ANALYSIS OF THE *ARABIDOPSIS* GENOME

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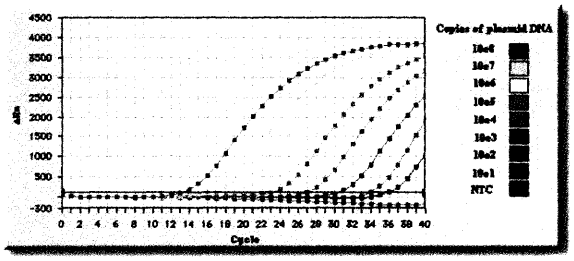

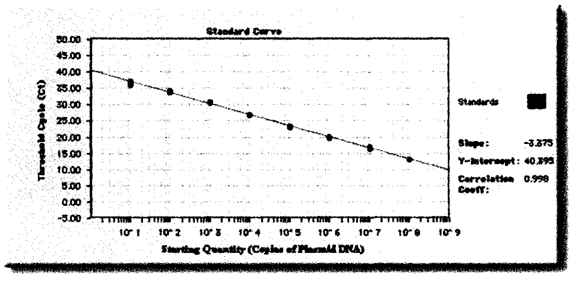

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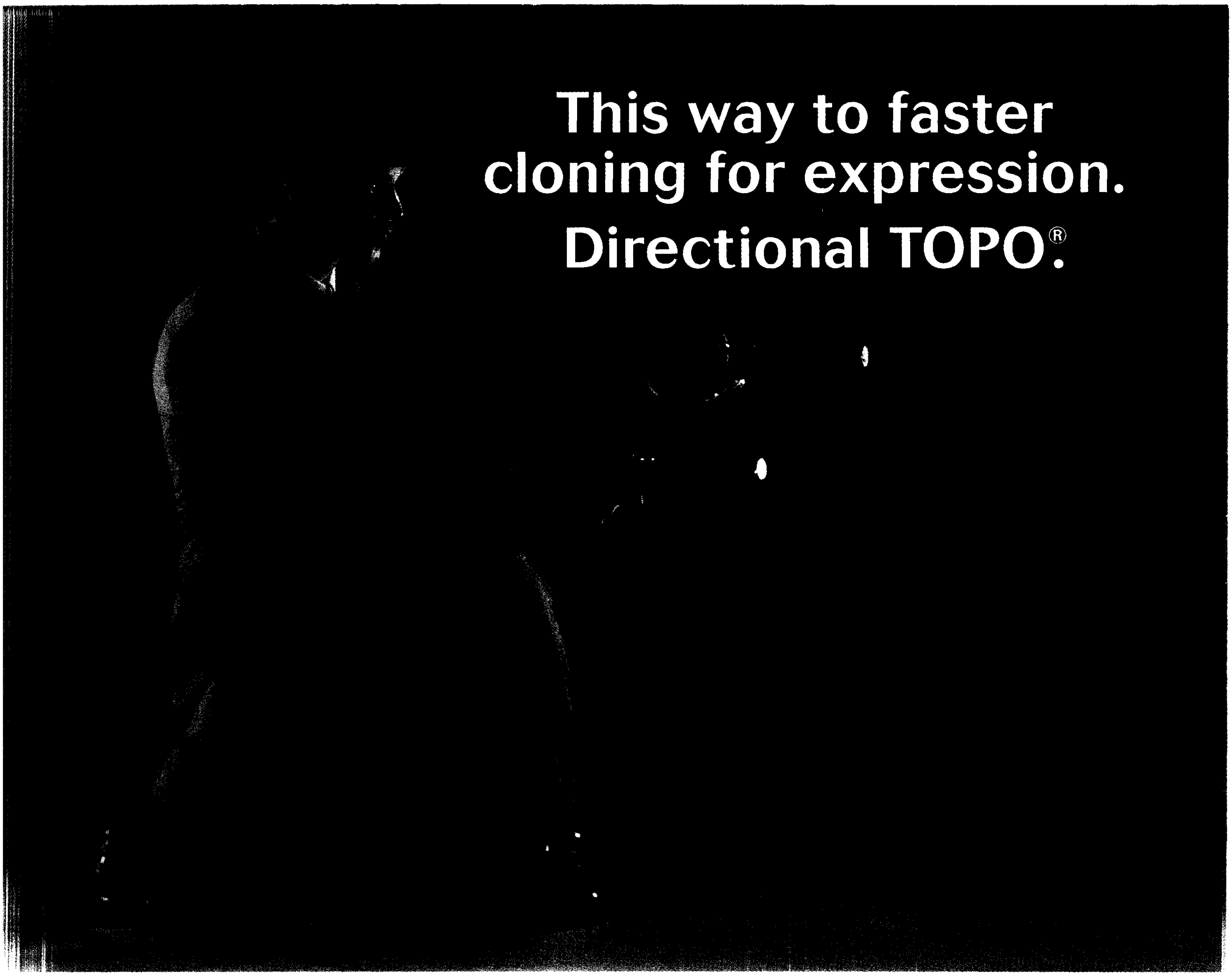

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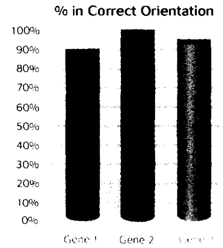

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COVER Molybdenum dioxide nanowires (300 nanometers in diameter) were electrodeposited from an aqueous solution onto this graphite surface, where each nanowire is formed at a preexisting defect. After reduction in hydrogen gas, metallic molybdenum nanowires are obtained. These nanowires can then be embedded in a polystyrene film and lifted off the surface intact, creating the potential for applications in microelectronics and chemical sensors. [Scanning electron microscope image: M. P. Zach]

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Arabidopsis sequence cuts the mustard

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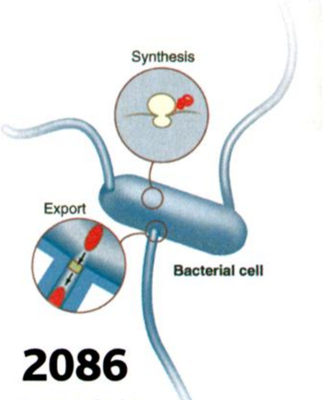

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Bacteria in motion

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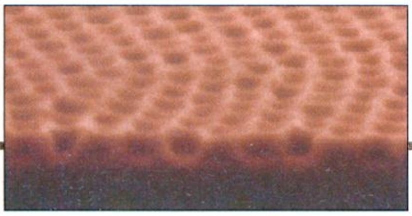

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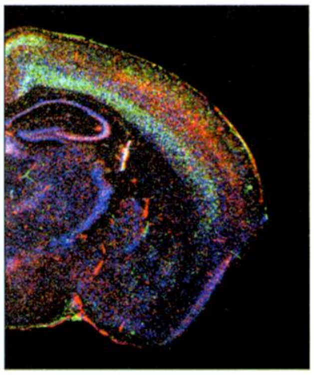

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Immune system molecules help build the brain

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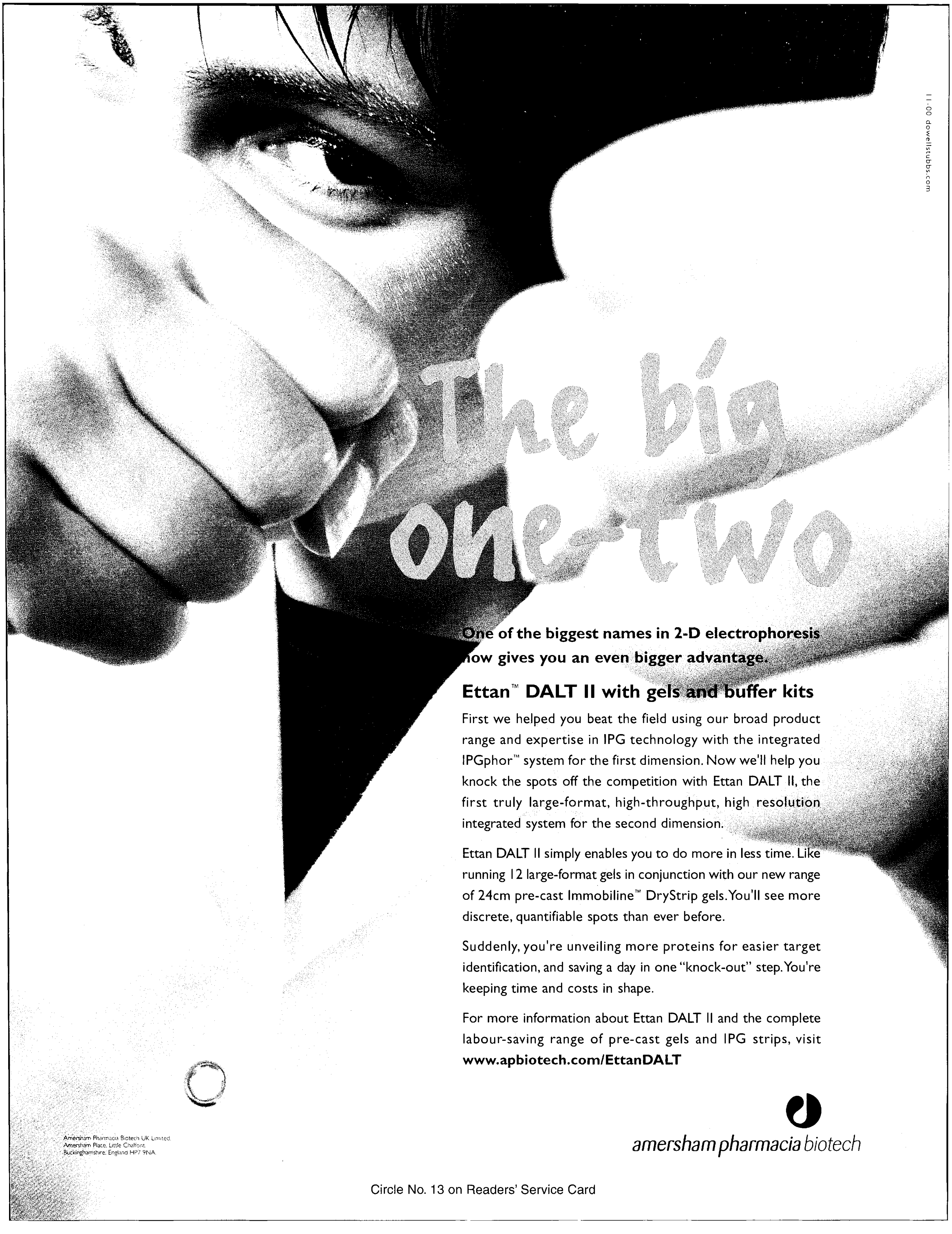

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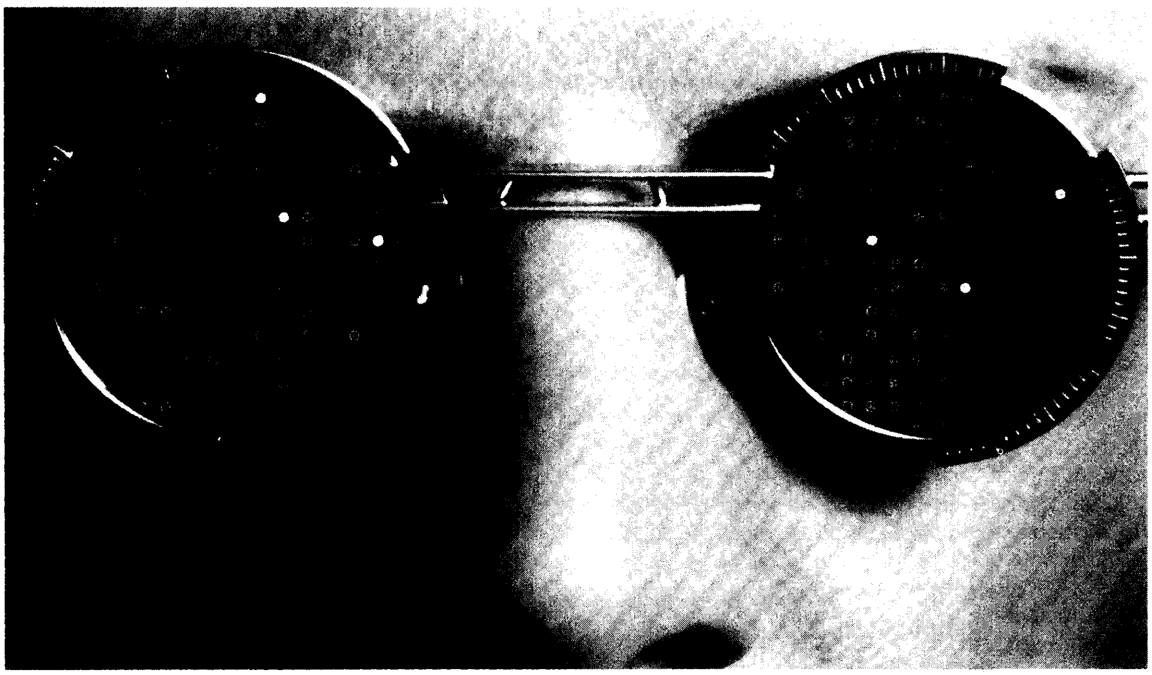

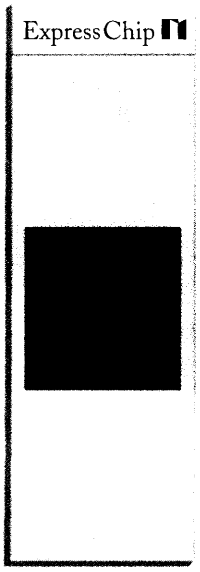

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THIS WEEK IN *SCIENCE*

edited by PHIL SZUROMI

PARITY VIOLATION AND STRANGE MAGNETISM

The magnetic properties of protons find widespread use in techniques such as magnetic resonance imaging, but there remains a lack of understanding of the fundamental physics underlying the generation of the proton's magnetic moment based on its internal structure. Hasty *et al.* (p. 2117; see the Perspective by Rosner) used the preferential scattering by protons of electrons with particular polarizations to probe strange quark interactions within the nucleus. Their results place constraints on the contribution of the strange quark-antiquark interactions to the proton magnetization to be –0.1 ± 5.1% of its total. The authors also present evidence for the existence of the anapole moment of the proton.

DENSELY PACKED MAGNETIC NANOWIRES

One route for making metallic nanowires is to grow them electrochemically in a nanoporous template. Although several types of templates can be made, it is often difficult to create templates that have narrow pores that are also closely and regularly spaced. Thurn-Albrecht *et al.* (p. 2126; see the news story by Service) field-aligned micrometer-thick block copolymer films of poly(methyl methacrylate) (PMMA) nanocylinder arrays within a polystyrene (PS) matrix; ultraviolet exposure removed the PMMA and cross-linked the PS. They could then grow densely packed, high-aspect ratio nanowires of copper or cobalt ($\sim 2 \times 10^{11}$ wires per square centimeter) and observed enhanced coercivities for the ferromagnetic cobalt wires compared with a continuous cobalt film of the same thickness.

NANOWIRES READY FOR LIFT-OFF

Flexible wire interconnects for nanodevices appear to be in reach. Zach *et al.* (p. 2120; see the cover) have made molybdenum wires on graphite that range from 15 nanometers to 1 micrometer in diameter and are half a millimeter in length. They could control the wire's diameter during its electrodeposition as an oxide, which was later reduced to the metal with hydrogen. The wires can be lifted off in polystyrene films and exhibit metallic conductivity—and they can be bent like the bulk metal. The method is applicable to other non-noble metals such as nickel.

BETTER AFTER A STRETCH

One potential use for self-assembled monolayers is as coatings for the tailoring of wetting behavior. However, for some materials, such as elastomeric silicones, it has proven difficult to generate sufficient attachment points for molecules to achieve packing densities high enough to change their surface properties. Genzer and Efimenko (p. 2130) show that by first stretching a silicone and then generating additional surface hydroxyl groups with ultraviolet light exposure and ozone, they could create high surface densities of semifluorinated hydrocarbon chains. The treated silicones retained high hydrophobicity and avoided surface reconstruction even after being stored under water for a week.

INDY-DEPENDENT LIFE-STYLE

Aging and life-span are still poorly understood aspects of basic biology, although it is widely accepted that genetic factors play a role. To identify specific genes that influence life-span, many researchers have turned to model organisms such as yeast, worms, and flies. Rogina *et al.* (p. 2137; see the news story by Pennisi) have found that altered expression of a single gene in the fruit fly *Drosophila* nearly doubles the life-span of the flies without adverse effects on fertility or physical activity. This gene, called *Indy* (for *I'm not dead yet*), encodes a protein with sequence homology to mammalian sodium dicarboxylate cotransporters, transmembrane proteins that transport Krebs cycle intermediates across the plasma membrane. Based on this sequence homology and the gene's expression pattern in the flies, the authors postulate that *Indy* affects life-span by altering absorption and utilization of metabolites, perhaps creating a metabolic state similar to caloric restriction.

TWISTING AND PUSHING

The bacterial flagellum is composed of subunits that are inserted at its tip. The basic mechanism of growth involves the transfer of subunits through a hollow channel along the flagellum, but how assembly at the tip is controlled has not been obvious. Yonekura *et al.* (p. 2148; see the Perspective by Macnab) evaluated the process using image reconstruction of electron micrographs. Their results yield startling information on how the cap structure at the tip of the flagellum appears to rotate to allow the insertion of new subunits while always maintaining at least one point of contact with the flagellum.

LESSONS FROM *ARABIDOPSIS* GENOMICS

Analysis of the genome of the tiny *Arabidopsis* plant is revealing new insights not only into plants and their evolution, but also into relations across kingdoms of organisms (see the Policy Forum by Somerville and the news stories by Pennisi and Mlot). The transcription of certain genes changes in a regular pattern throughout the circadian cycle. Harmer *et al.* (p. 2110) analyzed 8000 *Arabidopsis* genes with oligonucleotide microarrays and found that about 6% showed daily cycles of expression. Entire metabolic pathways exhibit coordinated circadian rhythms of their components. In this comparative survey of genomes, Riechmann *et al.* (p. 2105) analyzed major families of transcription factors. Comparisons of whole-genome sequences from *Arabidopsis*, *Caenorhabditis elegans*, *Drosophila*, and yeast show that some families of transcription factors are held in common across kingdoms, whereas other families appear to belong to only one kingdom. For those factors that are represented in all of the kingdoms, the DNA binding domain shows the most similarities—but these factors can show divergent functions. A comprehensive analysis of the *Arabidopsis* genome by Vision *et al.* (p. 2114) shows that this tiny plant went through an age of multiple, large-scale genome duplications before settling down into its current phase of relative stability. Chromosome fusions, inversions, and translocations have also helped shape the current *Arabidopsis* genome.

BACTERIAL CELL CYCLES

The array of genes that are expressed during the life cycle of a cell can be pictured as a complex genetic circuit. Laub *et al.* (p. 2144) provide a global survey of the part of that circuit that is expressed during the cell

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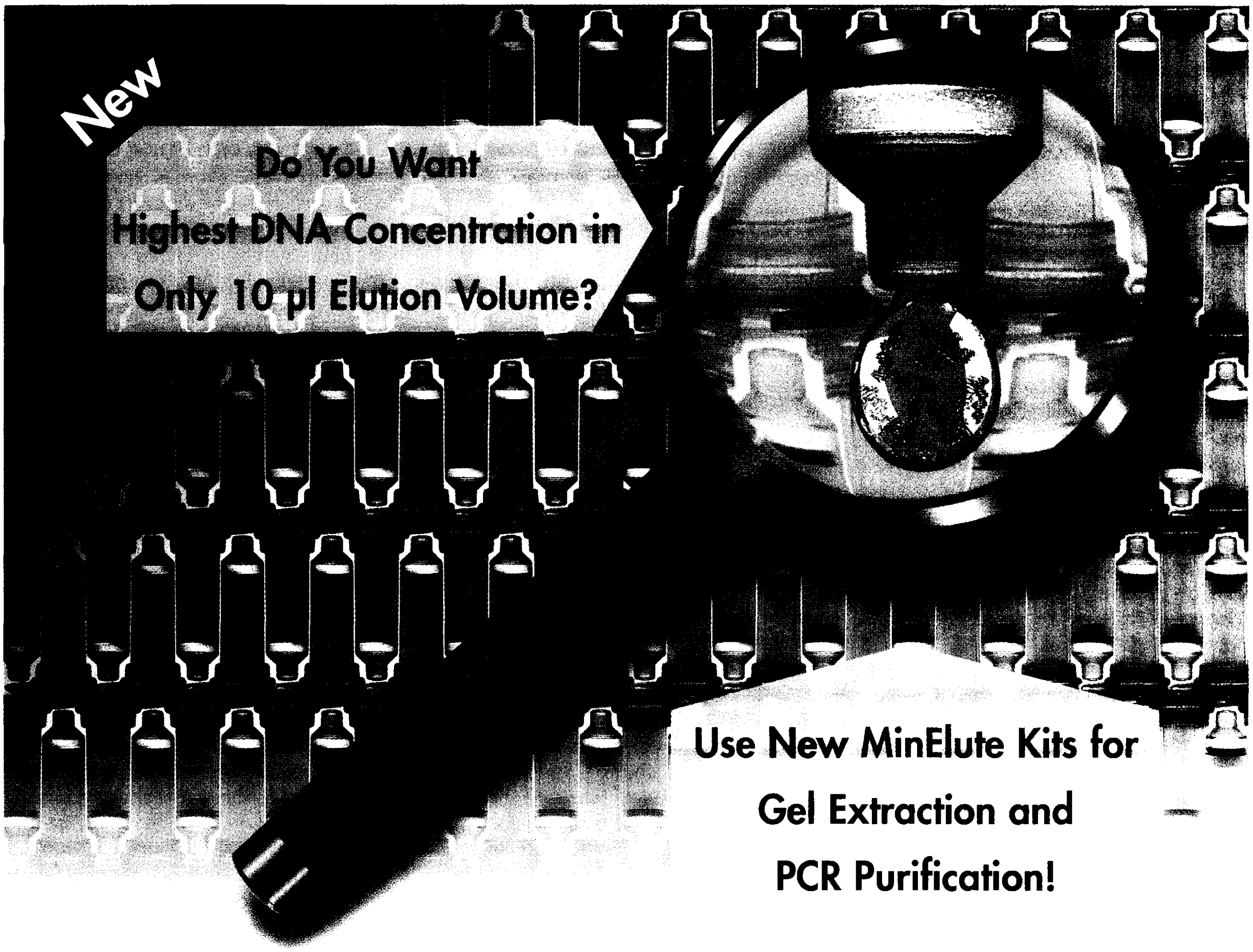

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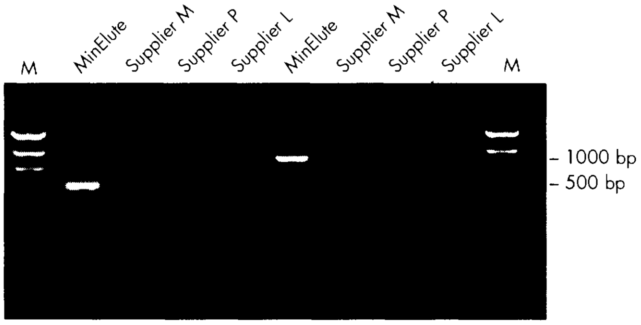

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CONTINUED FROM PAGE 2029

cycle of *Caulobacter crescentus*, a bacterium that differentiates during the course of its life. Out of nearly 3000 genes, 553 show cell cycle regulation. Temporal controls over genes involved in specific cell functions and coordinate regulation of proteins that are part of complexes were also observed. *CtRA* was shown to be a central regulator of the cell cycle in experiments with overexpressing or loss-of-function mutants. A histidine kinase and two RNA polymerase sigma factors were identified as possible regulators of early S phase.

BRAIN-BUILDING MHCs

In some ways, the nervous system and the immune system solve similar problems: They both have to distinguish and respond to an extremely large array of input from the external world, and both are exceedingly complex. Huh *et al.* (p. 2155; see the news story by Helmuth) show that class I major histocompatibility complex (MHC) molecules, used by the immune system to respond to antigens, are also necessary for accurate assembly of the brain. In mice genetically deficient for class I MHC molecules, the neural connections between the retina and their targets in the central nervous system are abnormal. Long-term potentiation, a form of cellular learning, is enhanced, and another form, long-term depression, is eliminated. The diversity and specificity of class I MHC molecules makes them attractive candidates for a role in establishing neural connections.

GETTING WARMER

Global annual mean near-surface air temperature increased during the 20th century in two major steps, the first between roughly 1910 and 1940 and the second (which is still continuing) after about 1975. It has been difficult to understand the causes of this overall rise, partly because anthropogenic forcing by fossil fuel combustion has grown steadily during that interval and partly because it was not as important a forcing factor in the first half of the century as in the second. Stott *et al.* (p. 2133; see the Perspective by Zwiers and Weaver) have used a state-of-the-art climate model, HadCM3, to examine the reasons for this increase. An ensemble of four simulations of the last 140 years indicates that a combination of natural climate variations and human-induced variability can explain the observed temperature rise, and that most of the multidecadal-scale global variations are not due to internal variability of Earth's climate system, but are externally forced.

DENDRITIC CELL ORIGINS

The expression of $CD8\alpha$—a cell surface molecule ordinarily found on cytotoxic T cells—has long been used to discriminate between two anatomically and functionally distinct subsets of dendritic cells (DCs). Much debate has revolved around whether each class of DC is derived from a discrete lineage of progenitors. It has been proposed that $CD8\alpha^-$ DCs are derived from a myeloid progenitor and that the less abundant $CD8\alpha^+$ DCs are lymphoid in origin. Thus, some of the differences in physiology of these cells have been attributed to these alternative pathways of development. Using transfer of clonogenic common myeloid progenitor cells, Traver *et al.* (p. 2152) demonstrate that both $CD8\alpha^+$ and $CD8\alpha^-$ can develop from a common myeloid ancestor. The distinct biology of each type of DC must depend on factors other than early differences in lineage commitment.

TECHNICAL COMMENT SUMMARIES

Genetic Polymorphism in CX_3CR1 and Risk of HIV Disease

The full text of these comments can be seen at www.sciencemag.org/cgi/content/full/290/5499/2029a

Faure *et al.* (Reports, 24 March, p. 2274), in a study of French Caucasian patients from three HIV-infected cohorts, found that patients homozygous for a specific single nucleotide polymorphism (SNP) in the chemokine receptor CX_3CR1—which is also a coreceptor for human immunodeficiency virus (HIV)—progressed to AIDS more rapidly than did those with other haplotypes. In a comment, a group including the senior author of the Faure *et al.* study report that they were unable to confirm these associations in a subsequent study of three North American cohorts. They suggest a number of possible explanations for the discrepant results, including the comparatively small number of patients homozygous for the suspect allele in both studies and known compositional differences (in characteristics such as gender, HIV risk category, and median length of patient follow-up) between the French and North American cohorts. "Nonetheless," the comment authors conclude, the results of the two studies, "taken together, do not support a clear and consistent role for CX_3CR1 in HIV pathogenesis."

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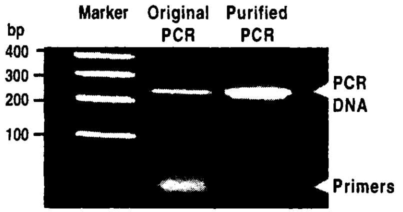

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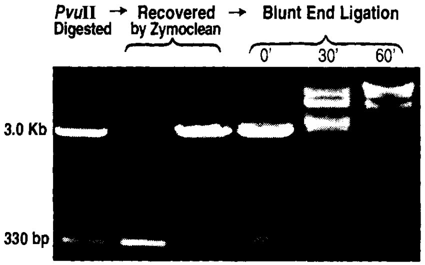

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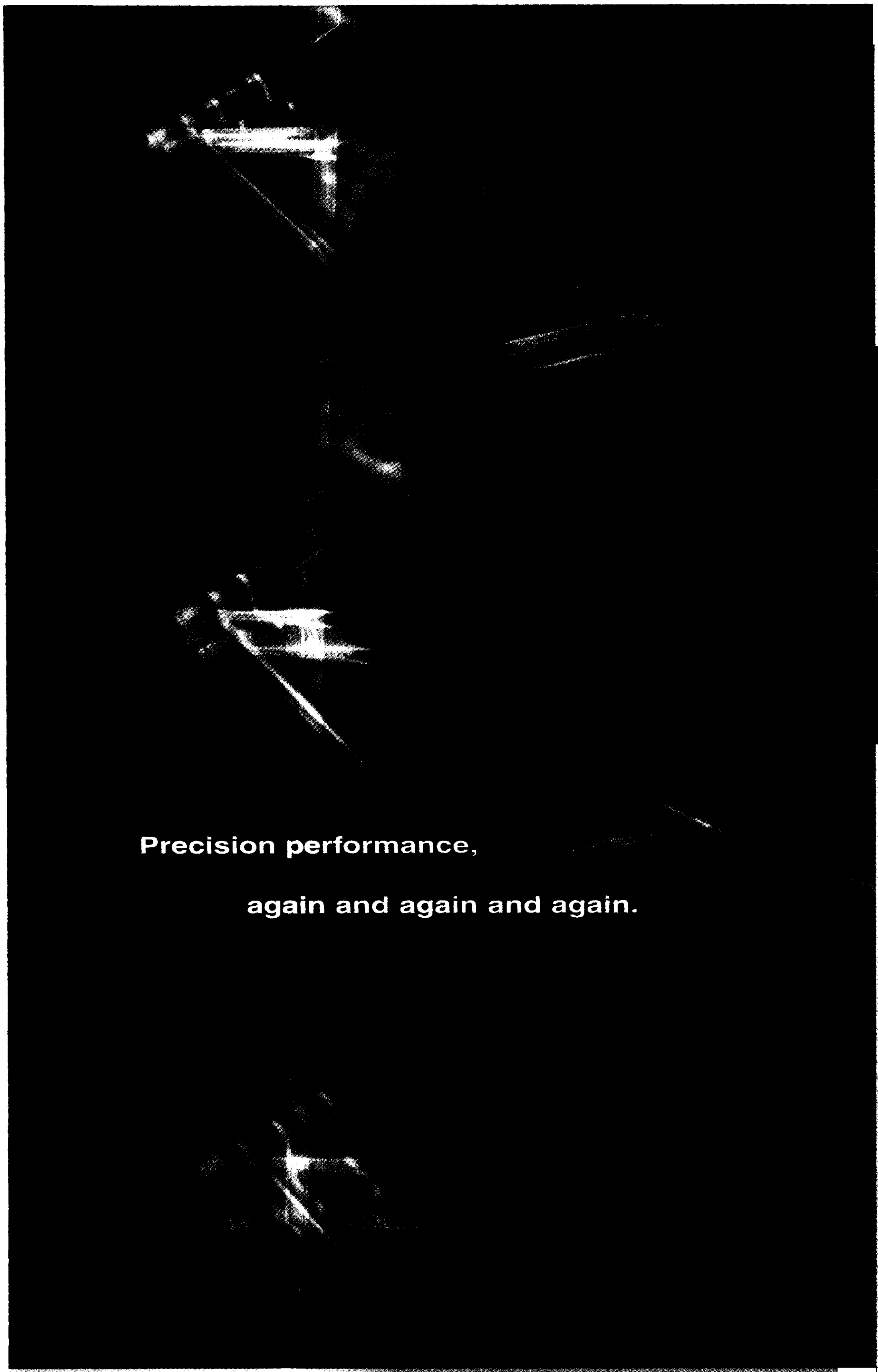

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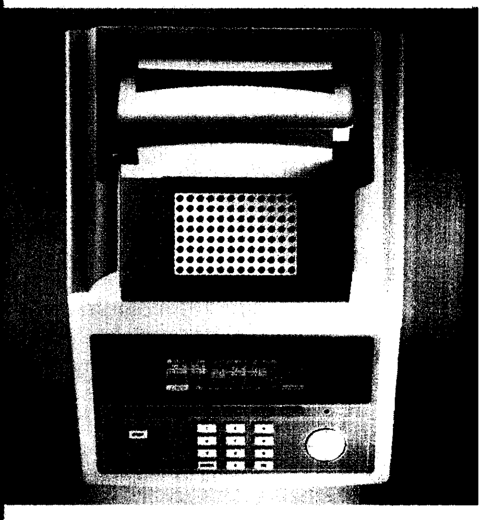

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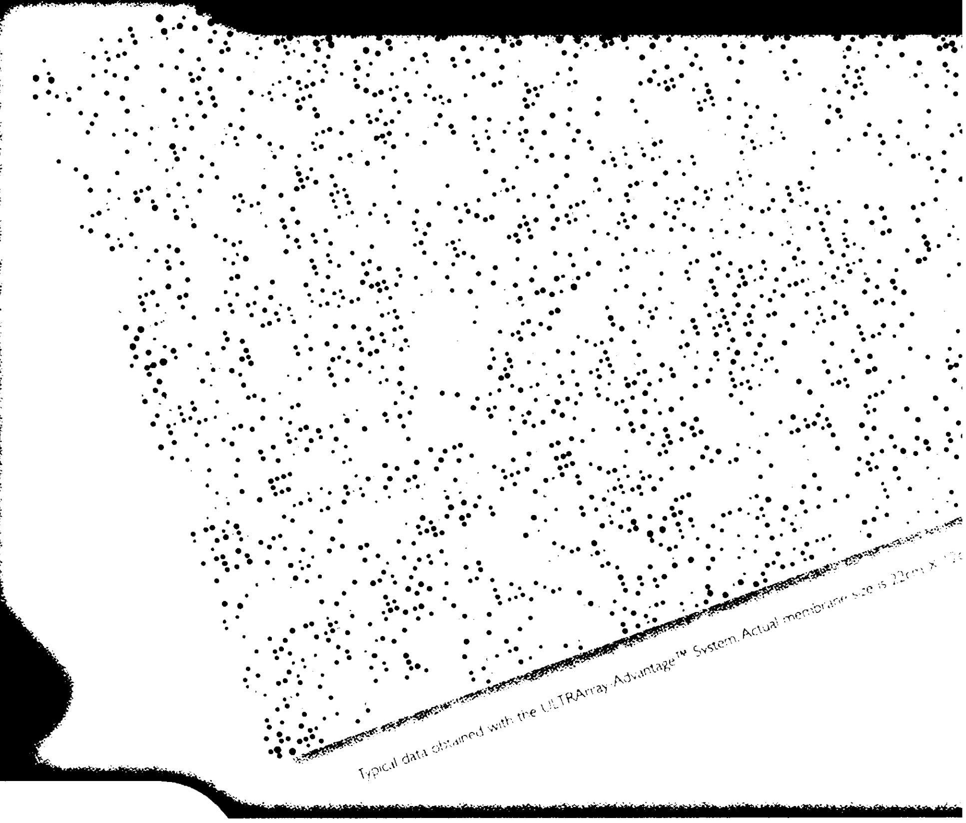
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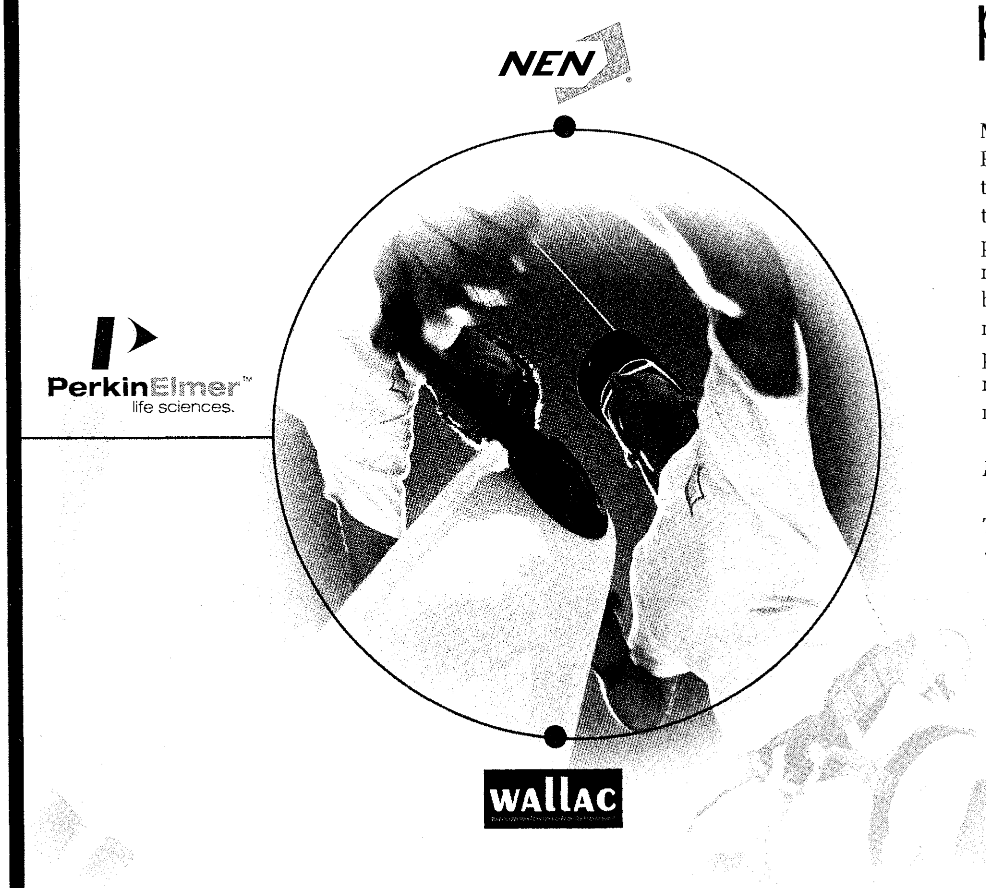

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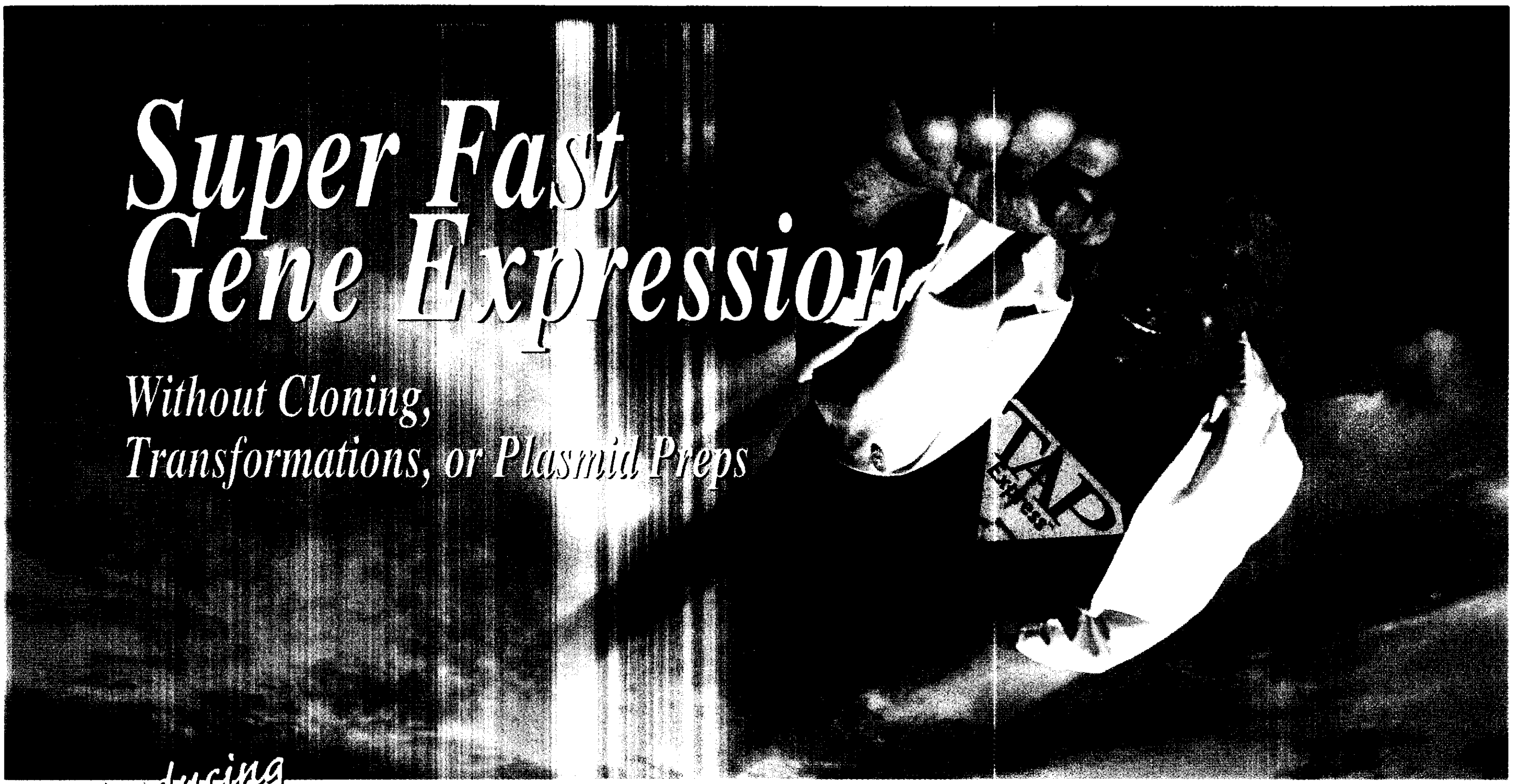

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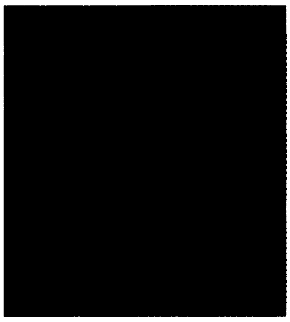

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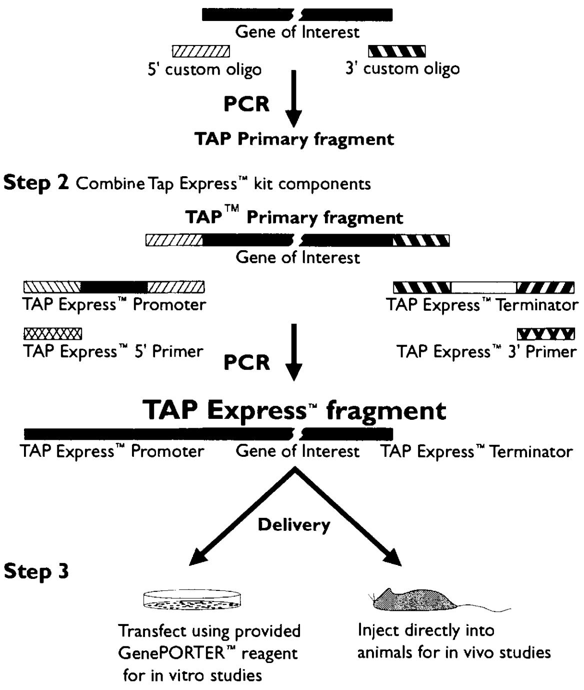

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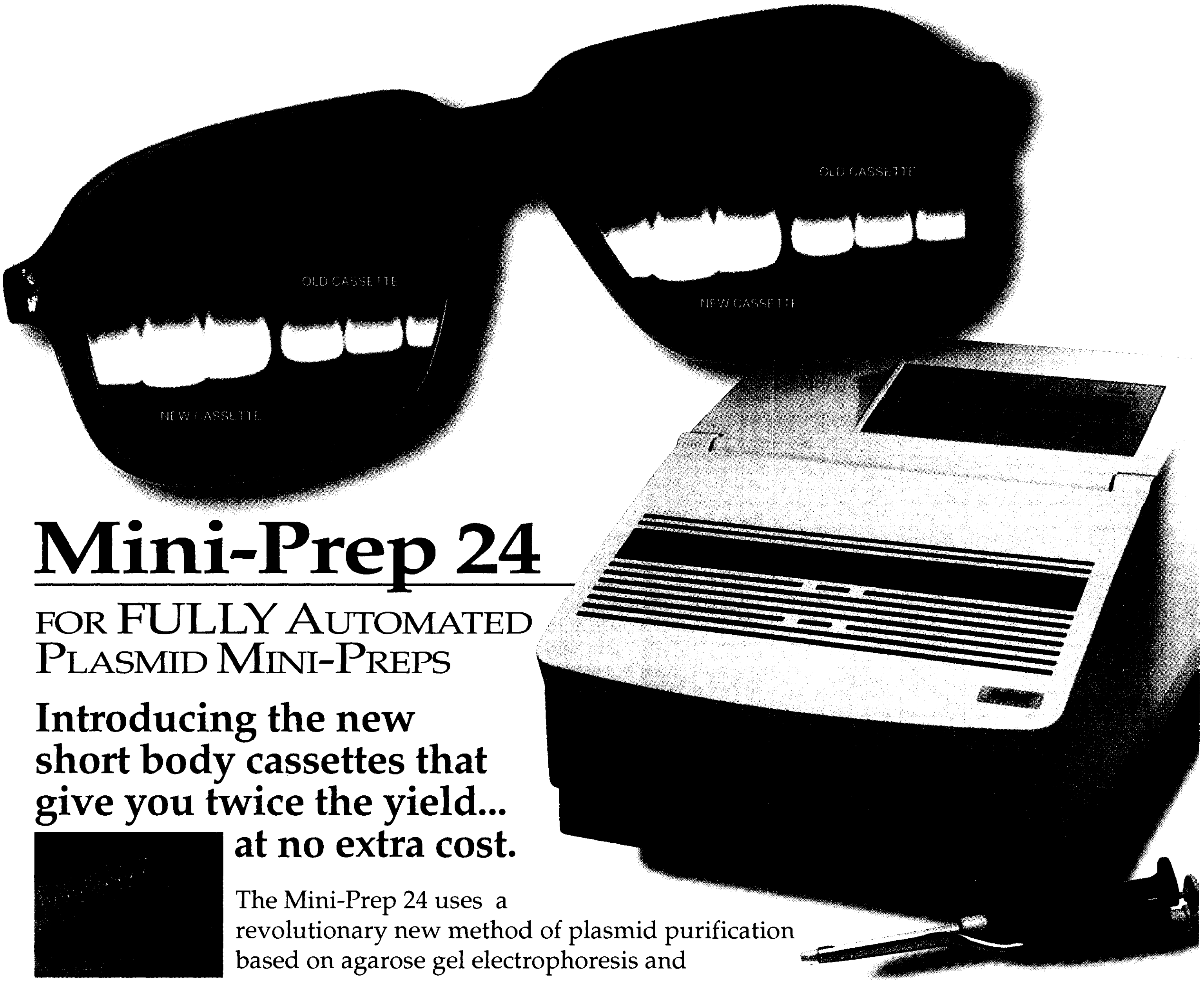

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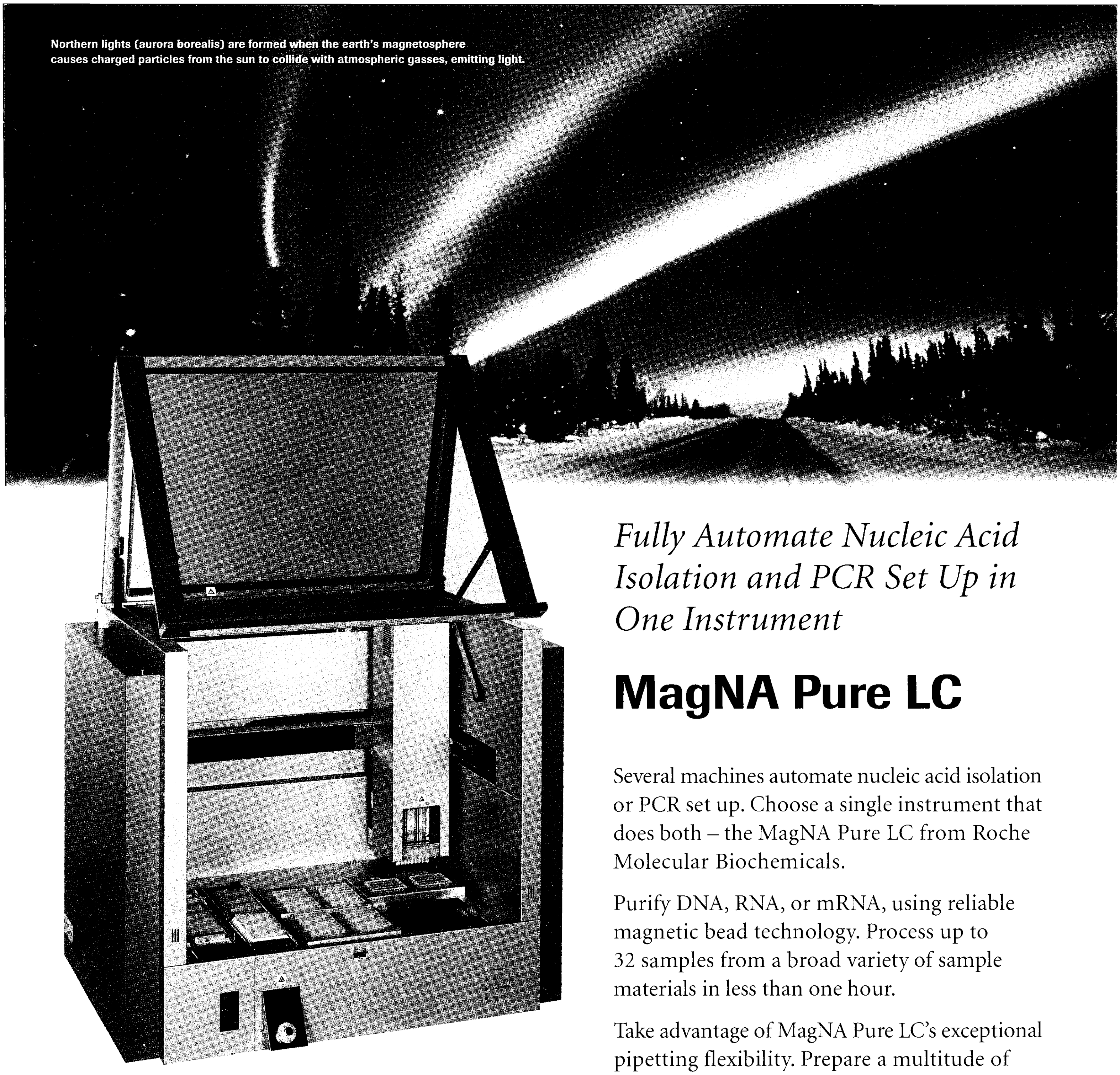

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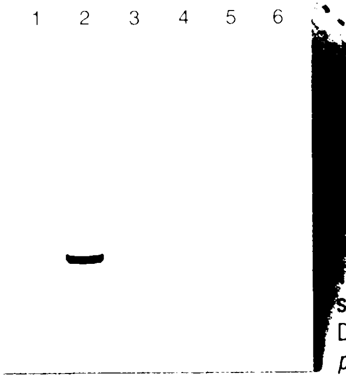

fferent sized products expressed using the TnT® Quick for PCR DNA System and FluoroTect™ reen$_{Lys}$ in vitro Translation Labeling System. he gel was visualized using a Hitachi FMBIO® II scanner. Lane 1. no DNA, Lane 2. Luciferase control DNA (61kDa), Lanes 3–6, APC (*adenomatous polyposis coli*) locus PCR products, 40–80kDa.

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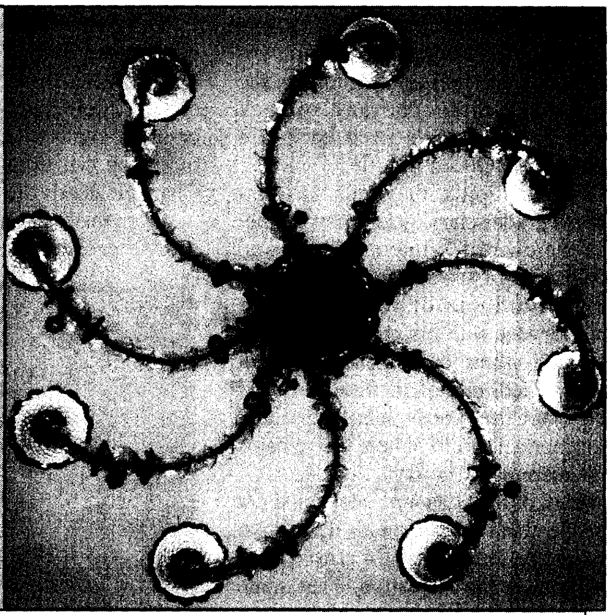

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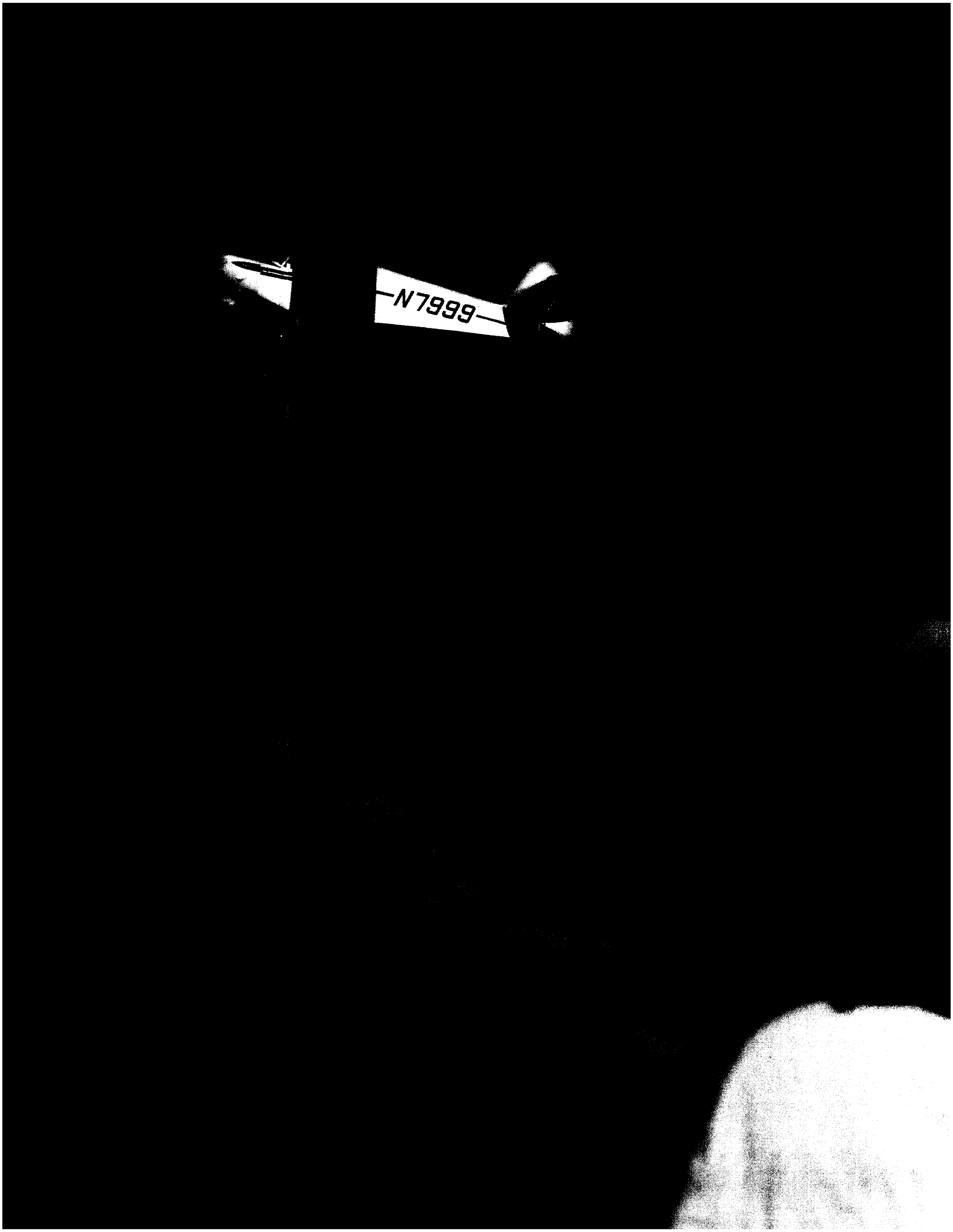
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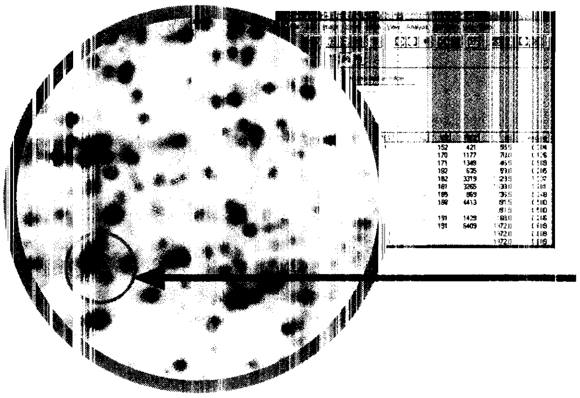

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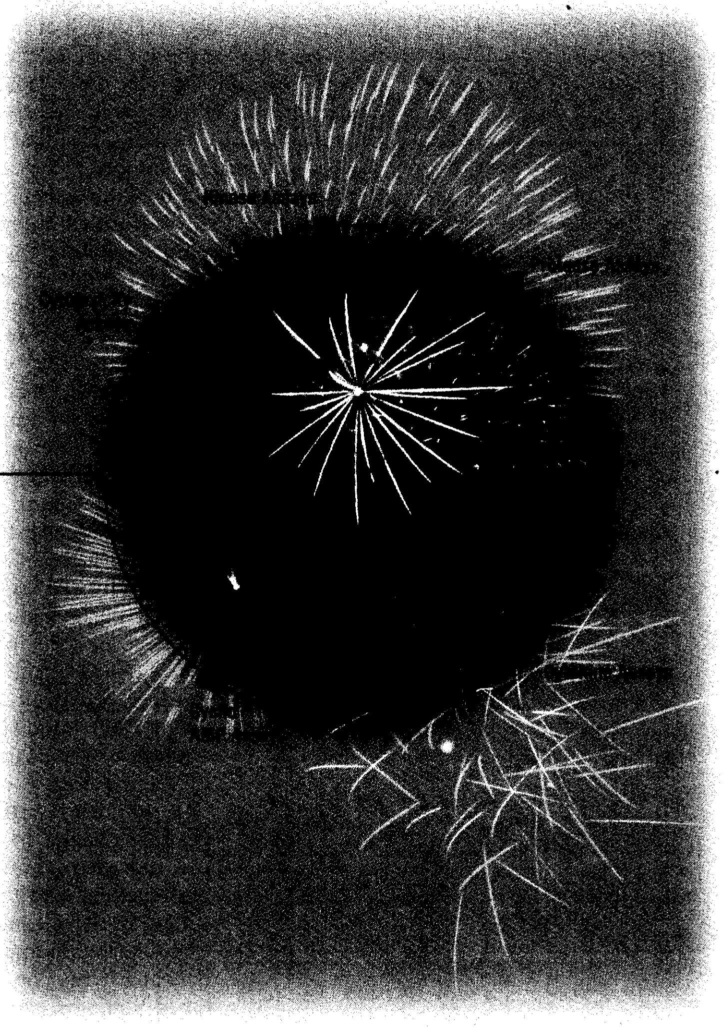

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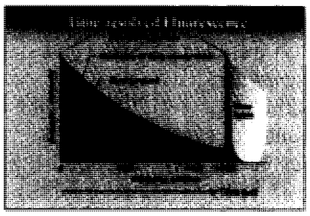

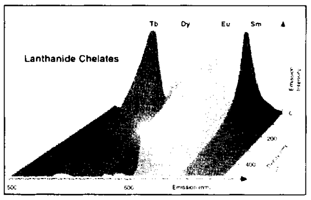

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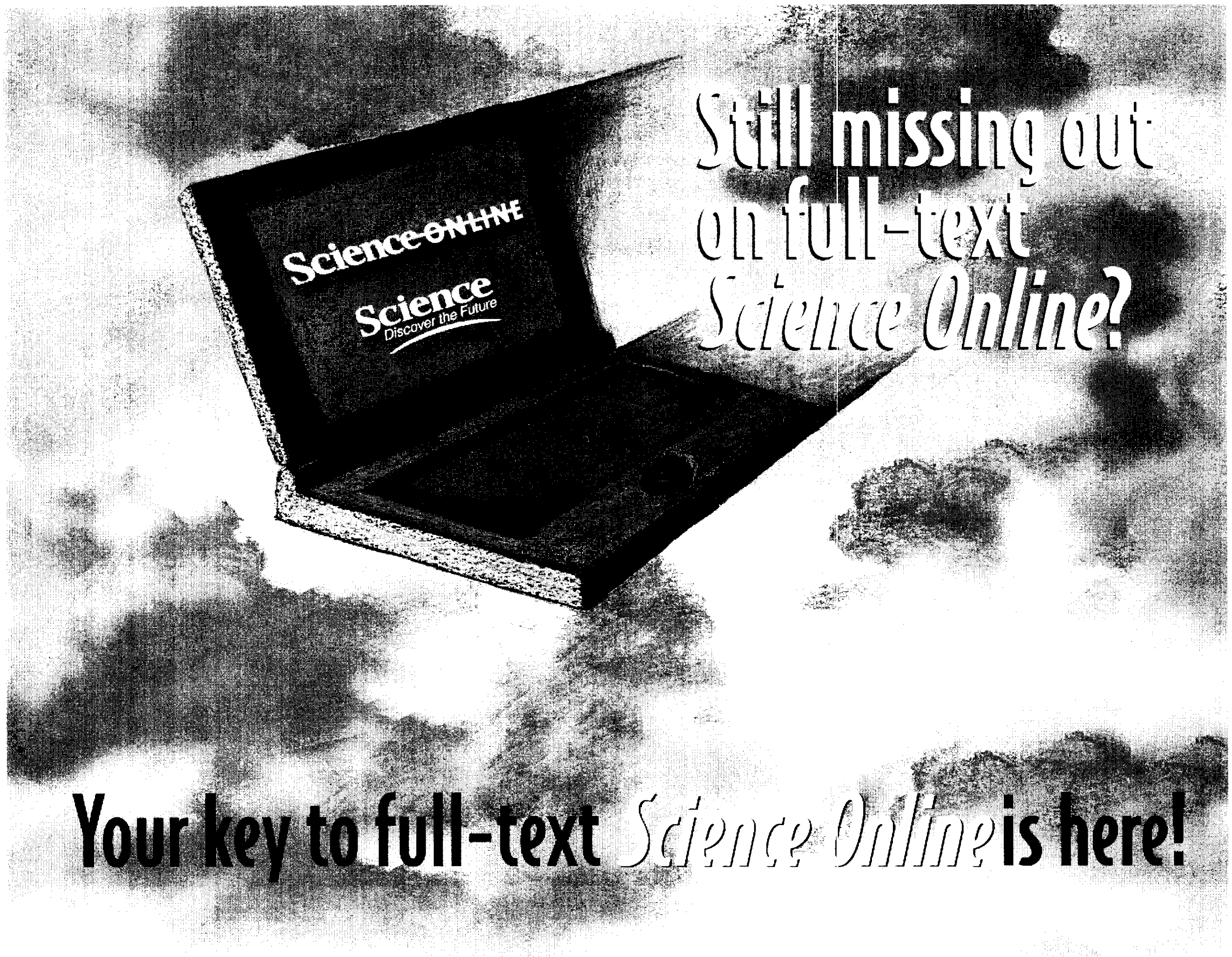

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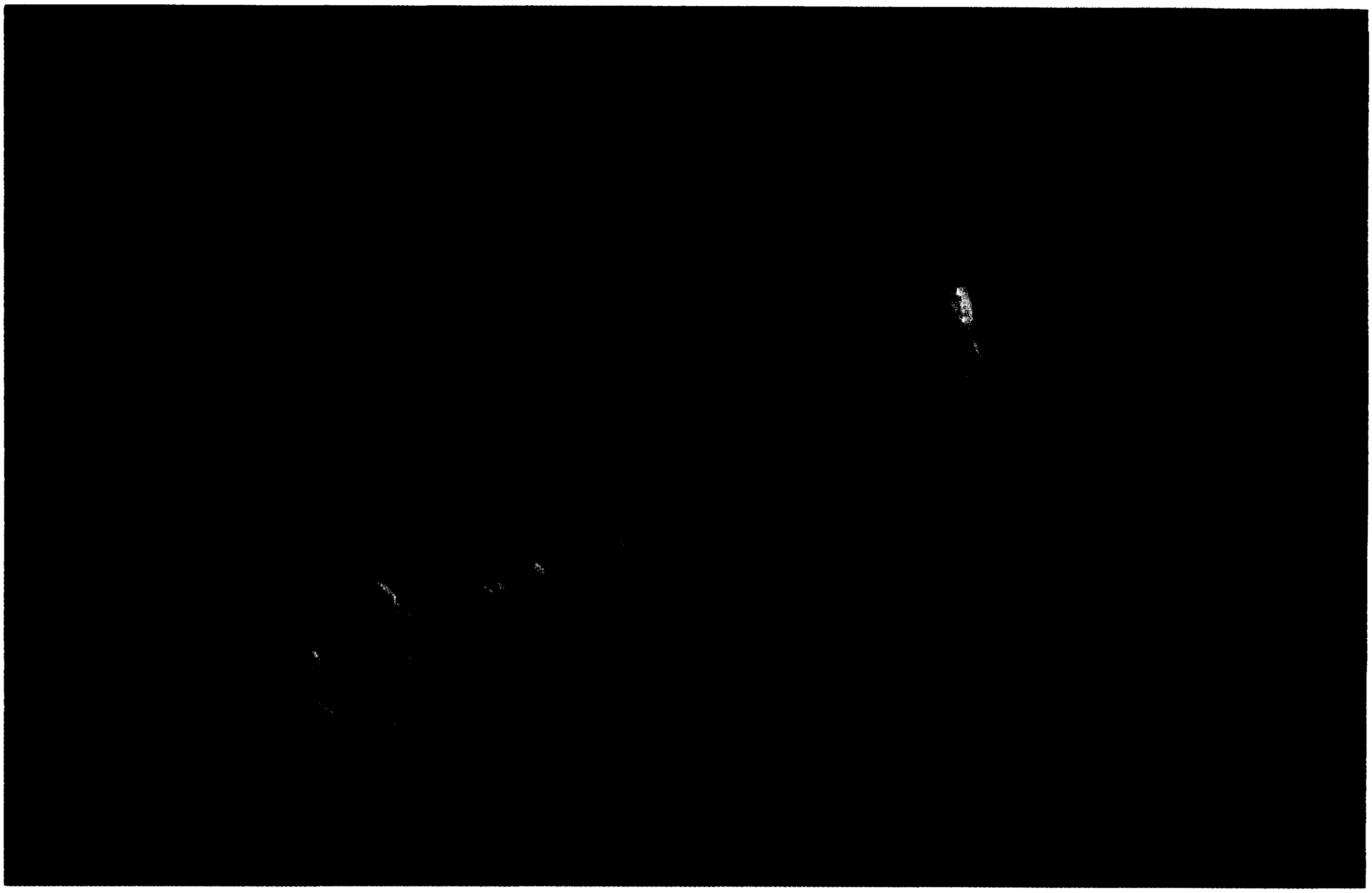

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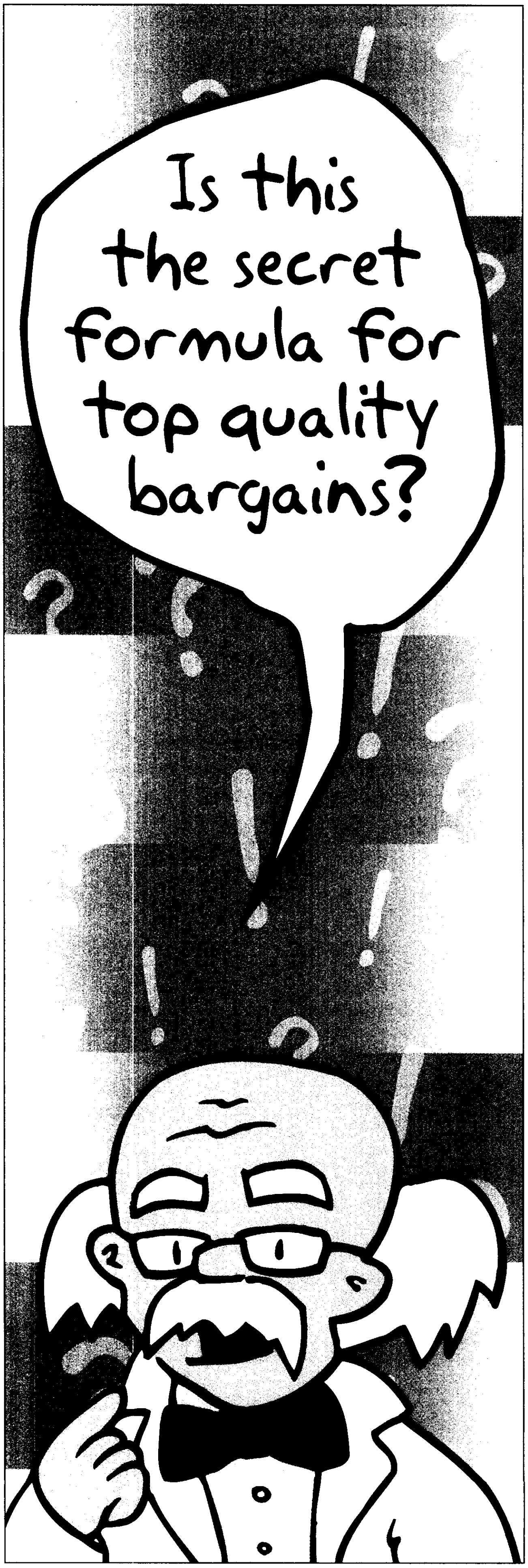

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2001 GENOME SEMINAR

Beyond the Human Genome

SATURDAY, FEBRUARY 17 AND SUNDAY, FEBRUARY 18, 2001 • SAN FRANCISCO, CA

The recent seauencing of the human genome, although it represents an enormous landmark in the history of science, is not the end but the beginning of a new era of research. From microarray technology to DNA vaccines to taking the first steps into the new frontier of proteomics—this two-day seminar explores the new kinds of research that will be possible and the new technologies being developed.

Organized by J. Craig Venter, Celera Genomics, Claire Fraser, TIGR and Barbara Jasny, AAAS and *Science*

The 2001 Genome Seminar is co-sponsored by AAAS, *Science* Magazine and The Institute for Genomic Research (TIGR)

Among the topics to be addressed are:

- whole genome sequencing
- comparative genomics regulatory regions
- proteomics
- microarrays
- SNPs
- functional genomics
- genetic networks
- pharmacogenomics
- artificial chromosomes
- DNA patenting
- genetic discrimination

The Genome Seminar is only one of the exciting events of the AAAS Annual Meeting. Among the many leaders of science and research scheduled to speak throughout the Annual Meeting are:

PLENARY LECTURERS:

- J. Craig Venter, Celera Genomics, Corp
- Francis Collins, National Center for Human Genome Research
- Karen Stephenson, NetForm and Anderson School of Management, UCLA

TOPICAL LECTURERS:

- Rita Colwell, National Science Foundation
- Troy Duster, University of California-Berkeley, *Human Genetic Technologies and Taxonomies: Old Wine in New Bottles and New Wine in Old Bottles*
- Donald Kennedy, Stanford University and *Science* Magazine, *New Tests for Science*
- Neal Lane,* Assistant to the President for Science and Technology, *The Grand Challenges of Nanotechnology*

*Invited, not yet confirmed

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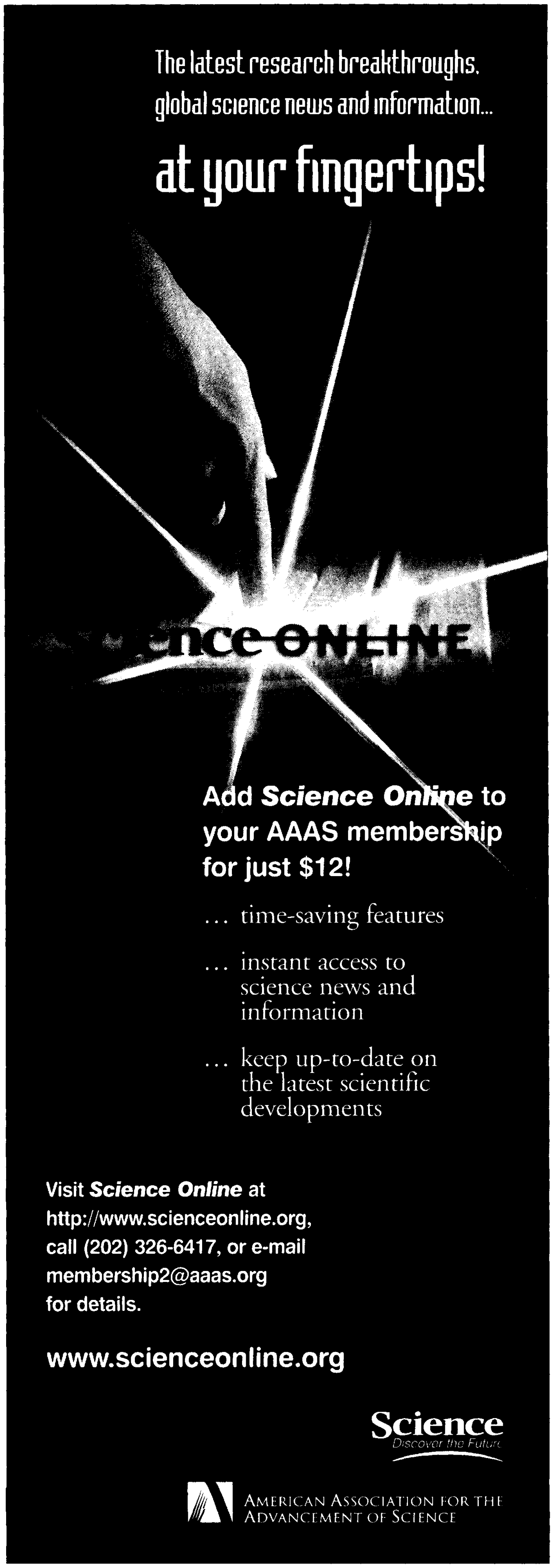

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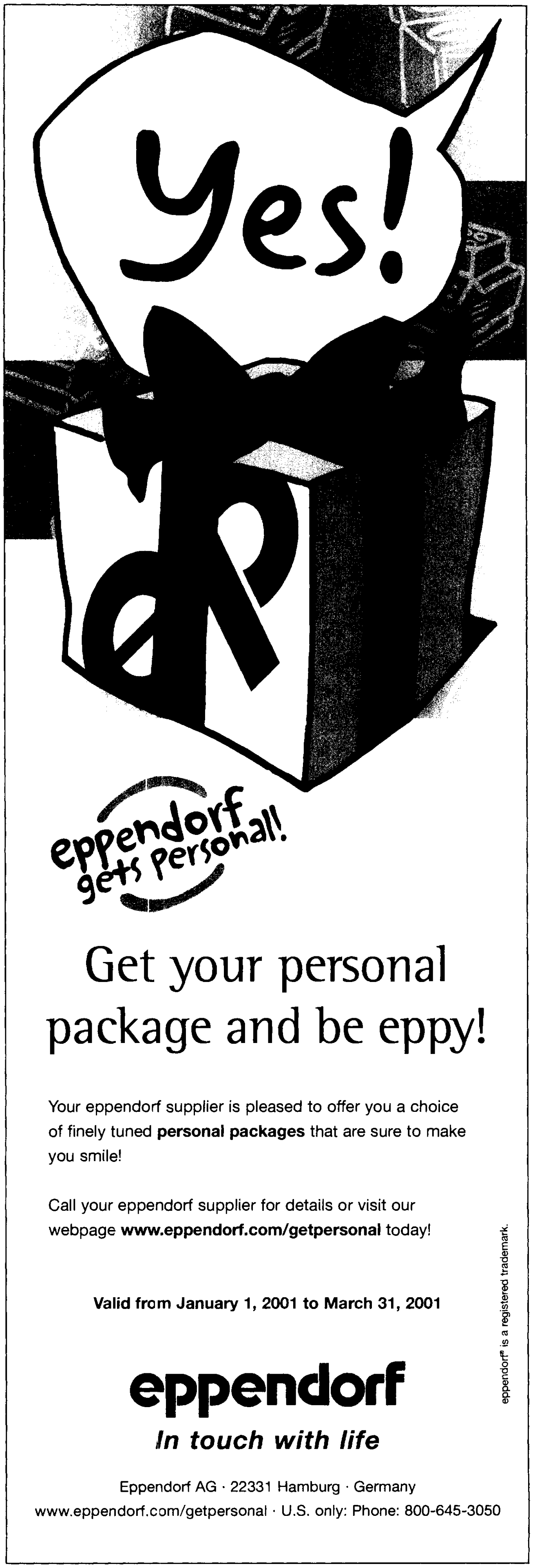

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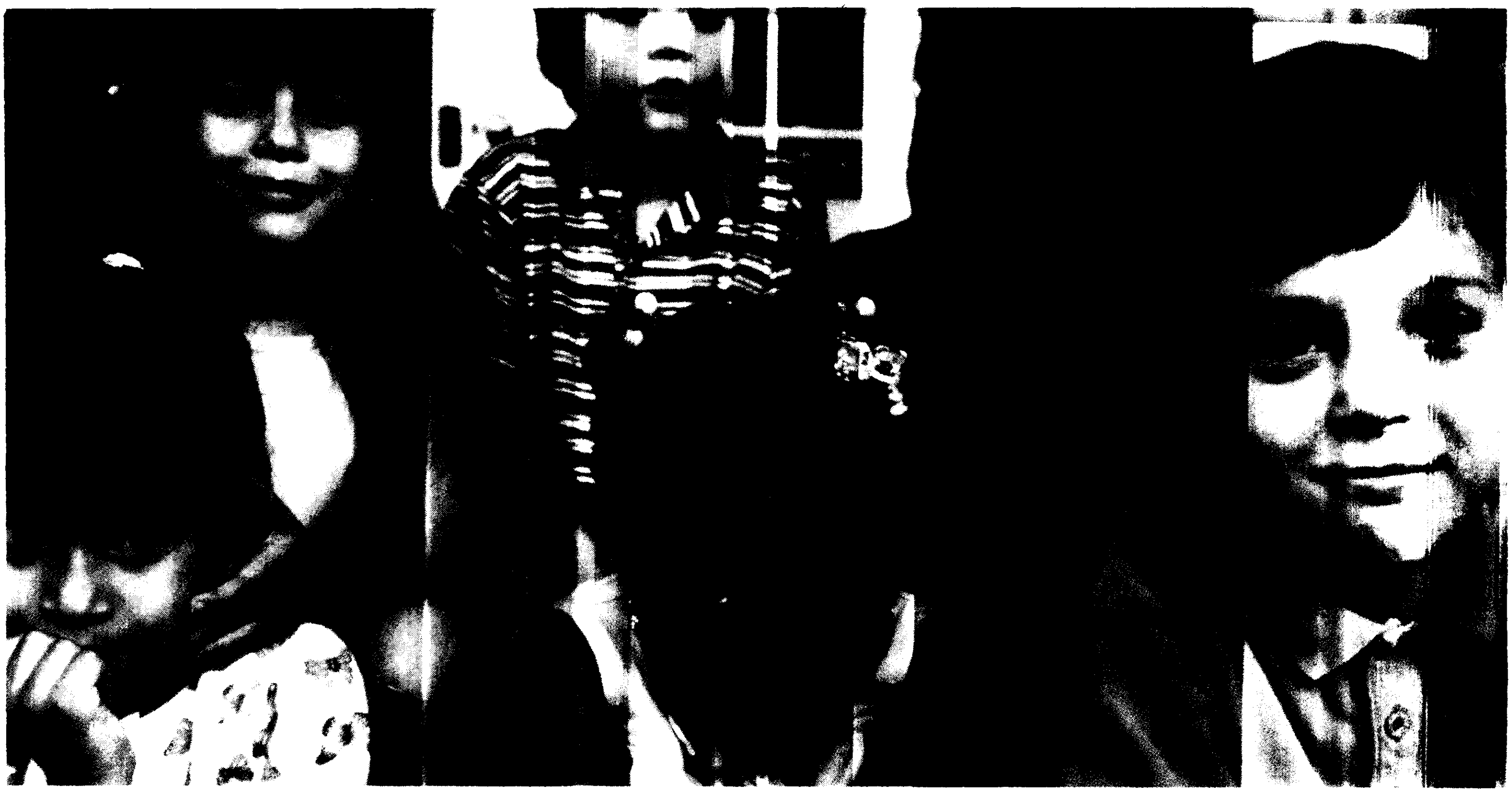

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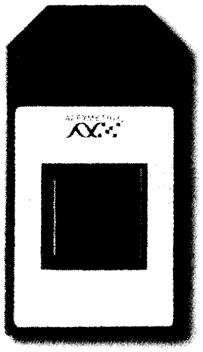

The Human Genome Project marks the beginning of what will truly be a Genetic Age. Understanding the genetic code may save and extend lives in ways we can only imagine. But first, the massive amounts of data produced by this extraordinary effort must be translated into specific genetic information. This will help scientists improve the quality of our lives and understand both how we are alike—and how we differ. Generating this information requires exceptionally powerful tools.

Affymetrix GeneChip® technology provides these tools. Based on semiconductor fabrication methods, GeneChip arrays contain vast quantities of genetic information where hundreds of thousands of experiments can be performed at the same time.

Many fields are poised to benefit from this technology. Already, leading pharmaceutical and academic researchers use Affymetrix technology to understand gene function, uncover medically relevant genetic variations and design targeted therapeutic products.

Yet, we have only begun to tap the potential. In the future, we can expect researchers throughout the world to become fluent in the language of genetics, for the benefit of us all.

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