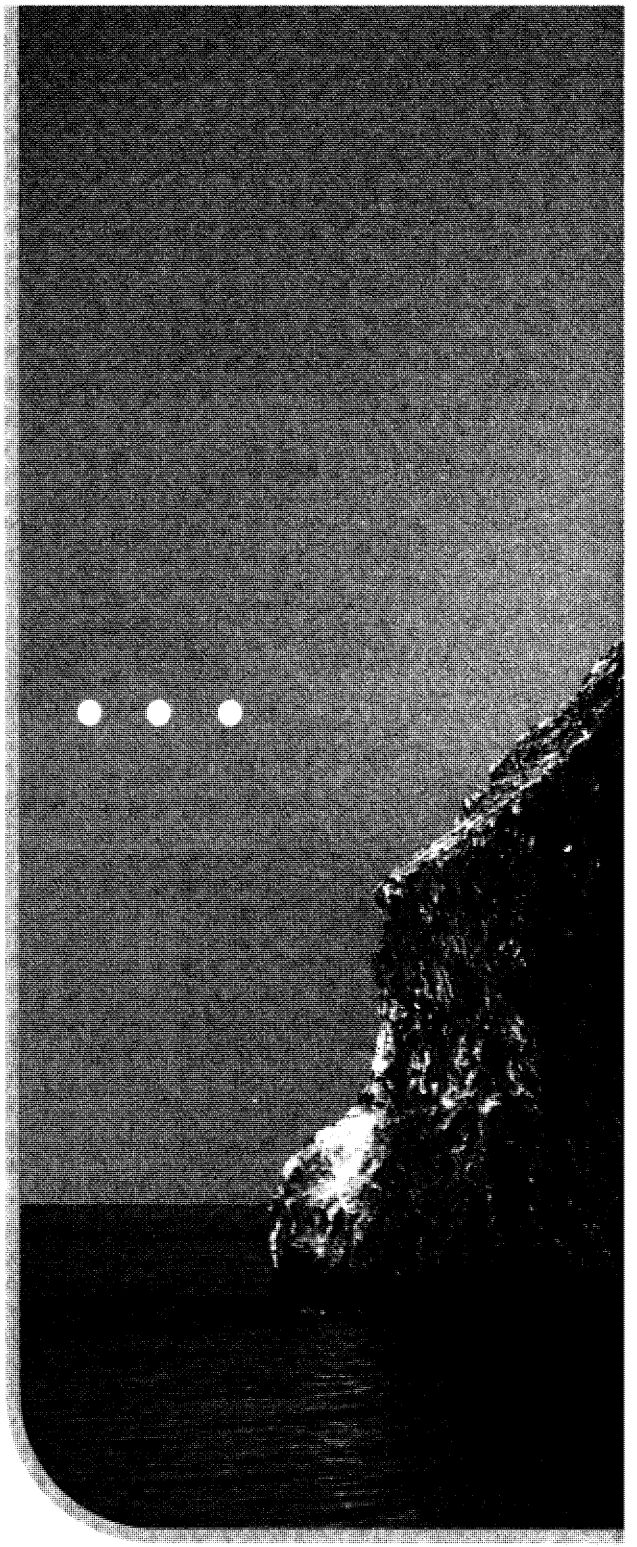

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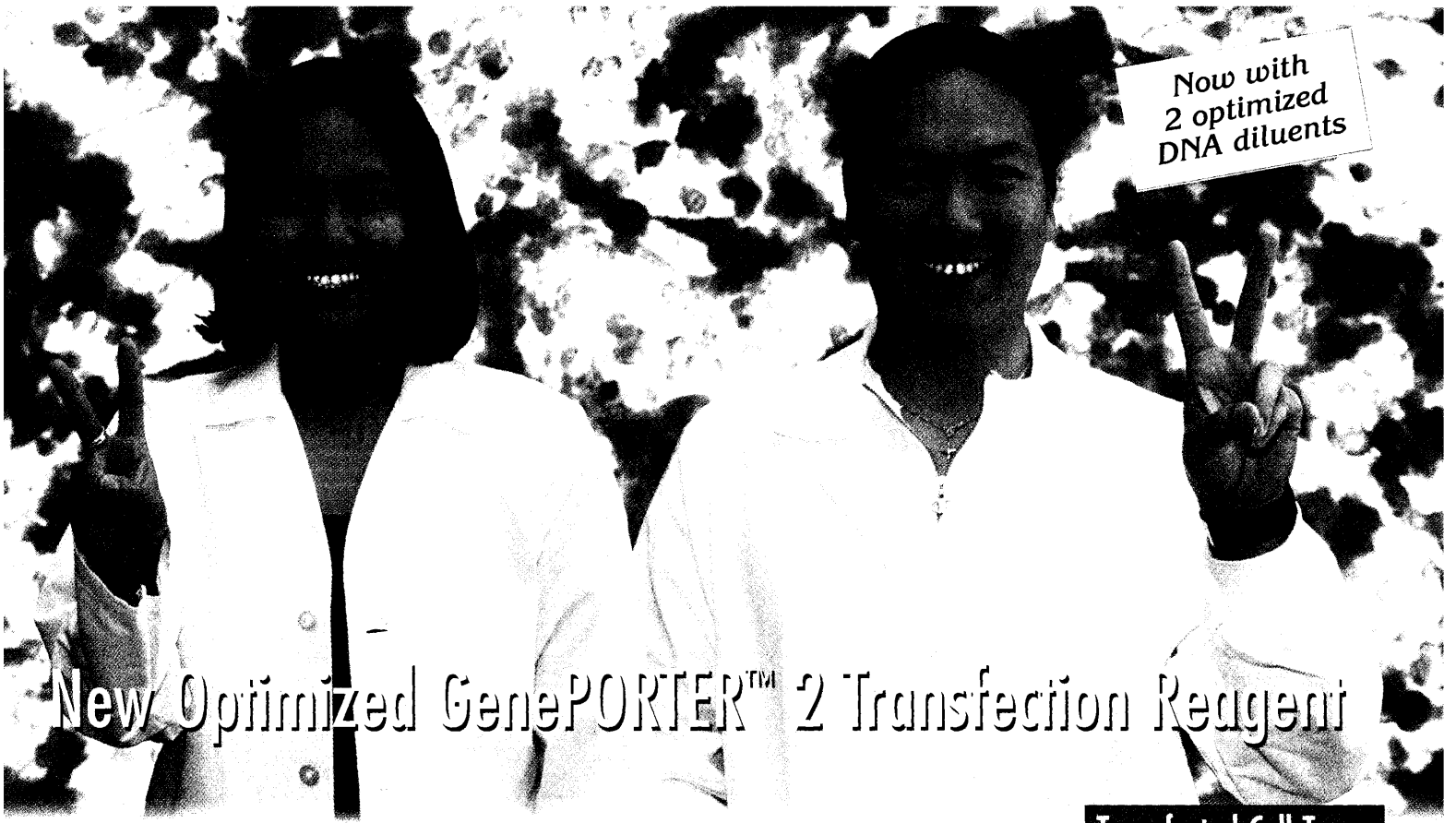

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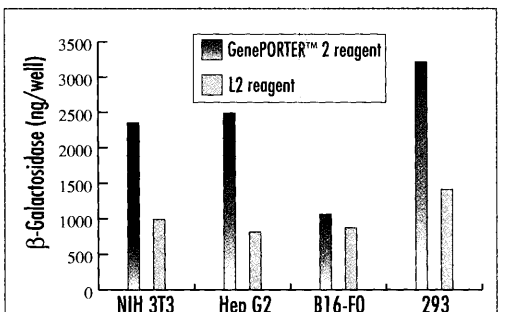

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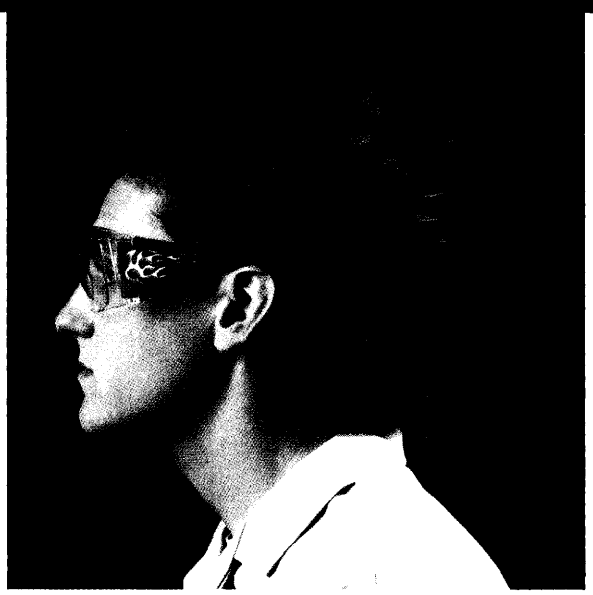

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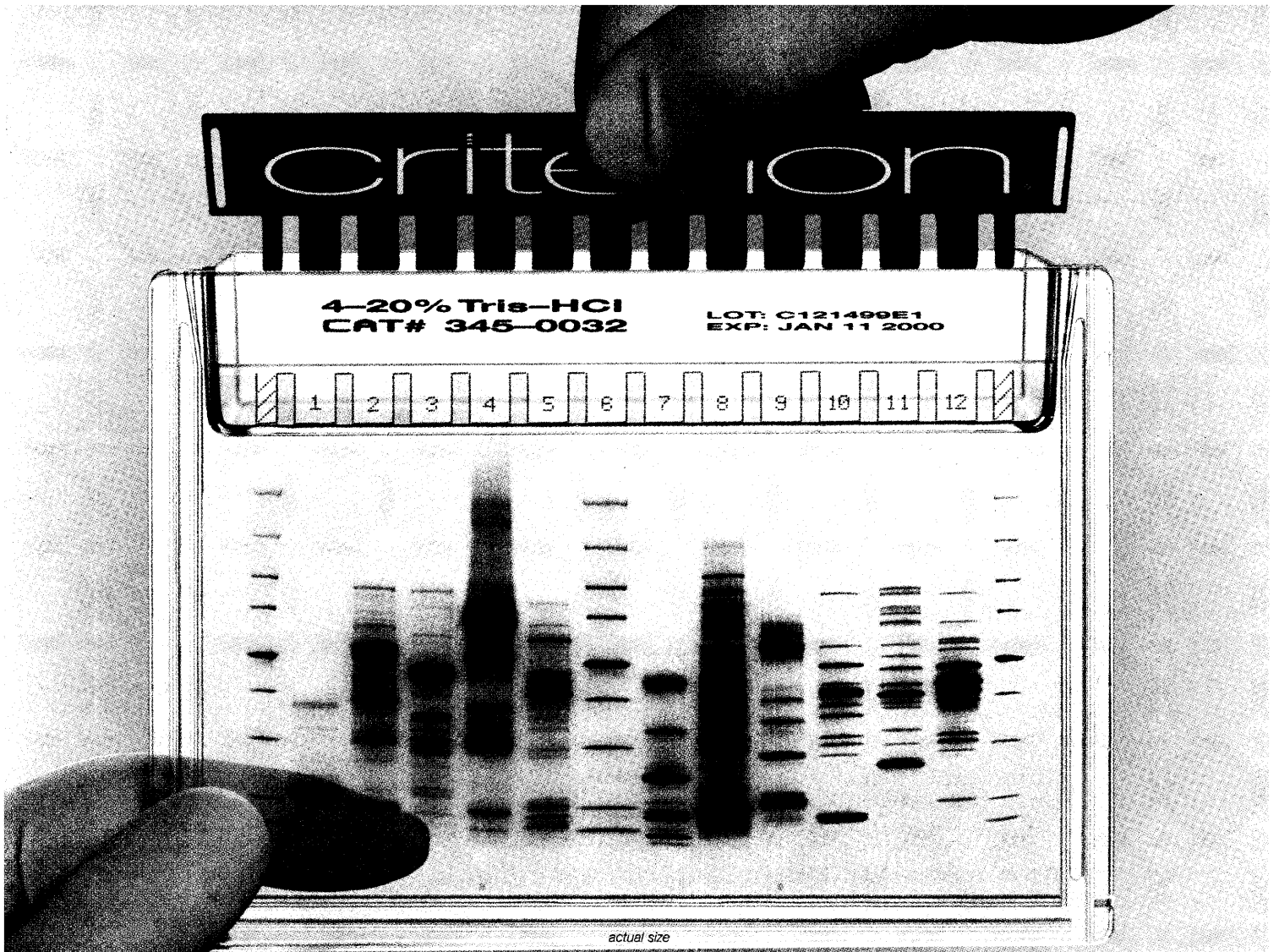

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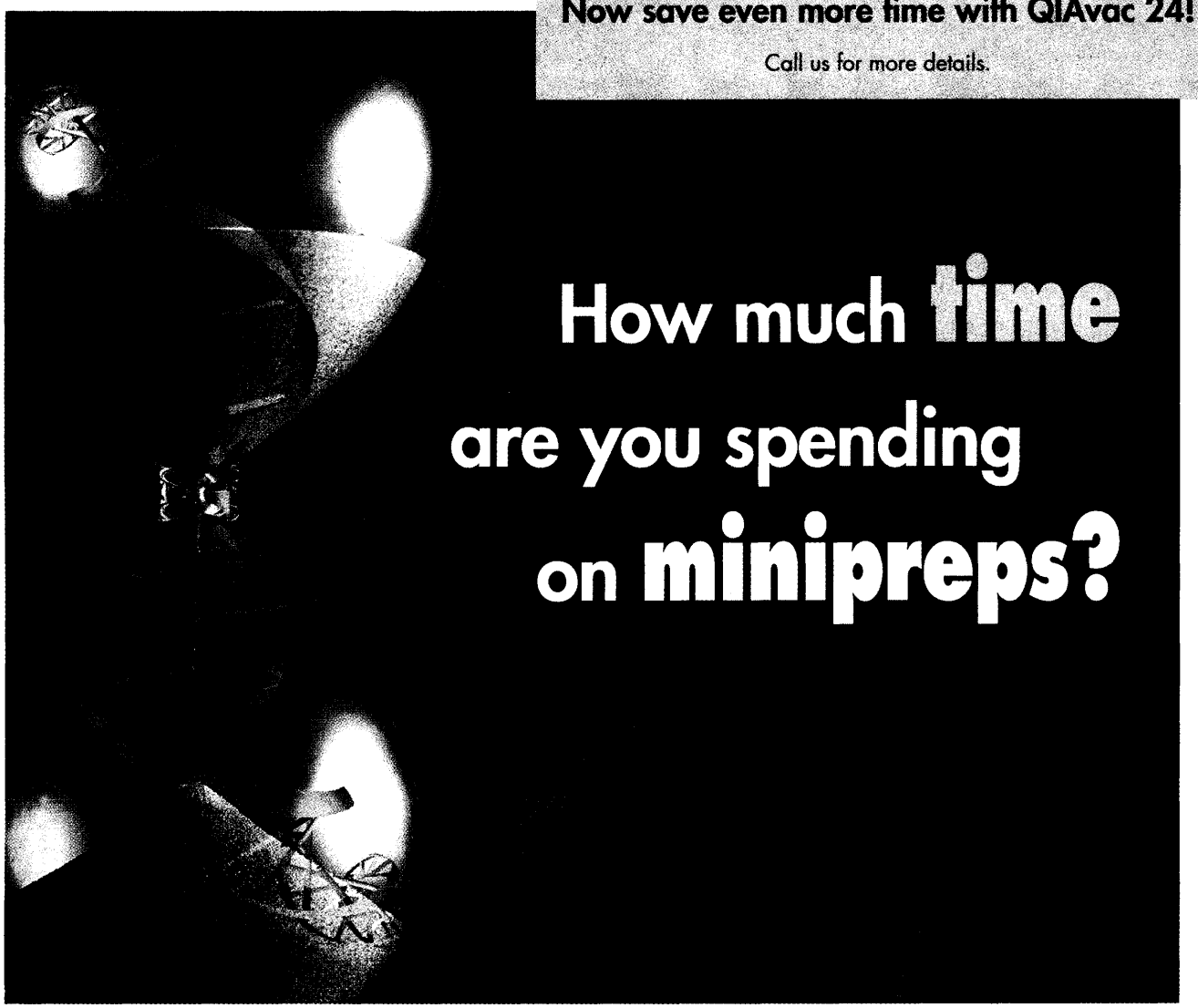

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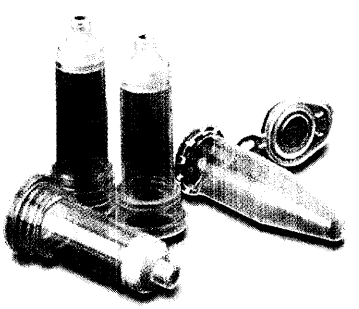

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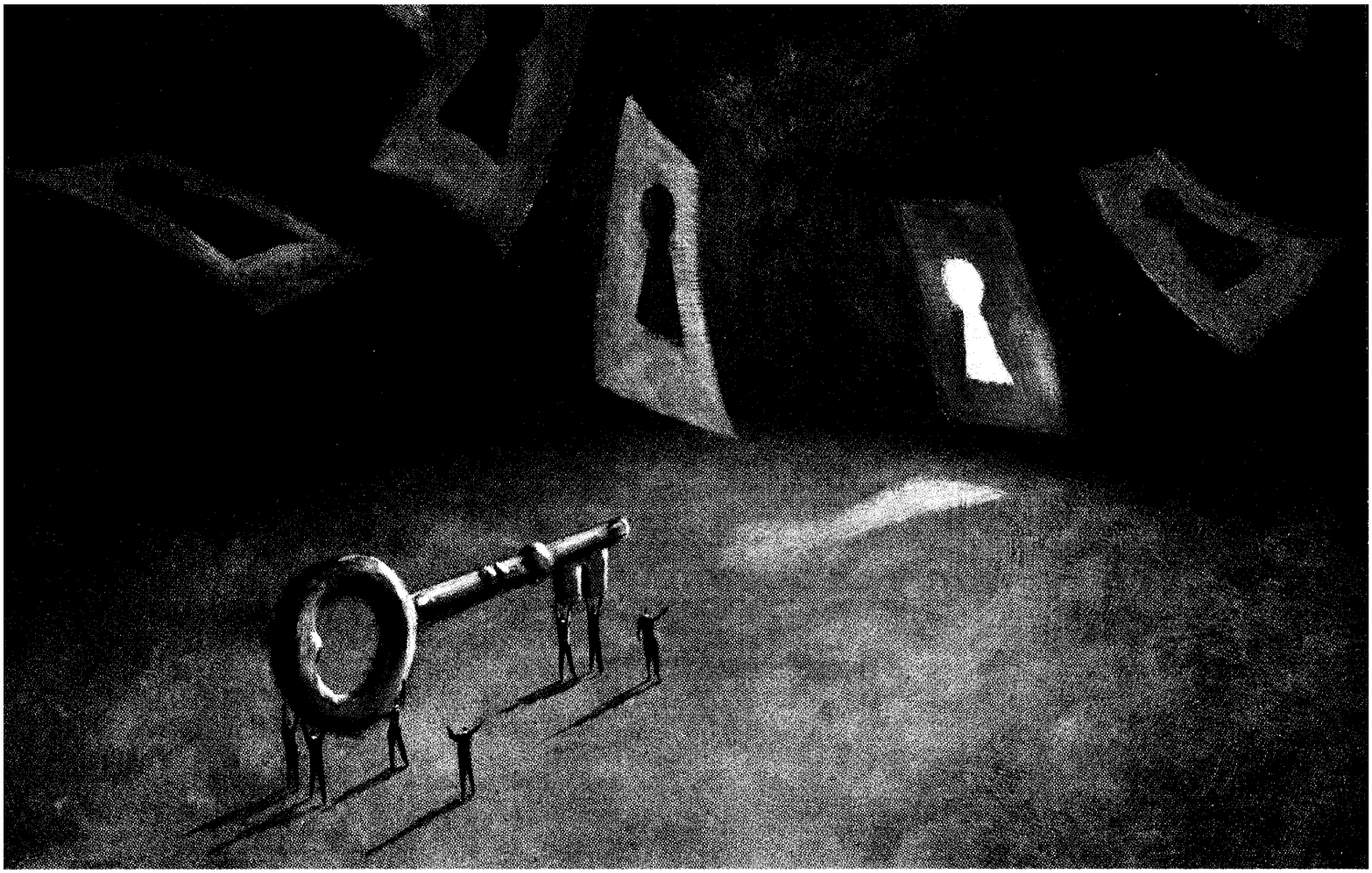

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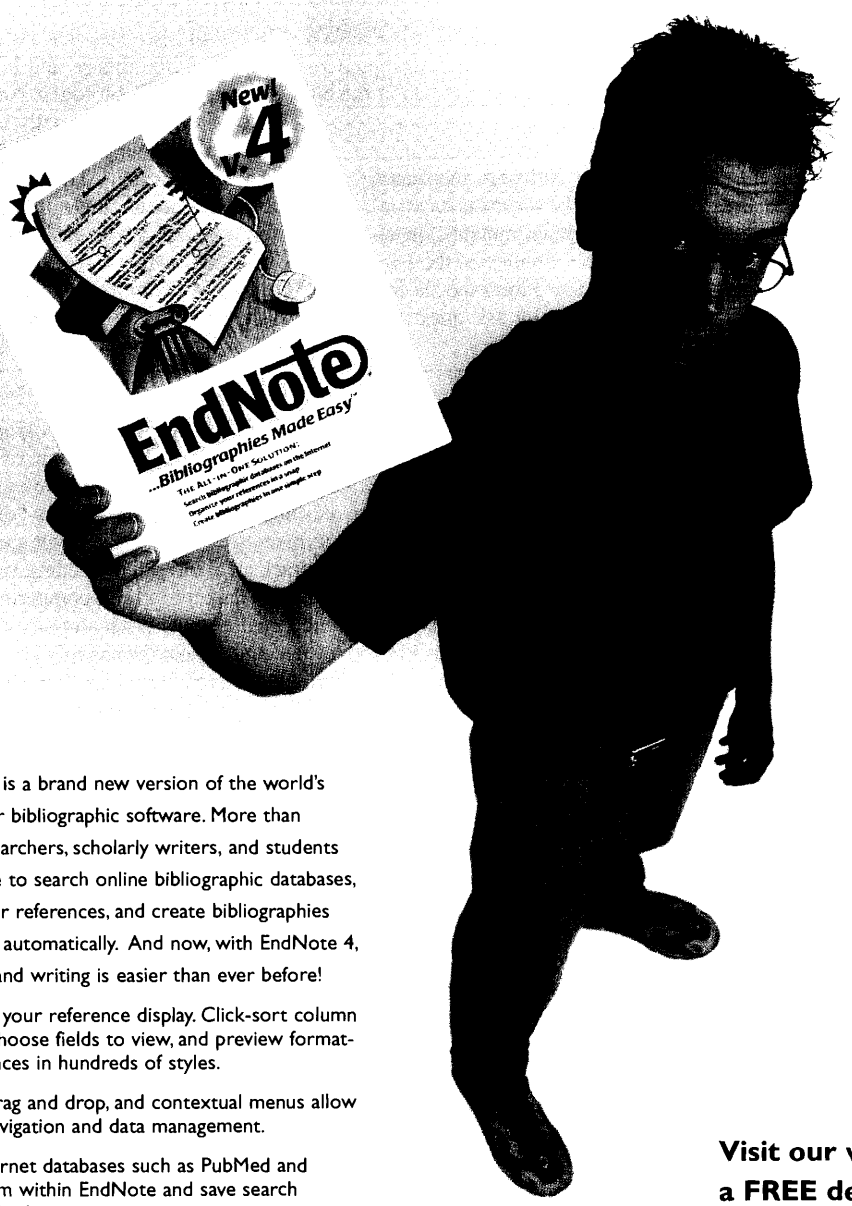

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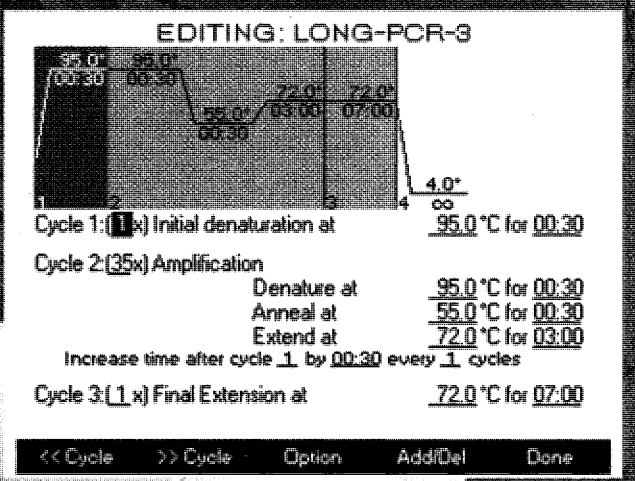

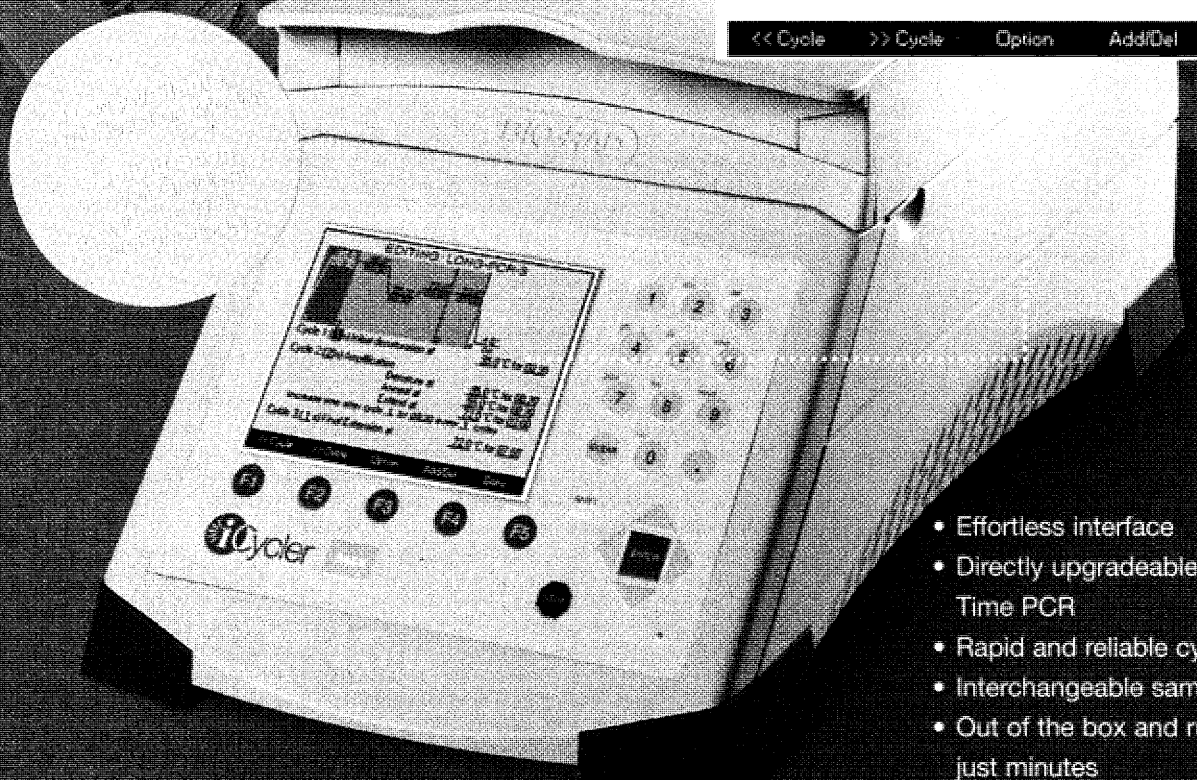

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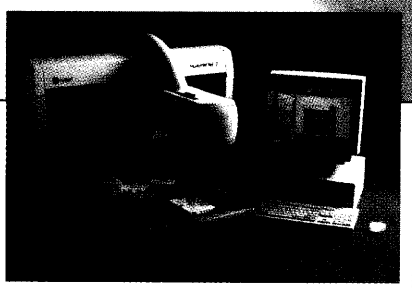

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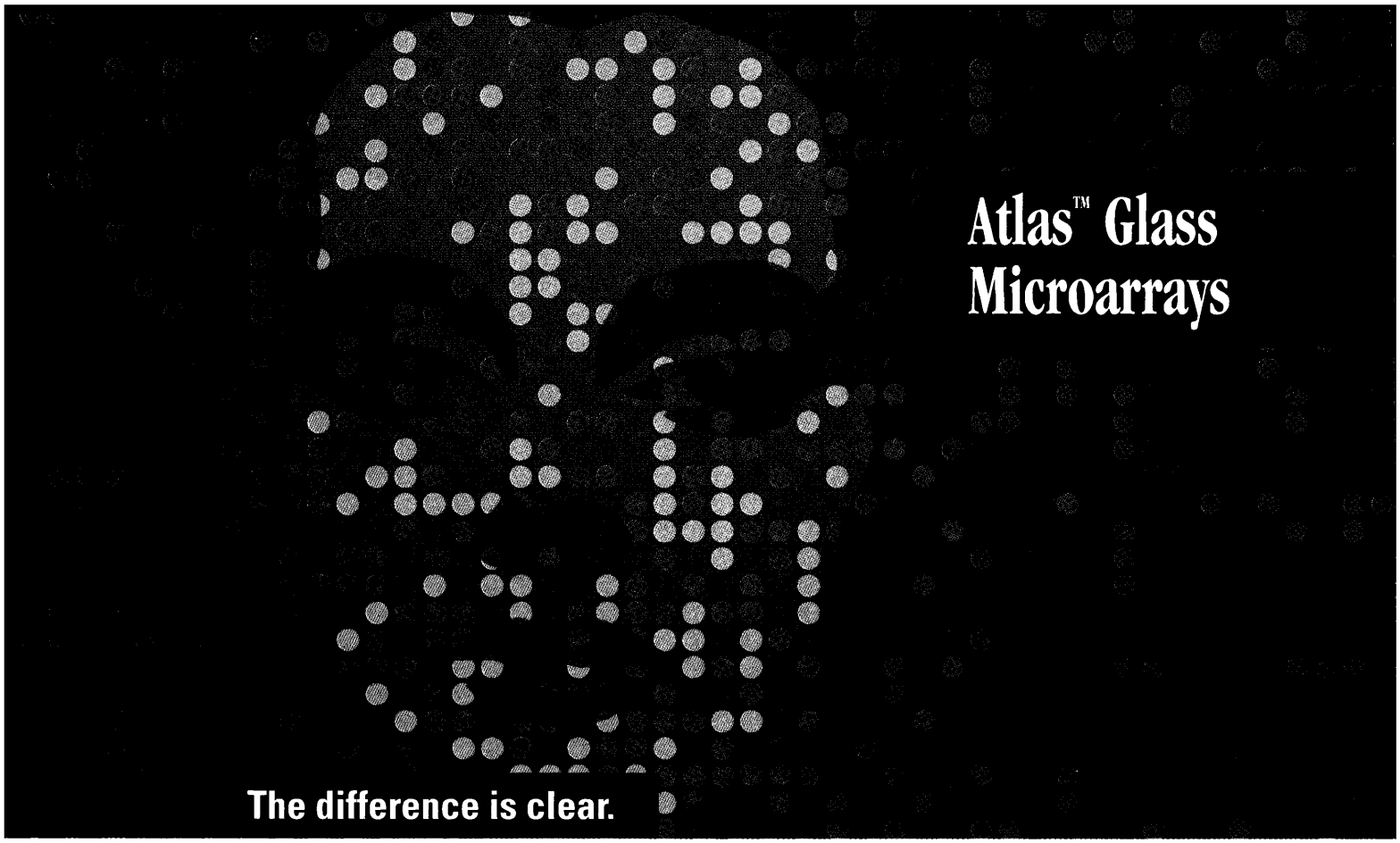

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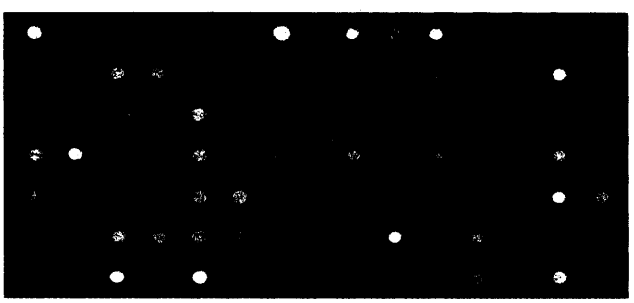

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