

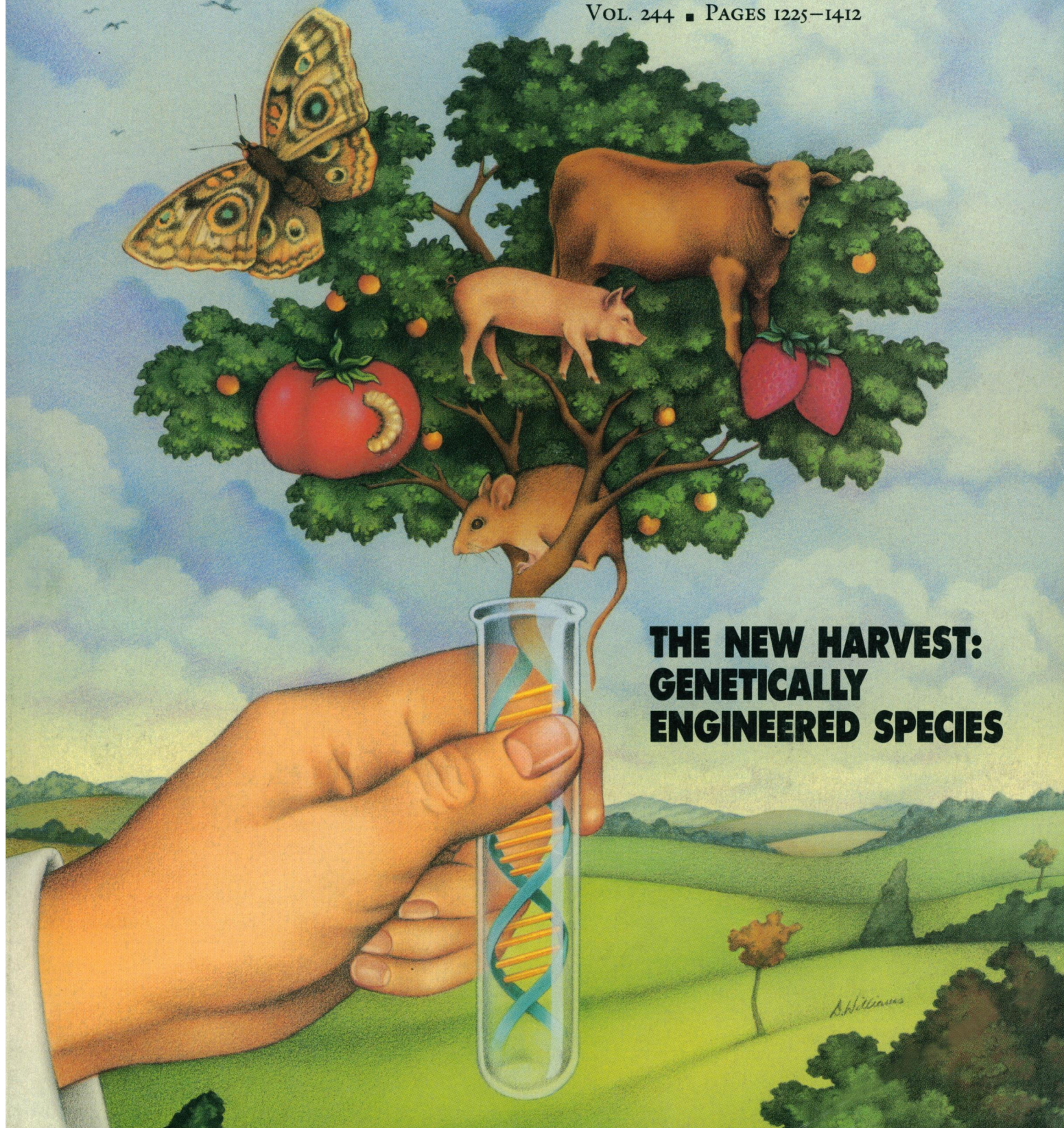
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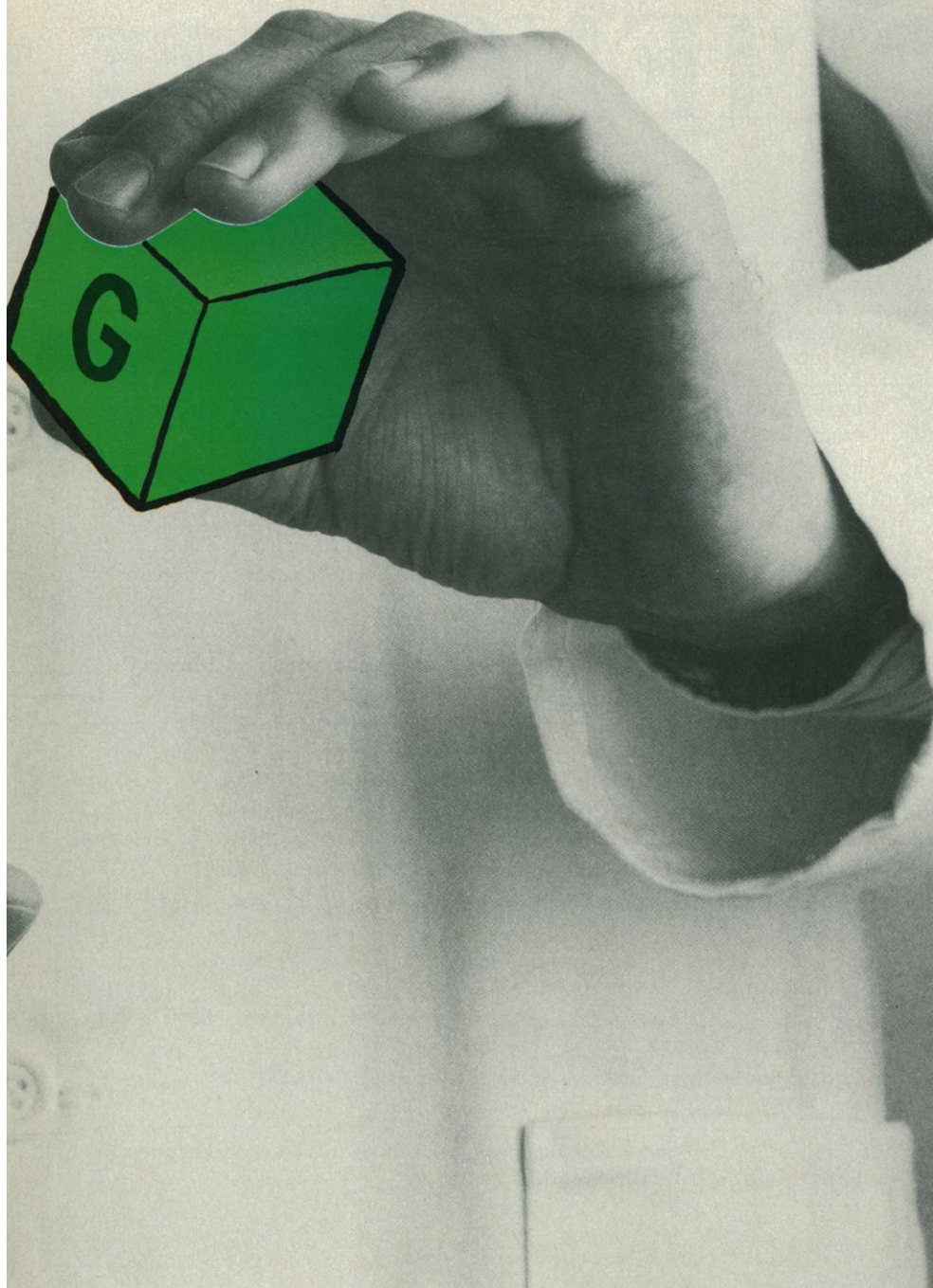
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COVER Advances in genetic engineering are bringing new variations of naturally occurring species to the research laboratory and into the field for testing and marketing. This issue of *Science* focuses on the applications of this technology that are already available and the prospects for the future. See page 1275. [Illustration by Donna Williams]

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This Week in SCIENCE

Human gene therapy

ACCCEPTANCE of gene therapy as a reasonable method for treating various human diseases and conditions has been growing. Unlike other therapies that treat symptoms, gene therapy would get at the root cause of a disease. Gene therapy includes the repair of aberrant genes or their replacement with genes that have normal structures or that function properly; in theory, it could be used for correcting genetic defects, for treating malignancies (diseases in which gene expression appears to be pathologic), and even for altering the genes of infectious agents so as to reduce their pathogenicity. Friedmann describes a number of technical advances that have been made in gene therapy, some immediate goals of gene therapy, and some ethical issues that are surfacing and must be addressed as the vision of gene therapy gets closer to becoming a reality (see pages 1233 and 1275 to 1317).

Fuels for fertility

FERTILITY problems have been noted among lean female athletes and dancers, women with eating disorders, and food-deprived animals. The problems were thought to be caused simply by individuals' low body weights. However, experiments in hamsters suggest that it is the availability of metabolic fuels—derived from sugars or fatty acids in the diet or from fatty acids stored in adipose tissues—that determines whether sexual cycling will occur (page 1326). Three measures of sexual readiness were followed—ovulation, vaginal discharge, and lordosis (arching of the back that indicates receptivity). Female hamsters were sexually receptive whenever at least one fuel source was available and were not receptive when inhibitors blocked metabolism of both sugars and fatty acids; a prerequisite to sexual cycling is therefore fuel availability, not some critical body weight or ratio of fat to lean. Schneider and Wade note that reproduction in many mammals can be put on hold when energy is needed for survival, for example, for

enduring cold winters. Similarly, monthly cycling may cease in thin women whose limited fuel supplies are being expended for other (for example, athletic) purposes.

Resetting human clocks

IN just 2 to 3 days, it is possible, with bright lights, to reset the human internal circadian pacemaker to a new, desired daily pattern (page 1328). Manipulation and adjustment of the pacemaker could be a great help to travelers who experience jet lag, to shift workers, to people suffering from certain sleep-wake disorders, and to individuals who perhaps experience "seasonal depression." In experiments with healthy subjects, Czeisler *et al.* show that the timing of exposure to bright light, indoor light, and darkness is key to determining how quickly the phase of the rhythm will be shifted and which direction—forward or backward—it will move. Body temperature, which drops to its daily low 2 to 3 hours before normal wake time, was used as a proxy for the internal pacemaker's rhythm; the daily rhythms of two other markers—urine output and plasma cortisol levels—shifted coordinately with shifts in body temperature, indicating that all three parameters are driven by the same pacemaker. The extreme light-sensitivity shown by the human pacemaker, a sensitivity that only insects and plants were thought to possess, indicates that the pacemaker is quite flexible and has great potential for change under the right inducing conditions. (See also page 1256.)

Troublesome antibodies

NOT all antibodies that are produced during viral infections help curb infections; some actually enhance the ability of viruses to enter cells (and then to proliferate and spread). The immune phenomenon of enhancement poses difficult problems for vaccine development because a safe vaccine must elicit only protective antibodies; it is necessary to identify viral

antigens that elicit enhancing antibodies and exclude them from vaccine preparations. A case in point is a vaccine for AIDS. Blood from patients with AIDS and from animals infected with the AIDS virus often contains enhancing antibodies. Homsy *et al.* found that complexes of enhancing antibodies and viruses attach to FcRIII receptors on the surfaces of macrophages (page 1357); other cells in the immune system also have FcRIII receptors (including lymphocytes, which play several key roles in AIDS). The experiments suggest that it may be necessary to block two kinds of receptors in order to prevent the AIDS virus from spreading in an infected individual—the FcRIII receptors to which viruses complexed with antibodies bind and a second receptor to which viruses bind when they enter cells on their own.

Damage from PCP and MK-801

A drug that has been under consideration for use in the treatment of neurodegenerative diseases may be too dangerous to use; although MK-801 provides protection to the nervous system—it interferes with excitatory and toxic actions of certain amino acids—it also produces major (though reversible) morphologic changes in certain brain cells (page 1360). MK-801 binds to the receptor in the brain used by PCP, which is a potent street drug that can induce psychotic behavior. Studies by Olney *et al.* indicate that MK-801, PCP, and two other compounds that have affinity for the "PCP receptor" are all toxic for nerve cells in restricted regions of the rat brain—the posterior cingulate and the retrosplenial cortices. Cells fill with large vacuoles and lose mitochondria (structures that contain metabolic machinery). Because the psychotic behaviors induced by PCP-type drugs resemble behaviors characteristic of schizophrenics, it is conceivable that endogenous substances like PCP induce psychoses in schizophrenics by acting on the same cells in the same regions of the brain affected by PCP.

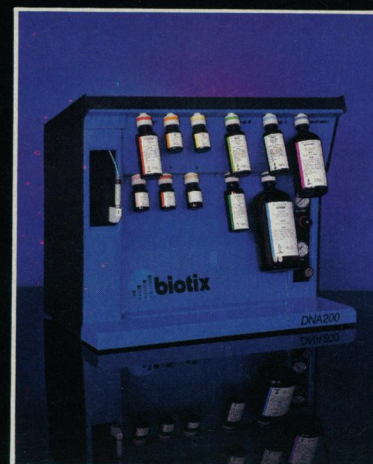
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The Engineering of Species

Somewhere in the vast pantheon of science a molecular biologist is saying, "I'd like to engineer a wolf into a dog." Somewhere else, the sepulchral voice of a geneticist will reply, "It's been done." For in fact, over evolutionary time, the friendliest of wolves (and possibly the most intelligent) learned that wagging their tails and delivering slippers was an easier way to earn a living than hunting caribou in the wilds. In modern times, scientists have accelerated evolution for the benefit of humans by deliberate selection techniques to improve livestock, crops, and other life forms. The difference between these techniques and the use of recombinant DNA is that direct gene alteration removes some chance and accelerates the pace at which new variants can be produced. This issue of *Science*, assembled with the insight and editing skills of Barbara Jasny, shows how various species are being genetically engineered.

The most controversial genetic engineering involves humans and Friedmann covers the latest exciting advances in the development of gene therapies. Gene transfer techniques that produce somatic mutations, such as by the introduction of viral vectors into bone marrow, have great potential for curing patients without affecting succeeding generations. Homologous recombination, as described in the article by Capecchi, allows the surgical removal of a single deficient gene and its replacement by a normal gene, the crucial step needed for efficient alteration of a germ line. It can reverse history in ending the progress of a deficient gene into new generations.

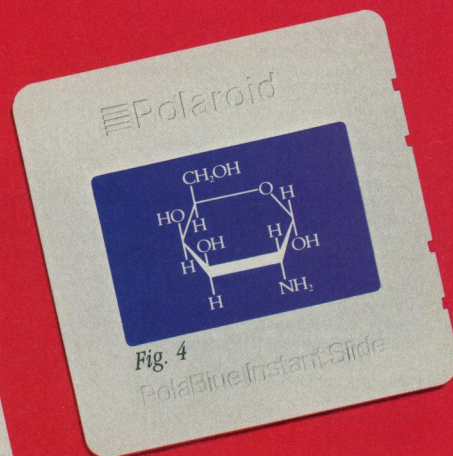
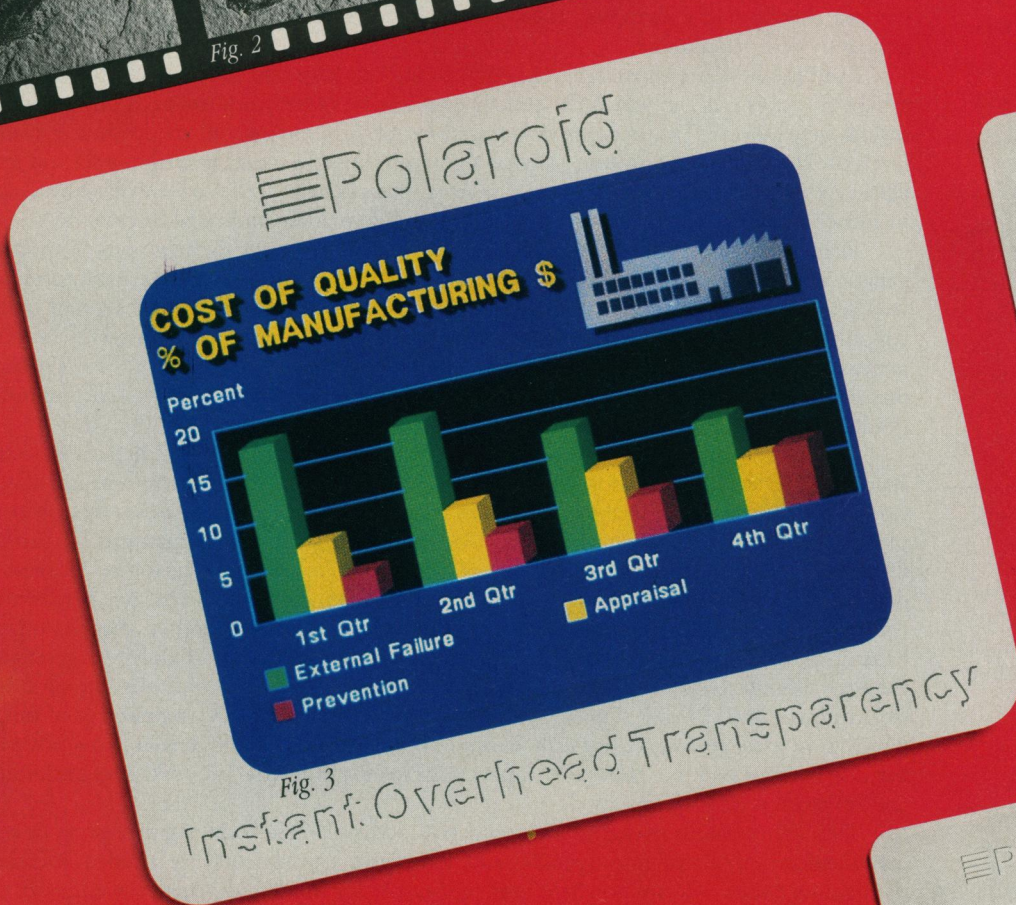
Even the best intentioned genetic engineering can have bad effects as illustrated in the article by Pursel *et al.*, in which the genetic engineering of livestock has been carried on for several generations. Two successive generations of pigs engineered to produce elevated levels of bovine growth hormone showed significant improvements in weight gain and feed efficiency and marked reduction in fat. However, these beneficial effects were offset by a high incidence of gastric ulcers, arthritis, cardiomegaly, dermatitis, and renal disease.

Plant research, as discussed by Gasser and Fraley, is one of the triumphs of modern genetic engineering; plants are being produced that are resistant to infectious agents or weed-control agents and can produce more and better food. As pesticides come under continual attack, the development of plants that naturally resist predators will become increasingly useful. An ironic feature is that some plant defenses involve synthesis of natural carcinogens. It is thus conceivable to get a plant that can be grown without pesticides but is deadly poisonous.

One alternative to pesticides is the use of biocontrol, a subject that is illustrated in the article by Lindow, Panopoulos, and McFarland. The famous "Ice-" bacterium is a classic case in which genetic engineering of a bacterial species results in an organism that protects plants against damage from freezing. The importance of microorganisms is further illustrated by the genetic engineering of *Rhizobium* to improve nitrogen fixation, a development that could increase plant yields and diminish the need for agricultural chemicals. Additionally, engineered bacteria are being used to improve the cleanup of hazardous waste sites. Techniques described by O'Connor, Peifer, and Bender can accelerate the ease and efficiency of genetic engineering, not only on bacteria, but possibly on other organisms as well. Finally, Timberlake and Marshall discuss genetic engineering of fungi, which have great relevance, not only because they are serious pathogens in many diseases, but also because they have potential applications for the industrial production of antibiotics and other important chemicals.

This issue reminds us that we must proceed cautiously in introducing new genes or new combinations of genes into species, and long-term experiments are needed to study detrimental effects. We are nowhere near the knowledge needed to genetically engineer the complex behavior of a wolf or a dog. An original wolf might say to the dog, "You have lost your freedom. Your obsequiousness is humiliating to the family Canidae." The dog could reply, "I am much less warlike, far more altruistic, and besides, it's a wonderful standard of living." Whether society prefers to have wolves or dogs remains to be seen.

—DANIEL E. KOSHLAND, JR.



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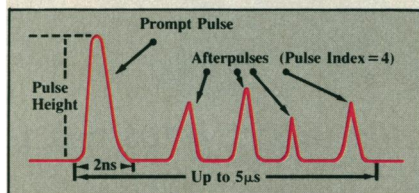
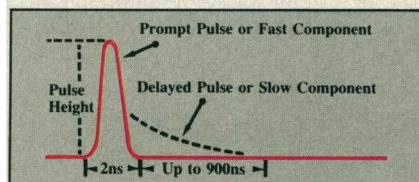
In the past, liquid scintillation counting used traditional technology to overcome background noise. Now, there's a new, more sensitive technology – TR-LSC or Time-Resolved Liquid Scintillation Counting – that reduces background noise by an additional 30%-40%, and more. This new patented technology is available only in Packard's Tri-Carb® liquid scintillation analyzers.

Originally developed for extremely low level counting, TR-LSC technology has now been applied to a broad range of applications. While these don't always require high sensitivity, additional benefits have been realized. By increasing sensitivity, TR-LSC reduces sample and cocktail consumption while shortening the time required for accurate counts. The benefits? Lower cocktail costs, lower disposal costs, and increased throughput.

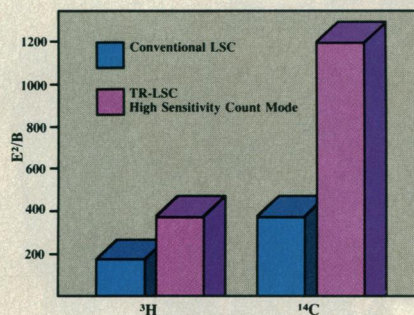
How TR-LSC is superior to older technology

Traditional counters are based on two-dimensional pulse analysis: pulse height and pulse counts. They provide a level of sensitivity that's merely adequate for most applications.

Patented TR-LSC adds a third dimension to pulse analysis: a pulse index that measures over time the afterpulses associated with background. In doing so, TR-LSC clearly distinguishes between beta pulses and background pulses. By identifying, and reducing, background noise, TR-LSC provides a great level of sensitivity (see chart comparing E^2/B values) and more accurate counts.



The typical beta scintillation pulse (top) is very fast and may be followed by a delayed component. The typical background pulse is followed by a series of afterpulses. Patented TR-LSC distinguishes between the two.



Typical E^2/B values for ^3H and ^{14}C using traditional and TR-LSC counting.

Achieve accurate counts on samples as small as 25 µL

Traditional technology limits sensitivity. The improved sensitivity of TR-LSC, however, allows you to achieve accurate DPM results for single and dual label samples in volumes as small as 25 µL. That can add up to substantial savings in sample and cocktail costs.

Slash radioactive waste disposal costs

Counting smaller samples will also reduce radioactive liquid disposal costs, which can be \$500 per drum, or higher. While you may not pay this cost directly, your operating budget could be affected. With TR-LSC you can cut operating costs while reducing environmental hazards.

Increase sample throughput by over 80%

Just as TR-LSC reduces the volume of sample and cocktail required for accurate counting, it also reduces the time required for an accurate count. By cutting background in half, high sensitivity TR-LSC lets you count nearly twice the number of vials of a 250-DPM sample, in the time it would

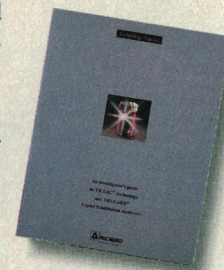
take to count a single vial using conventional technology. For lower activity samples, the increase in throughput with TR-LSC is even greater.

Automatic data interpretation, too

Another advanced feature available only with Tri-Carb analyzers is automatic tandem processing. This unique capability processes your counting data automatically using one software program after another – RIA packages, spreadsheets, word processing, or custom-written programs – until the results are printed in whatever format you have specified. All this is done automatically, without operator intervention, for up to 30 users.

Free Investigator's Guide provides a complete explanation of the benefits of TR-LSC

More information on TR-LSC, and other exclusive Packard features, is available in a new publication, the Investigator's Guide to TR-LSC Technology and Tri-Carb Liquid Scintillation Analyzers. For your free copy, mark the reader service number below or call us today.



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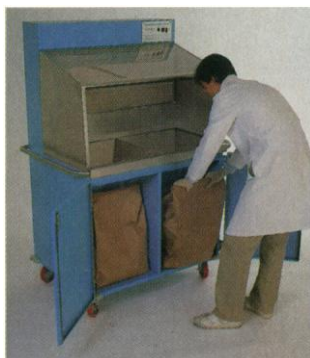
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How can this exciting new system help protect both your laboratory animals and personnel from contamination?

The dumping of cage bedding and animal waste can create—and then lead to—the inhalation of aerosolized contaminants by animals and lab personnel. Such animal exposure can interfere with—or even jeopardize—research studies. And inhalation of contaminants by personnel can result in serious health consequences. Up until now, *this* has been the weak link in the animal facility contamination-containment chain.



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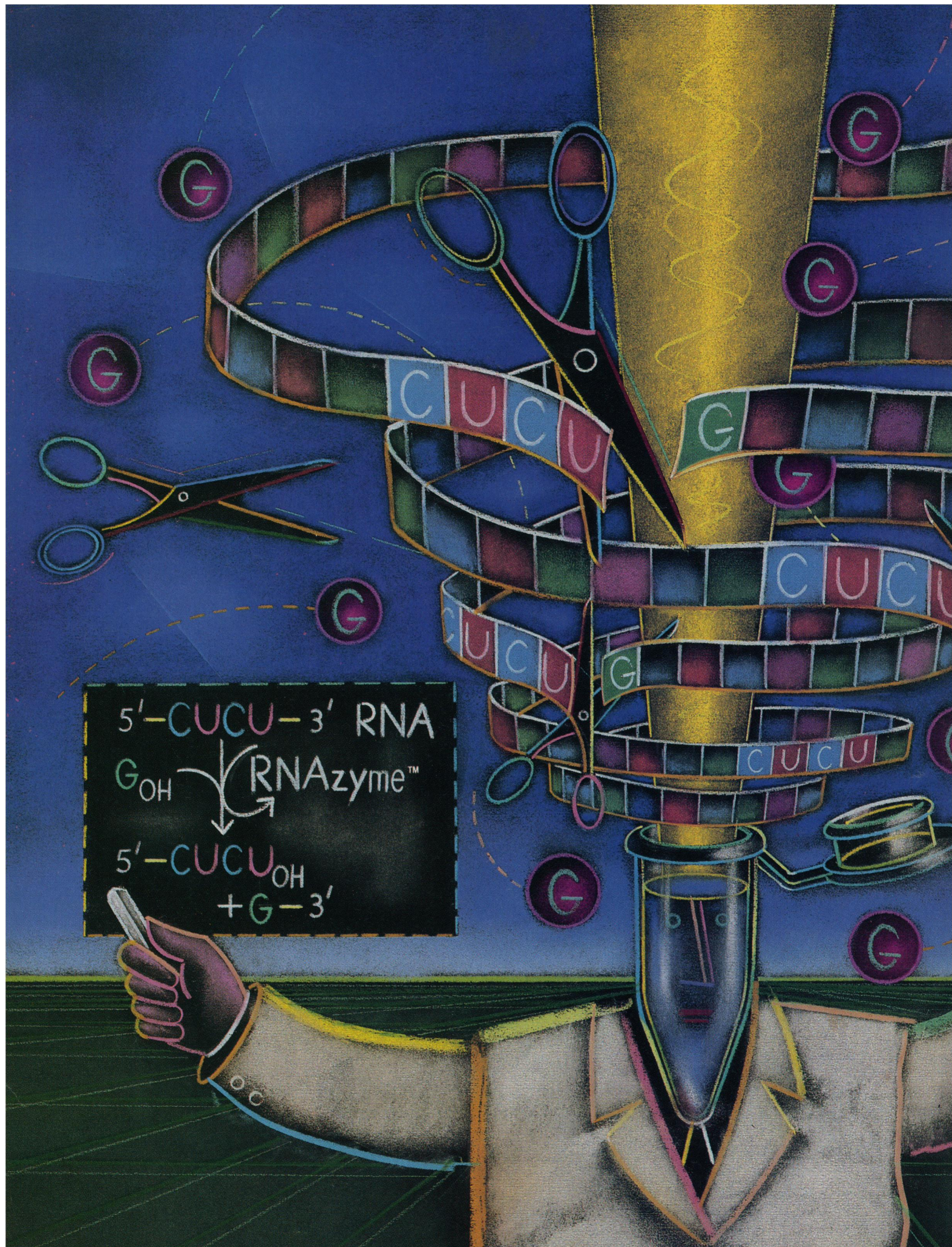
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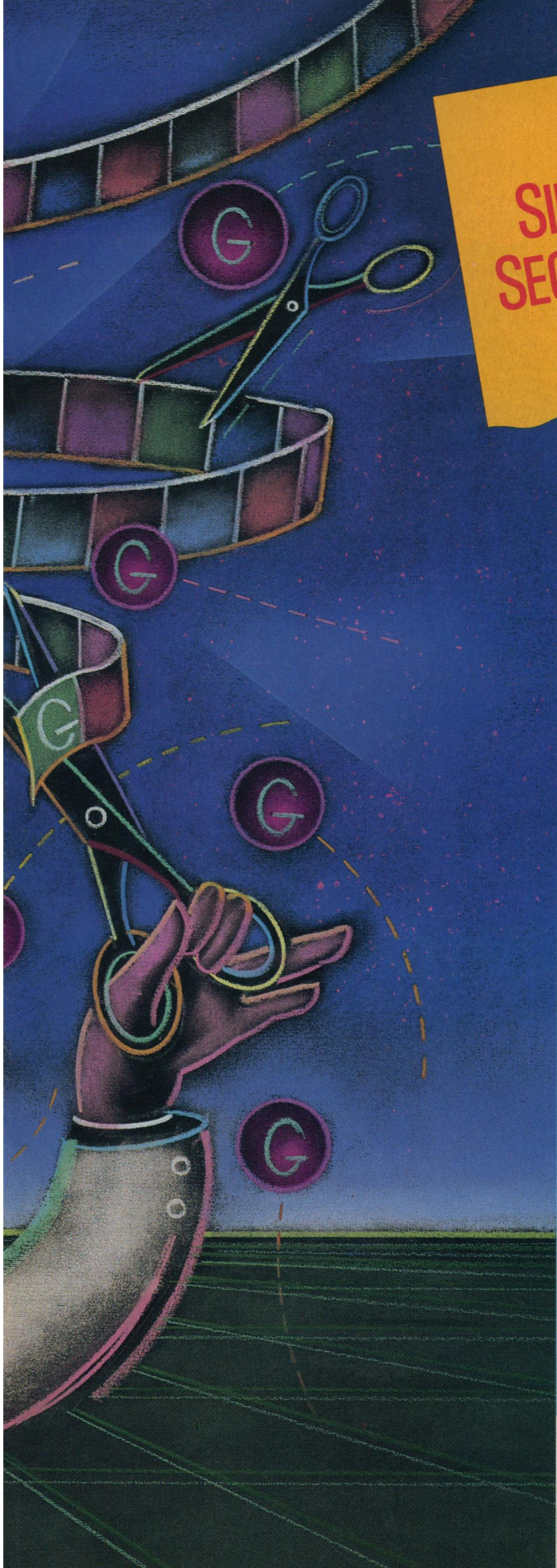
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The discovery of ribozymes — novel enzymes composed entirely of RNA that cleave RNA in a sequence-specific manner — represents a tremendous opportunity to expand the scope of RNA studies.

Now USB scientists have produced the first commercially-available ribozyme from a naturally-occurring, self-splicing group I intron of *Tetrahymena* RNA (1).

RNAzyme™ Tet 1.0 (Ribozyme Tet 1.0) cucu specific is one of a group of important ribozymes (sequence-dependent RNA endonucleases), that promise to be powerful tools in experiments involving all aspects of RNA. RNAzyme™ Tet 1.0 (Ribozyme Tet 1.0) cucu specific resembles a DNA restriction endonuclease in that it will cut RNA into discrete segments at a specific nucleotide sequence; in this case, cleaving RNA at sites having the sequence cucu. As with DNA restriction endonucleases, the concept

of using a ribozyme as a molecular scissors is simple. However, its potential value lies in the development of imaginative applications which, until now, have been difficult or impossible to achieve.

One primary application will, of course, be in the physical mapping of related RNA species. In addition, consider RNA sequencing, secondary structure analysis and *in vitro* RNA metabolic studies.

We are excited to take the leading role in the development of this newly-discovered field, and dedicated to fulfilling the promise ribozymes represent as extremely useful tools in basic molecular biological research, as well as in other areas as diverse as oncology, virology, pharmacology and agriculture.

USB RNAzyme™ Tet 1.0 (Ribozyme Tet 1.0) cucu specific is offered in a kit with all the accessory reagents necessary to calibrate the ribozyme activity with any RNA substrate and begin RNA analysis.

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(Additional information on next page.)

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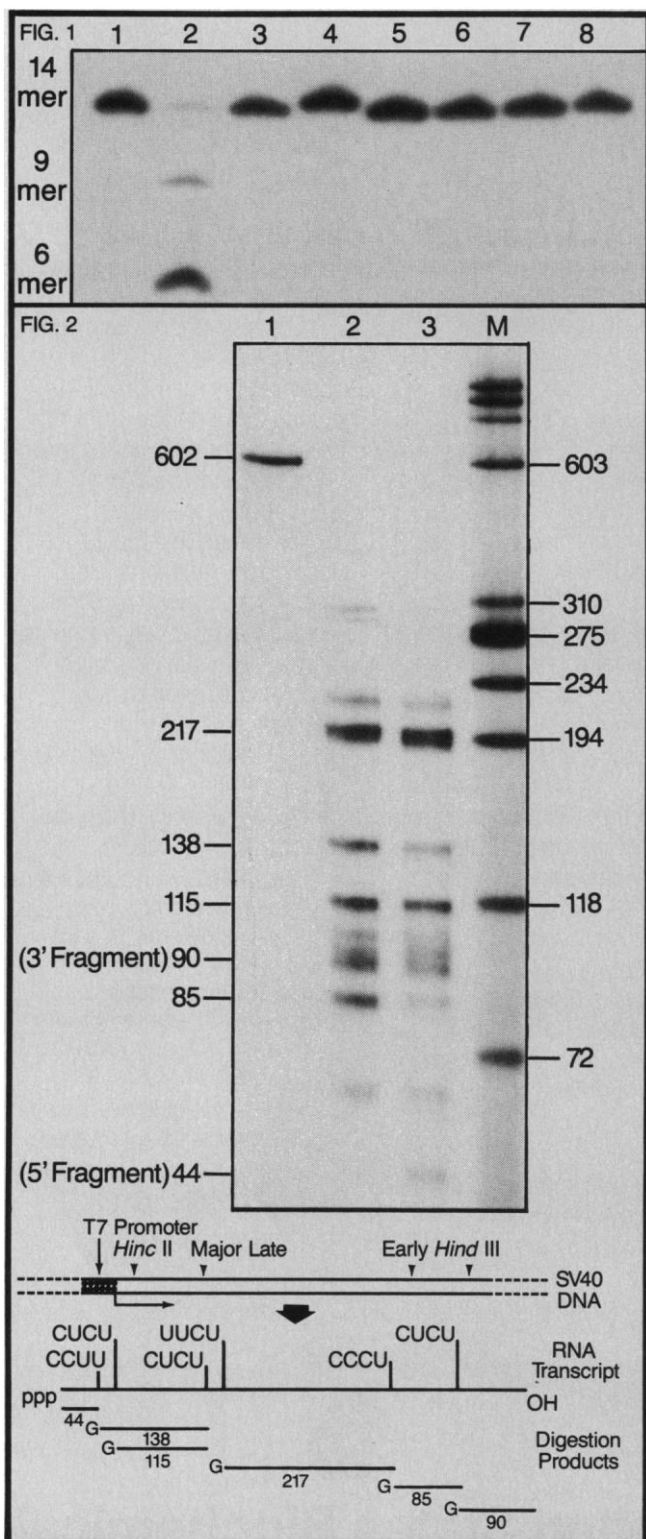


FIG. 1 Demonstration of the Specificity of Cleavage.

RNAzyme™ Tet 1.0 was incubated with seven different oligomeric RNA substrates: lanes 1 and 2, 5' GGGACCCUCUAAAAA3'; lane 3, 5' GGGACAUUUAAAAA3'; lane 4, 5' GGGACGGCUAAAAA3'; lane 5, 5' GGGACACCUAAAAA3'; lane 6, 5' GGGACACAUAAAAA3'; lane 7, 5' GGGACUAAUAAAAA3'; lane 8, 5' GGGACGAAUAAAAA3'. Lane 1 is a no ribozyme control. The reaction contained 0.10 μM substrate ([α-³²P] ATP labeled), 0.01 μM RNAzyme™ Tet 1.0, 2.5M urea, 0.5mM GTP, 20mM MgCl₂, 50mM Tris-HCl (pH 7.5). Incubation was for 1 hour at 50°C. Samples from each reaction were electrophoresed on a high percentage acrylamide denaturing gel and the bands of substrate and digestion products were identified by autoradiography. Only the matched substrate in lane 2 was cleaved.

FIG. 2 RNA Fragments of SV40 and Physical Map.

SV40 RNA (610-nt) was glyoxalated and then cleaved with RNAzyme™ Tet 1.0 at 50°C in a reaction containing 1.5M urea. The RNA fragments were detected by two different labeling schemes which together identify the 5'-terminal fragment. The lanes are as follows: lane 1, ³²P-labeled RNA transcript uncut; lane 2, unlabeled RNA cut with ribozyme in the presence of [³²P]GTP; lane 3, body-labeled RNA cut in the presence of unlabeled GTP; M, glyoxalated HaeIII fragments of φX DNA. The fragments were separated by electrophoresis in a 4% acrylamide gel containing 8M urea and the bands were visualized by autoradiography. The physical map shows the locations and sequences of the RNAzyme™ Tet 1.0 cleavage sites in SV40.

*RNAzyme™ Tet 1.0 (Ribozyme Tet 1.0) cucu specific
RNAzyme™ is USB's brand of Ribozyme.
Ribozymes — Patents pending.

The results shown illustrate the site-specific cleavage activity of RNAzyme™ Tet 1.0 on both oligomeric and larger RNA. They confirm the results originally reported for the *Tetrahymena* group I intron derived ribozymes (1,2). This work provides the basis for the experimenter to generate digestion patterns of larger RNA and to attempt studies involving the detection of different forms of RNA (e.g., alternatively spliced RNA) in complex populations. Studies involving *in vitro* transformation of purified RNA fragments could also be possible. The development of RNAzyme™ Tet 1.0 to its full potential as a biological tool will depend upon further characterization of its enzymatic activity as well as the development of specific protocols.

The RNAzyme™ Tet 1.0 kit includes sufficient ribozyme and reagents to allow a variety of investigations. The Control Substrate in the kit is provided to allow calibration of the RNAzyme™ Tet 1.0 activity since activity is dependent upon the concentration of GTP, urea, and cleavage sites as well as the ribozyme concentration. Selection of various conditions for cleavage depends upon the fraction of sites needed to be cleaved; the amount of radiolabel needed to be incorporated into the fragments and the degree of sequence specificity desired.

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References:

1. Zaug, A.J., Grosshans, C.A., and Cech, T.R., *Biochemistry* 27, 8924-8931 (1988).
2. Zaug, A.J., Been, M.D., and Cech, T.R., *Nature* 324, 429-433 (1986).



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Corrections

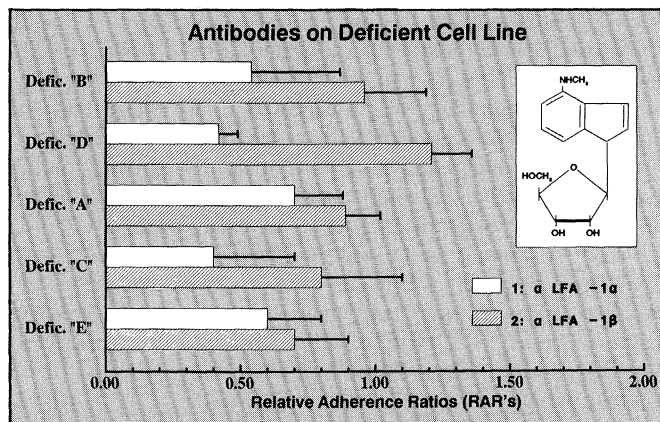
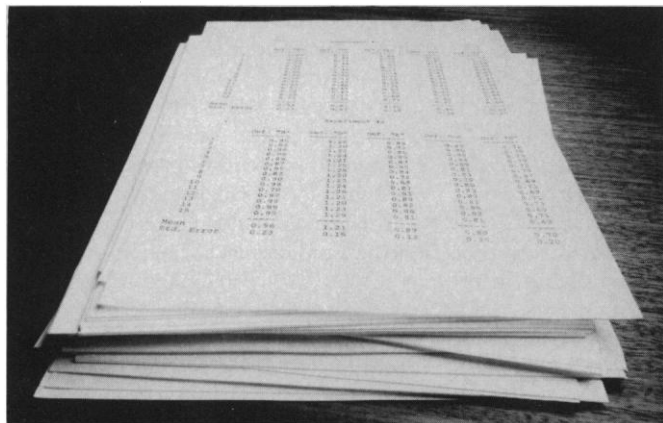
The Perspective "Gamma-ray observations of orbiting nuclear reactors" by Joel R. Primack (28 Apr., p. 407) incorrectly identified the Gamma-Ray Spectrometer on the Solar Maximum Mission satellite as having been blinded by radiation from Soviet satellites. The seventh paragraph should have read, in part, "Gamma-ray detectors are surrounded by charged-particle detectors, so that events initiated by gamma rays can be distinguished from background events initiated by electrons. But positrons can annihilate on other parts of the gamma-ray detector spacecraft such as the SMM shield, and the resulting 511-keV gamma rays can appear to be astronomical gamma-ray signals. The SMM-GRS picked up such signals an average of eight times per day for much of 1987 and early 1988, each time causing brief interference with astronomical observations. The data storage capacity of the Gamma-ray Burst Detector (GBD) on the Japanese Ginga satellite was sometimes saturated by such events, so that it could take no more data until

the next pass over its ground station (which could be on the same orbit or as many as 14 orbits later); this effectively blinded the GBD about 20% of the time. The sensitive detectors aboard Gamma Ray Observatory" [The remainder of this paragraph is as published.]

In the report "Geomagnetic origin for transient particle events from nuclear reactor-powered satellites" by G. H. Share *et al.* (28 Apr., p. 444), the following corrections should be noted. The last sentence of the second full paragraph on page 445 should have read, "Their report provides detailed confirmation of the origin of the SMM events." On page 446, the last sentence of the caption of figure 3 should have read, "Rate is in counts per 0.5 s." On page 447, text references to figures 2 and 3 were interchanged. The sixth sentence of the fifth full paragraph should have read, "The concentration of particles on this L shell explains the peak observed by the GRS." The fourth sentence of the sixth paragraph should have read, "The spike near 12 min coincides with the time when SMM reached L shells on which positrons had been deposited about a minute earlier." Reference 12 should have read, "Solar Geophysical Data Prompt Reports, No. 535 (Pt. 1), H. E. Coffey, Ed. (National Geophysical Data Center, Boulder, CO, 1989)."

In the report "Distribution and detection of positrons from an orbiting nuclear reactor" by E. W. Hones and P. R. Higbie (28 Apr., p. 448), the following corrections should be noted. The first sentence of the caption for figure 1 should have read, "Locations of SMM (dots) and Cosmos 1176 (triangles) at the times of 21 of the most intense 511-keV gamma events recorded by SMM during the 29 April to 2 September 1980 operating period." The first sentence of the caption for figure 3 should have read, "Estimated differential energy spectrum of positrons escaping from Cosmos 1176 per joule of fission energy." On page 450, the second sentence of the first full paragraph should have referred to event 5, not event 59.

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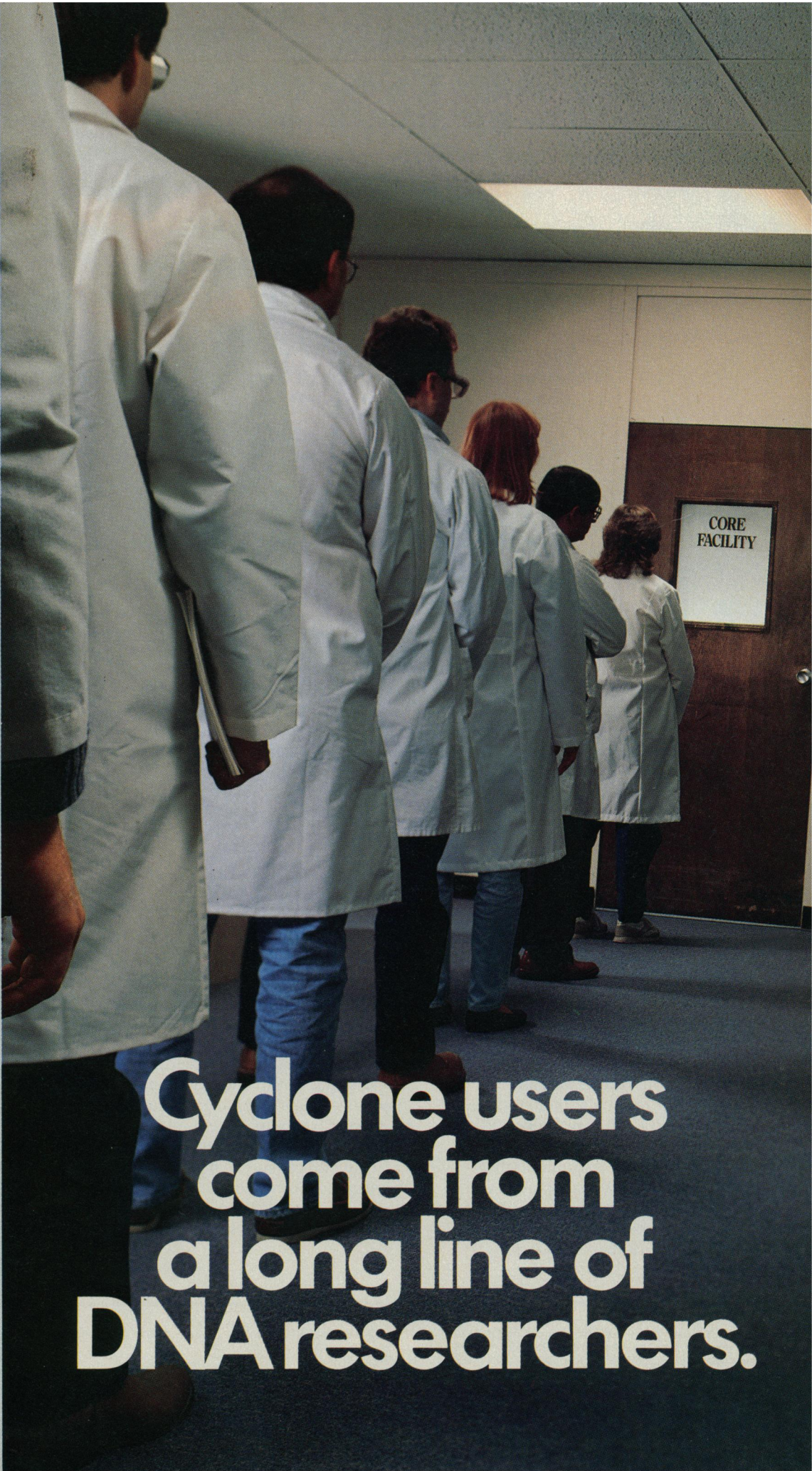
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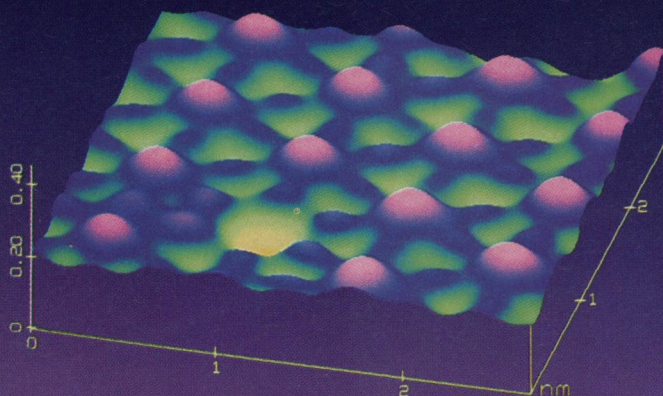
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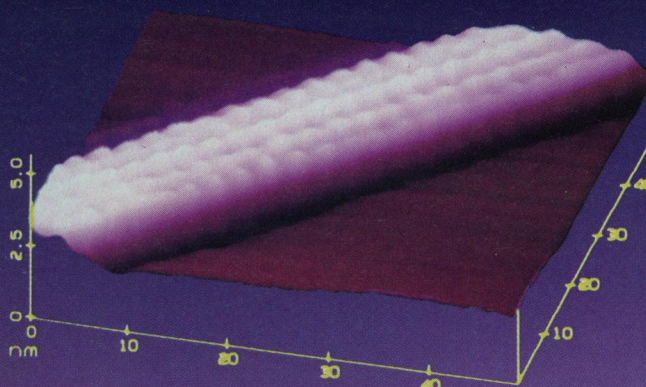
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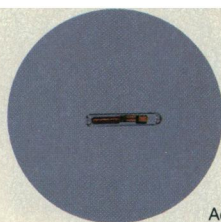
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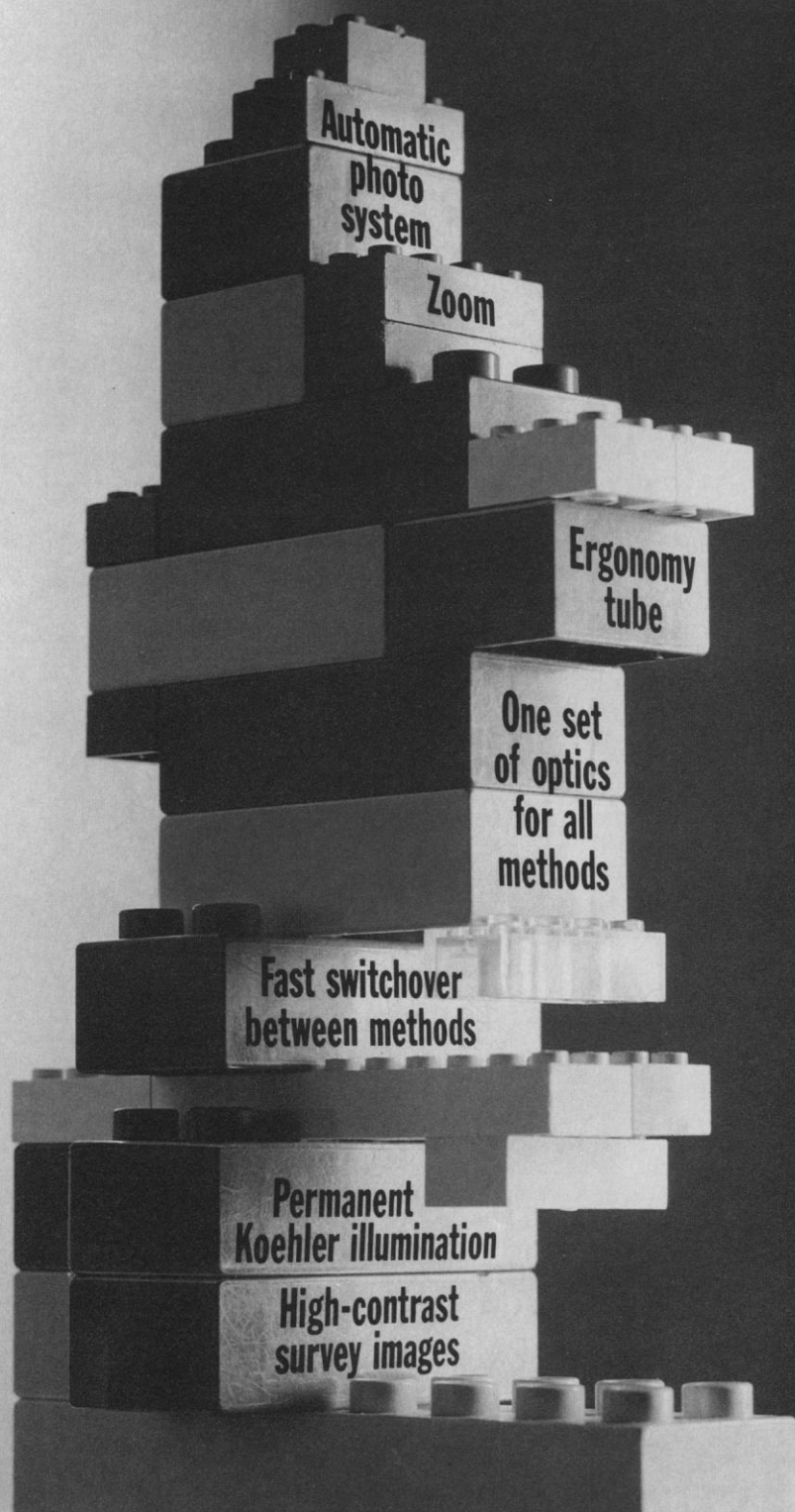


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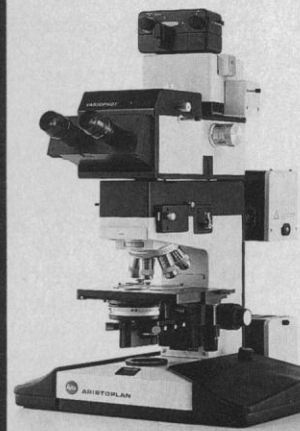
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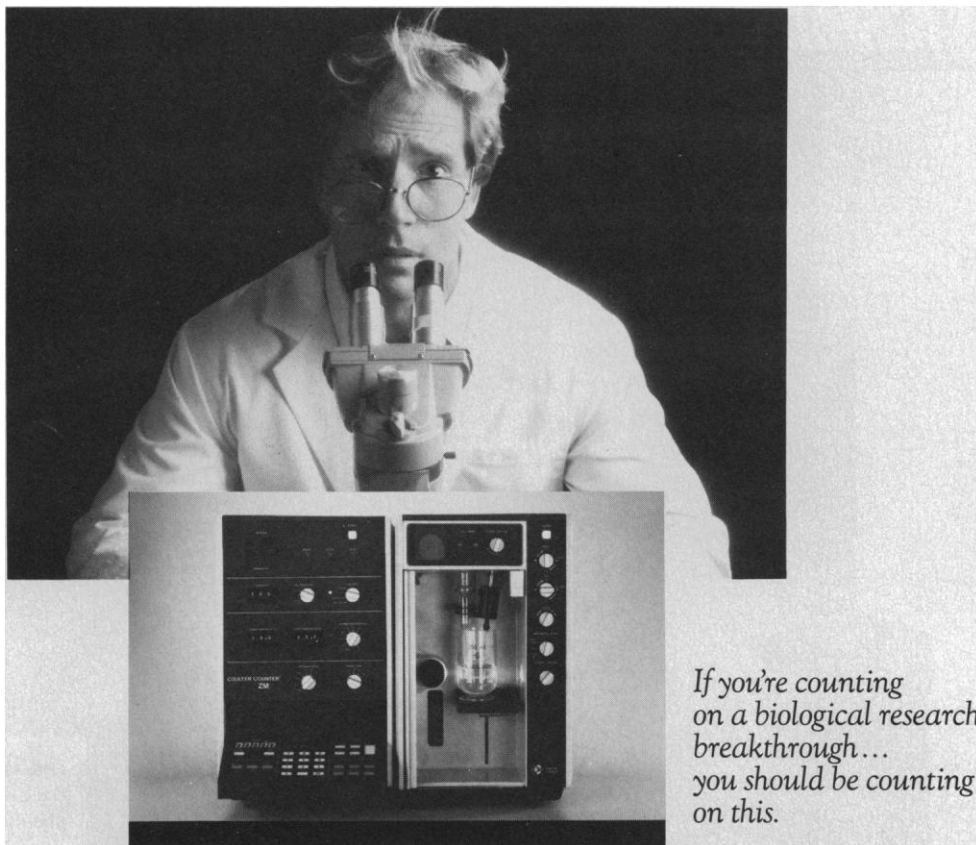
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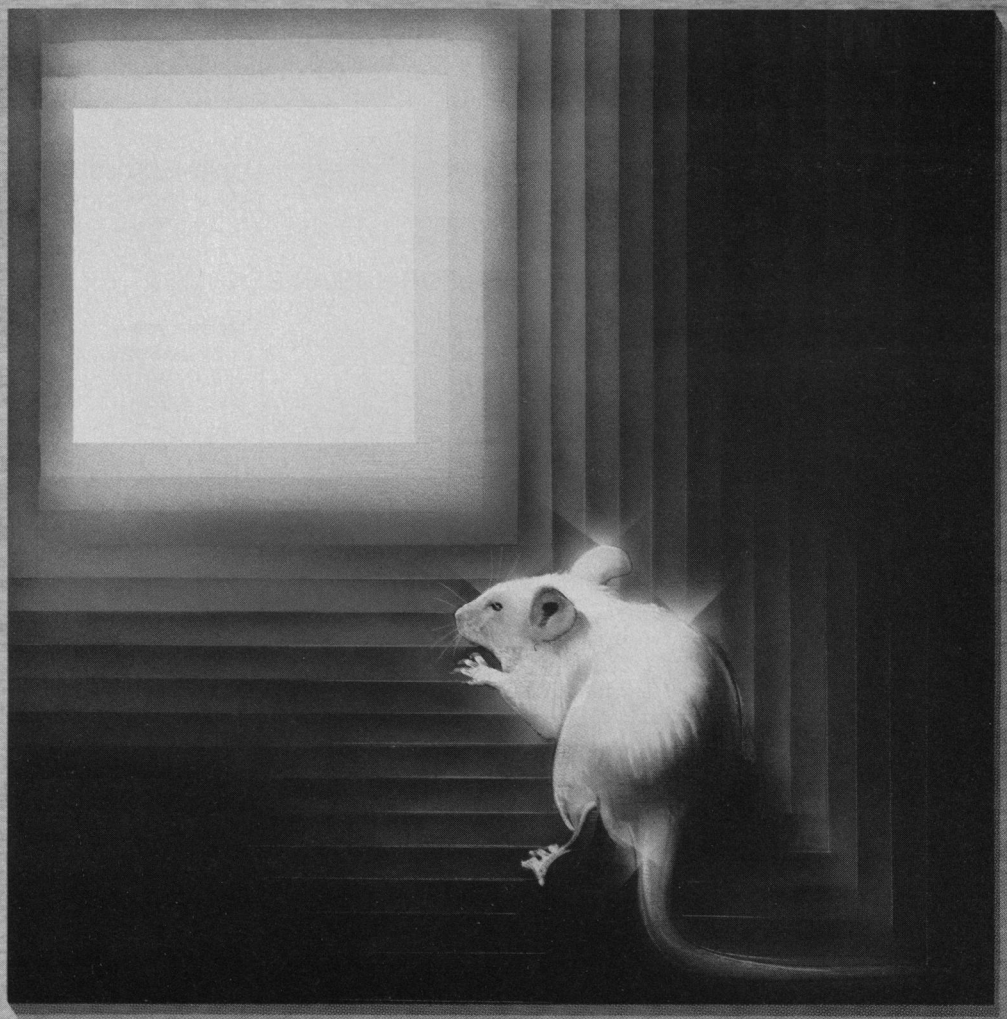
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PARTIAL LIST OF SPEAKERS FOR HUMAN GENOME I

Sydney Brenner
*Director, MRC Molecular Genetics Unit
Cambridge, England*
Eric Lander
*Fellow of the Whitehead Institute for Biomedical Research
Cambridge, Massachusetts*
Robert Moyzis
*Genetics Group Leader
Los Alamos National Laboratory*
Charles Cantor
*Professor of Molecular Biology
University of California, Berkeley
Director, Human Genome Center
Lawrence Berkeley Laboratory*
James Watson
*Director, Cold Spring Harbor Laboratory
Associate Director, NIH Human Genome Project*
Victor McKusick
*University Professor of Medical Genetics
Johns Hopkins University School of Medicine
President, International Human Genome Organization (HUGO)*
Francis Collins
*Associate Investigator, Howard Hughes Medical Institute
Chief, Division of Medical Genetics
University of Michigan Medical Center*

Tasuku Honjo
*Professor of Medical Chemistry
Kyoto University Faculty of Medicine*
Jean Dausset
*Professor, College de France
President, Human Polymorphism Study Center (CEPH)*
Hans Zachau
*Professor, Institute for Physiological Chemistry
University of Munich*
Ronald Davis
*Professor of Biochemistry
Stanford University School of Medicine*
Peter Pearson
*Chairman, Department of Human Genetics
Sylvius Laboratories, Leiden*
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*Distinguished Research Professor and Acting President
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Michio Oishi
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PARTIAL LIST OF SESSION TOPICS

- Organization of the Human Genome Project
- State of our Current Knowledge
- Advances in Technology: New Methods for Mapping and Sequencing
- Progress in Interesting Regions of the Human Genome
- The Diversity of the Human Genome in Different Populations

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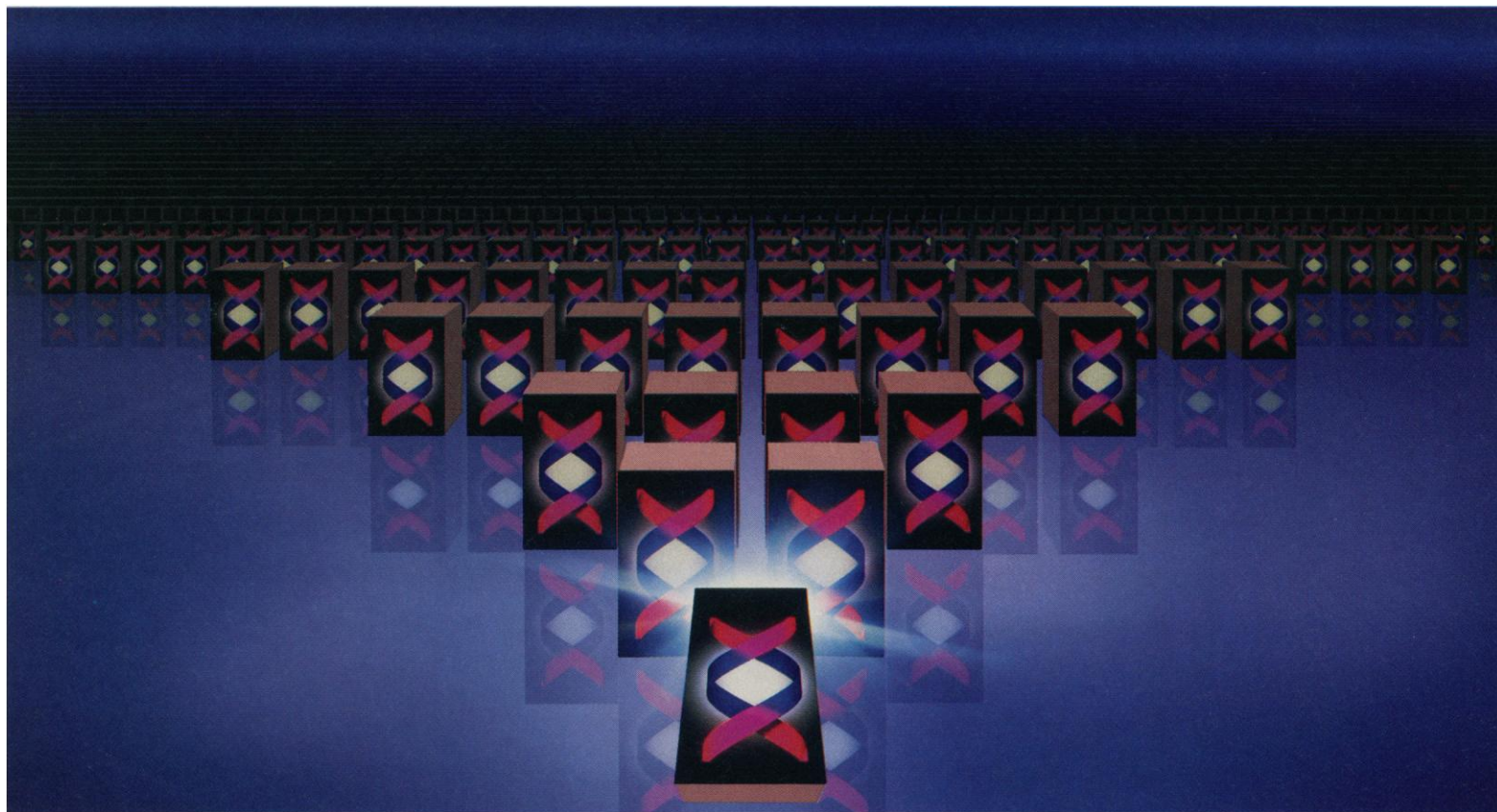
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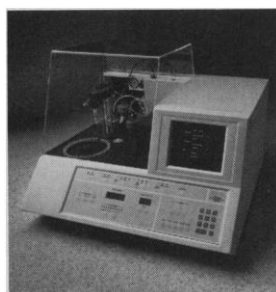
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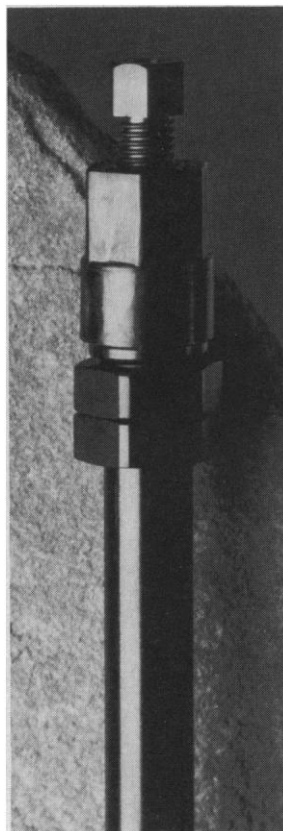
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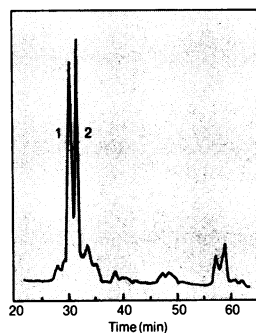
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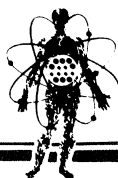
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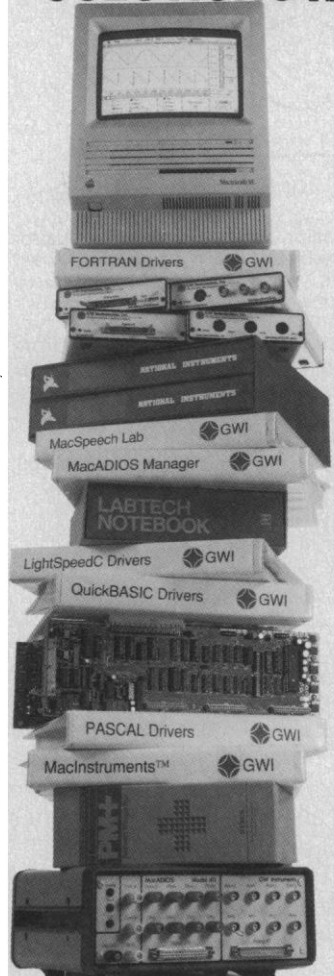
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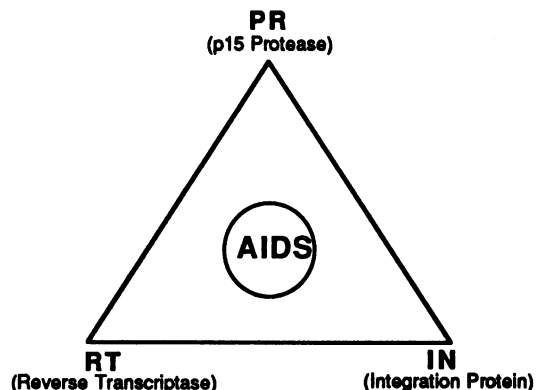
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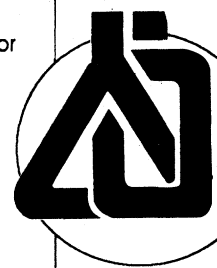
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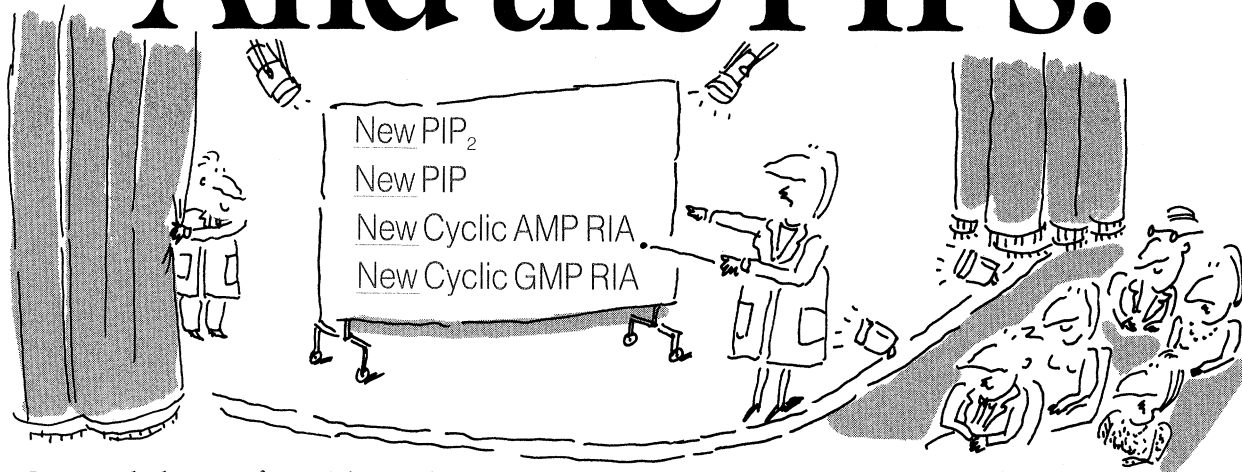
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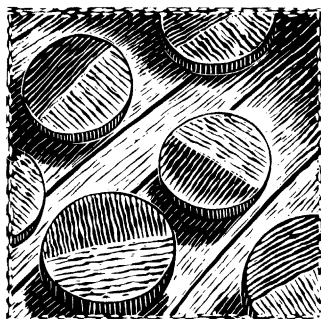
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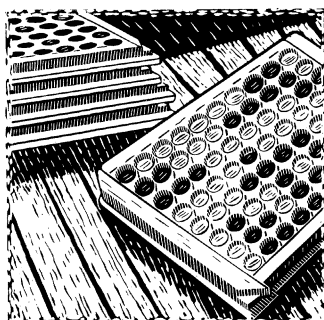
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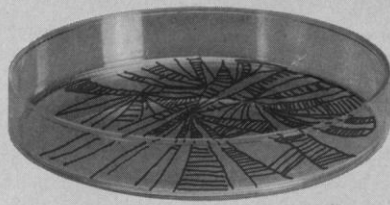
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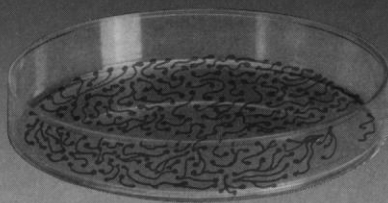
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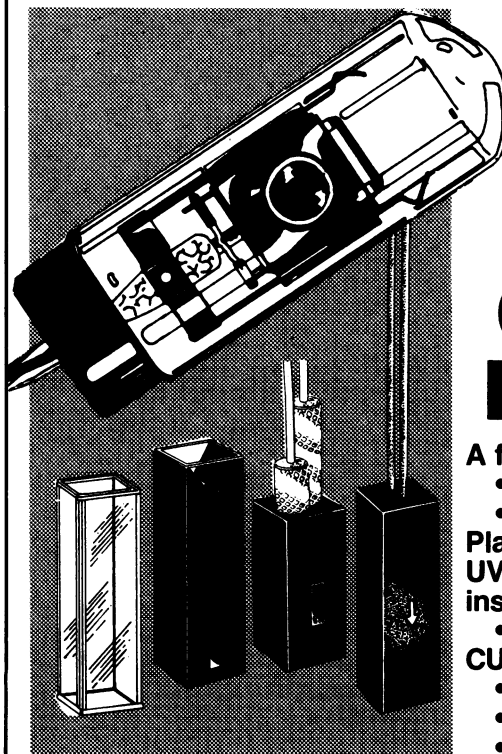
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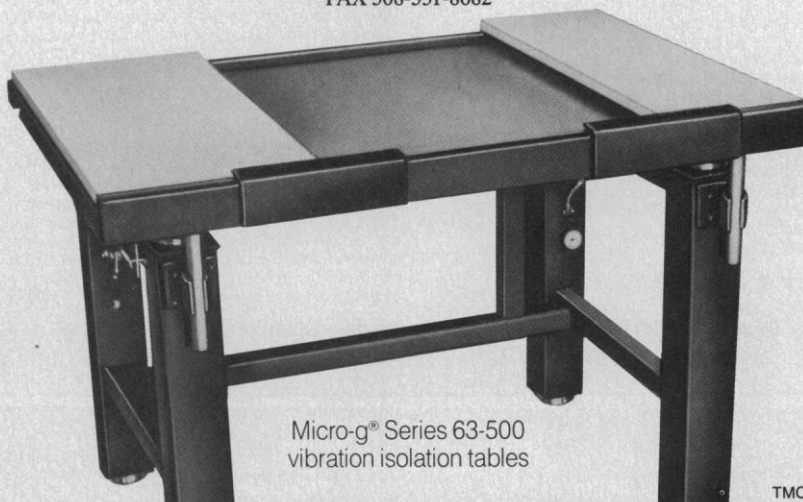
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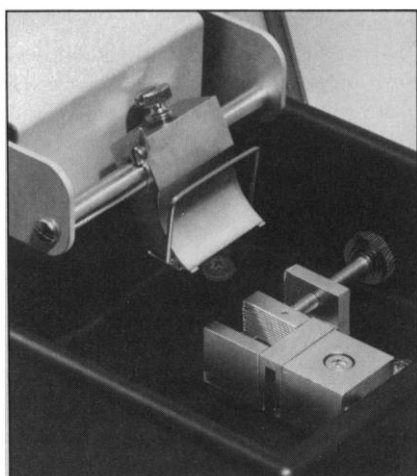


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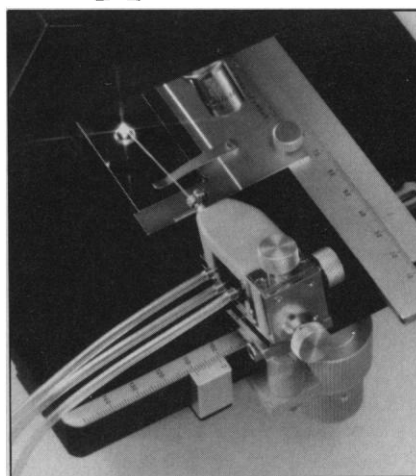
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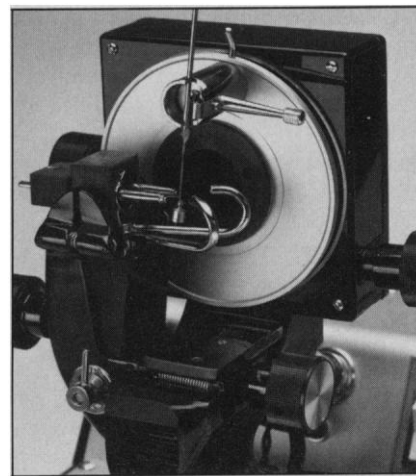
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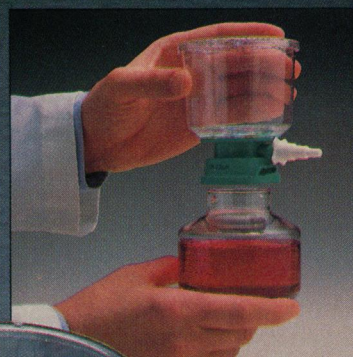
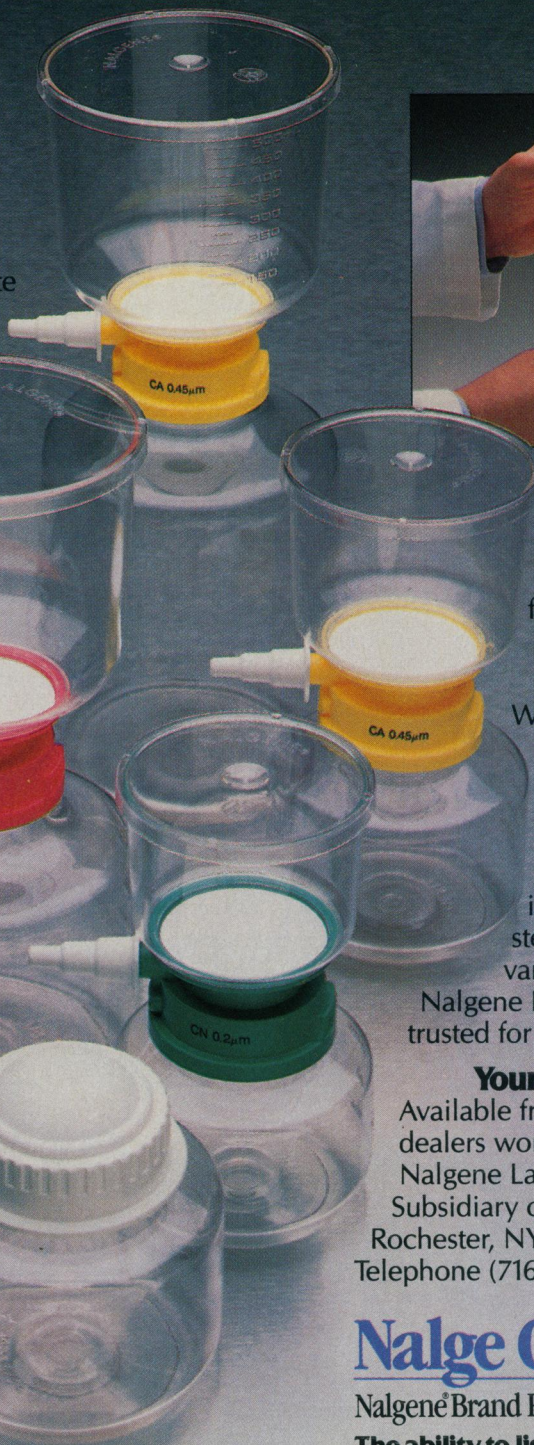
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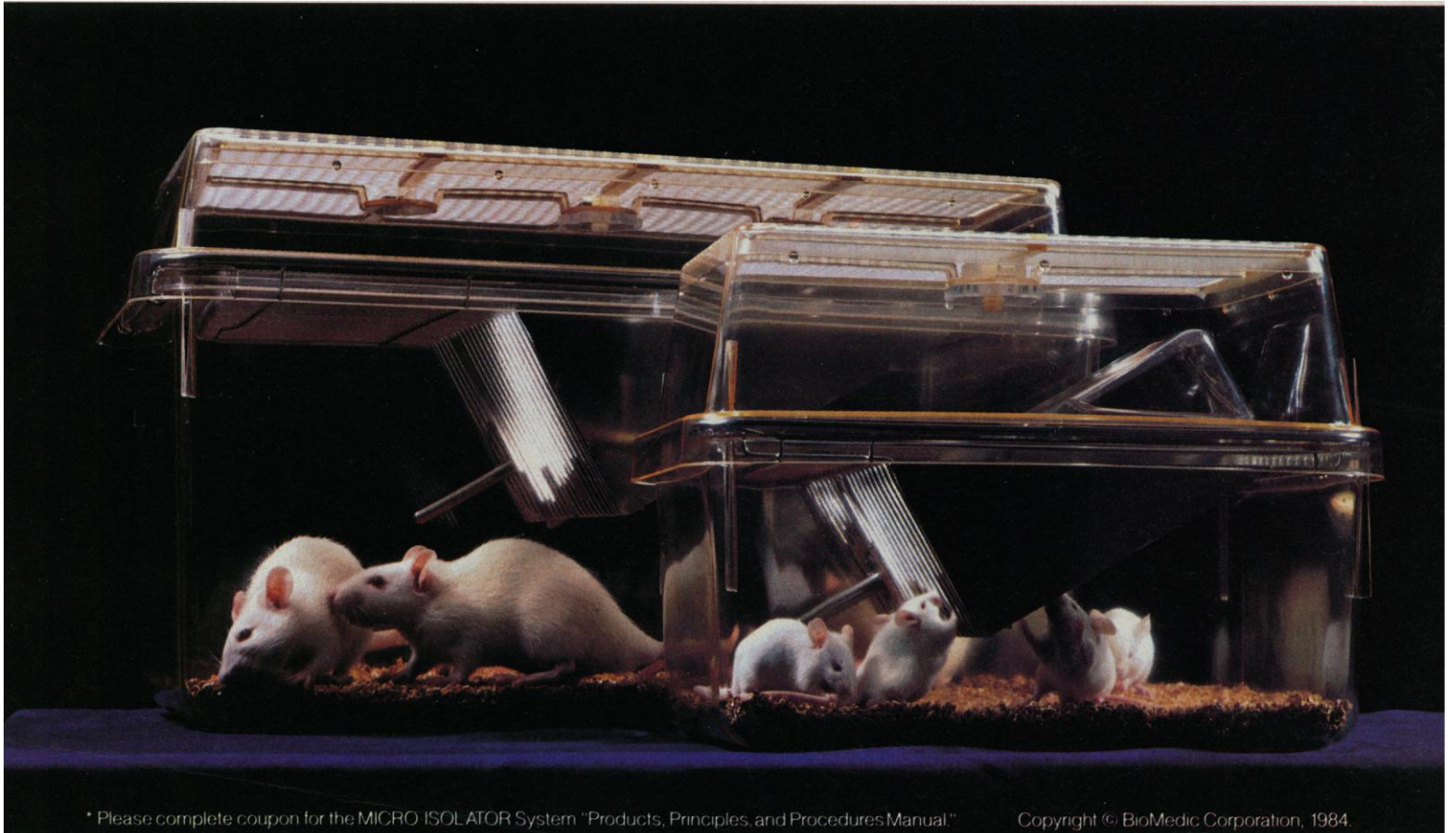
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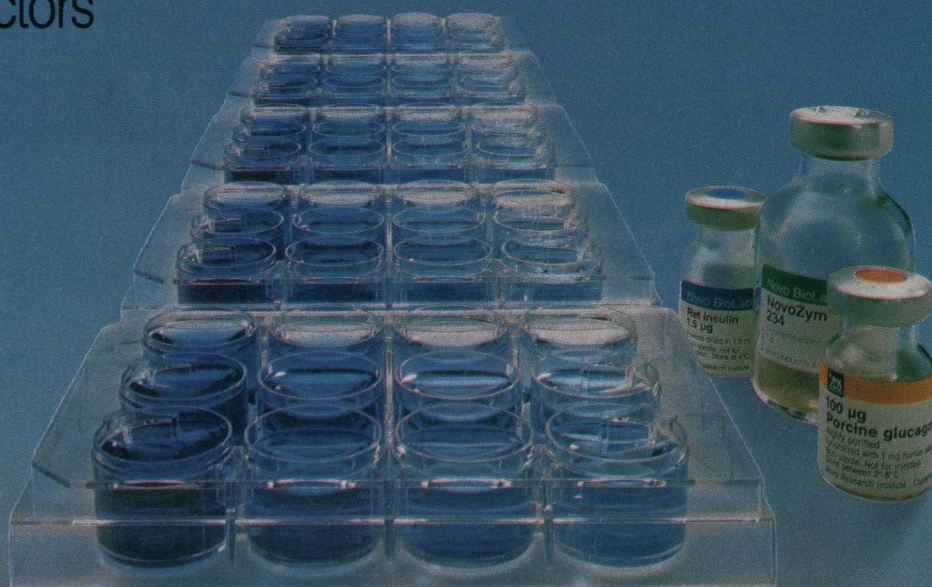
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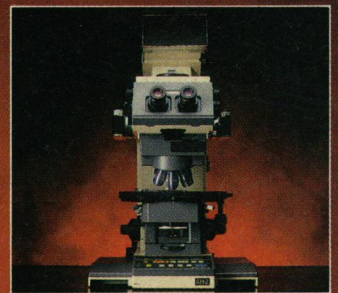
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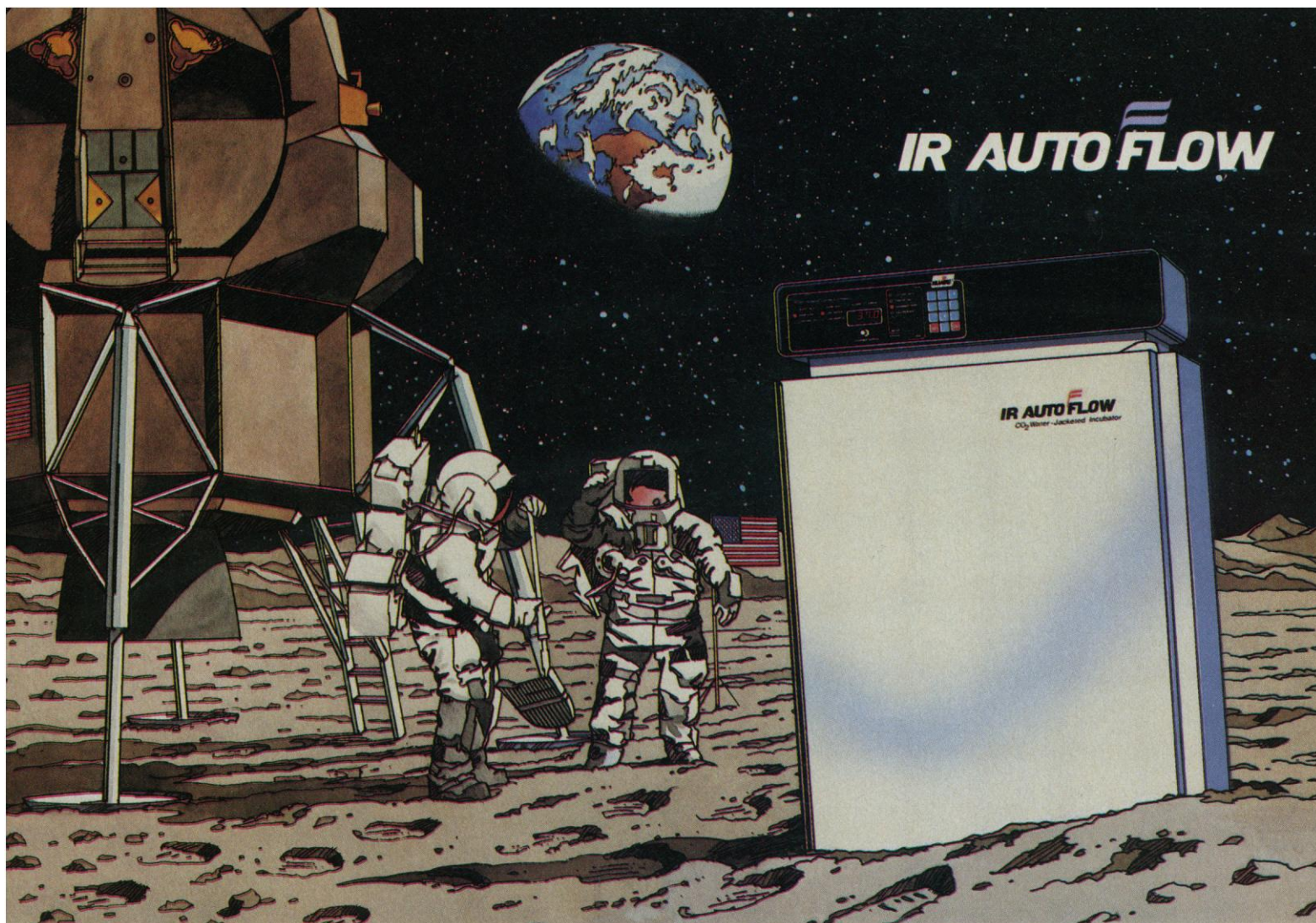
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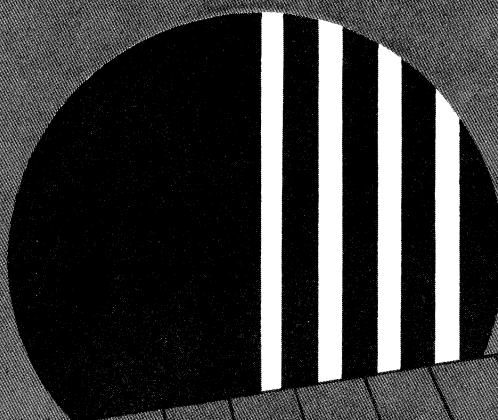
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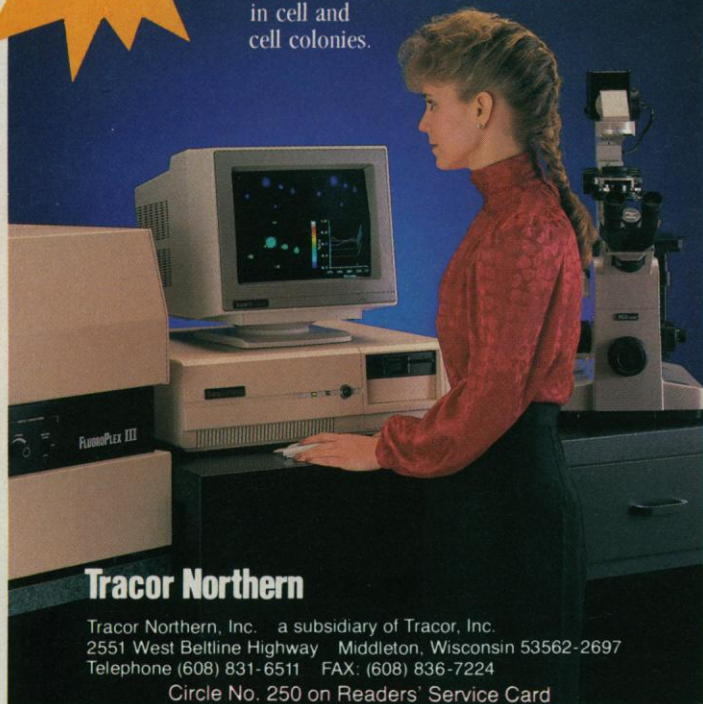
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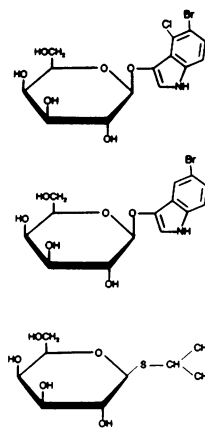
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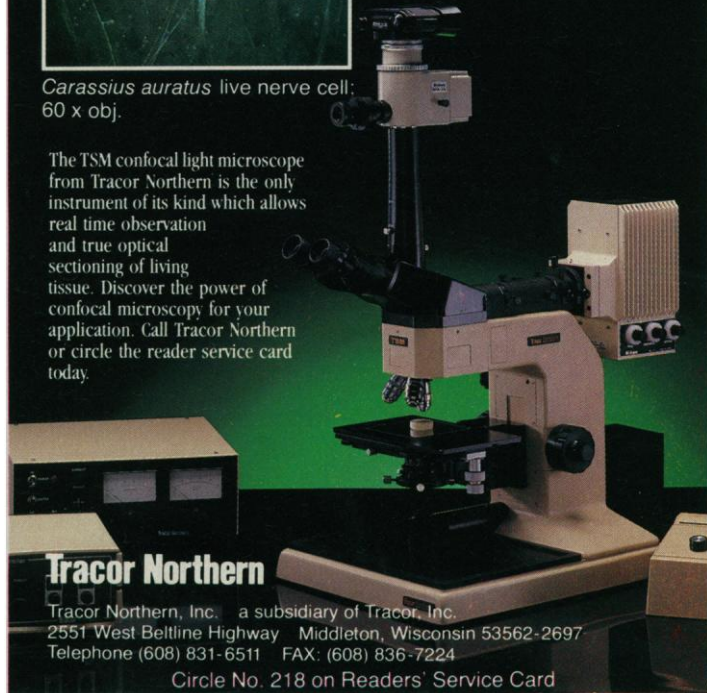
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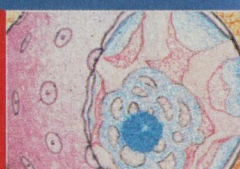
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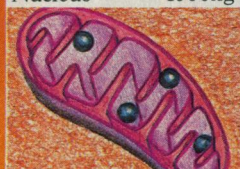
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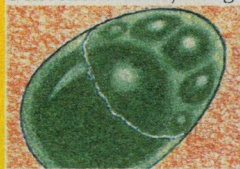
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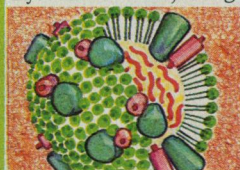
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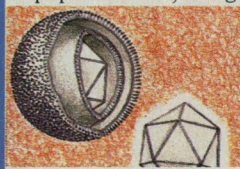
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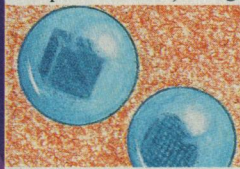
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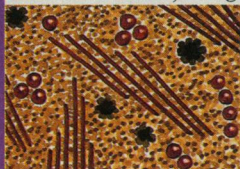
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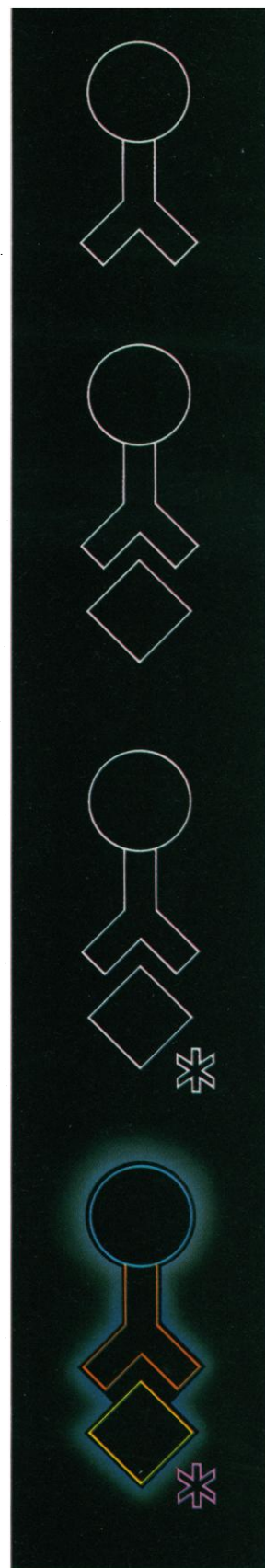
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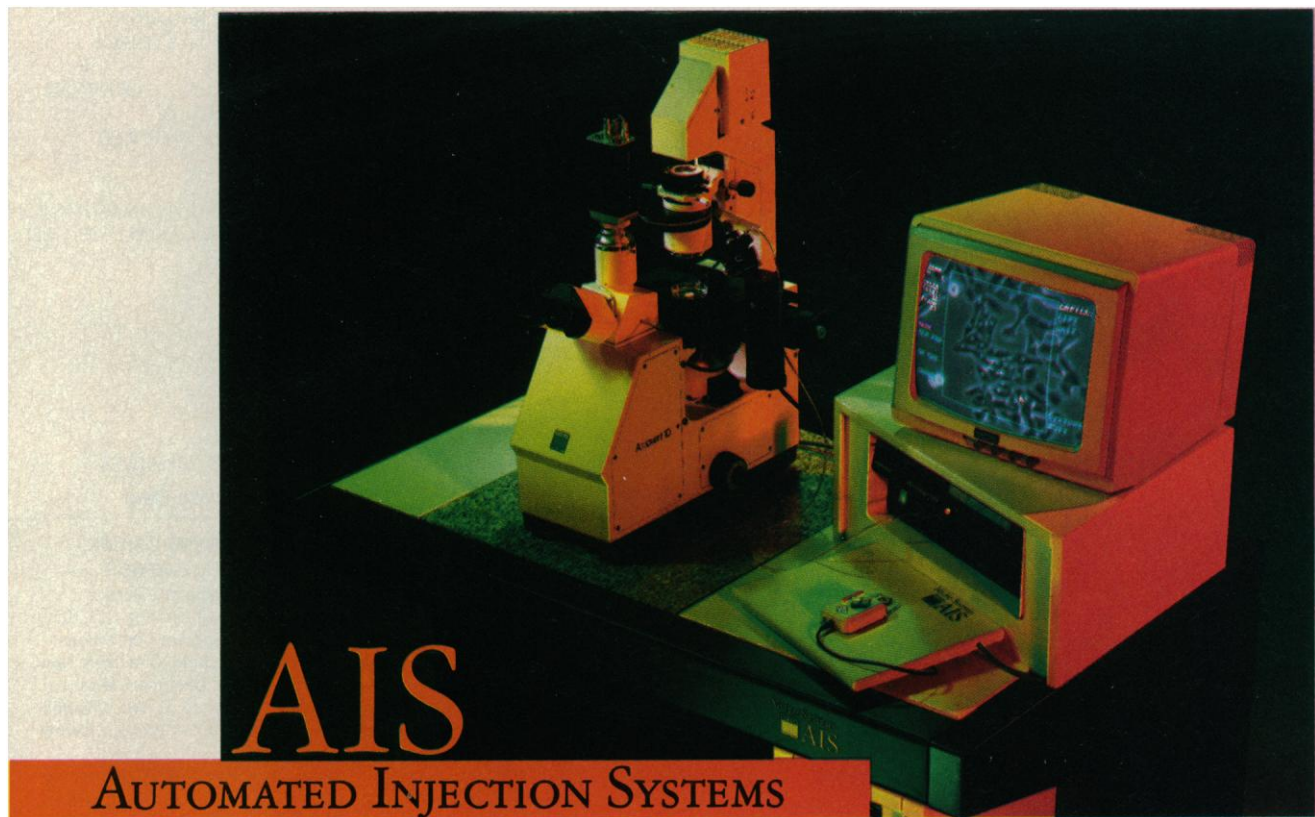
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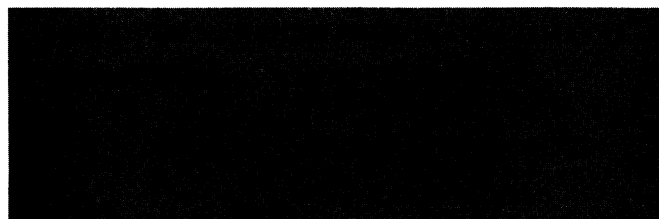
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FUDAN INTERNATIONAL SYMPOSIUM ON NEW FRONTIERS OF GENETICS

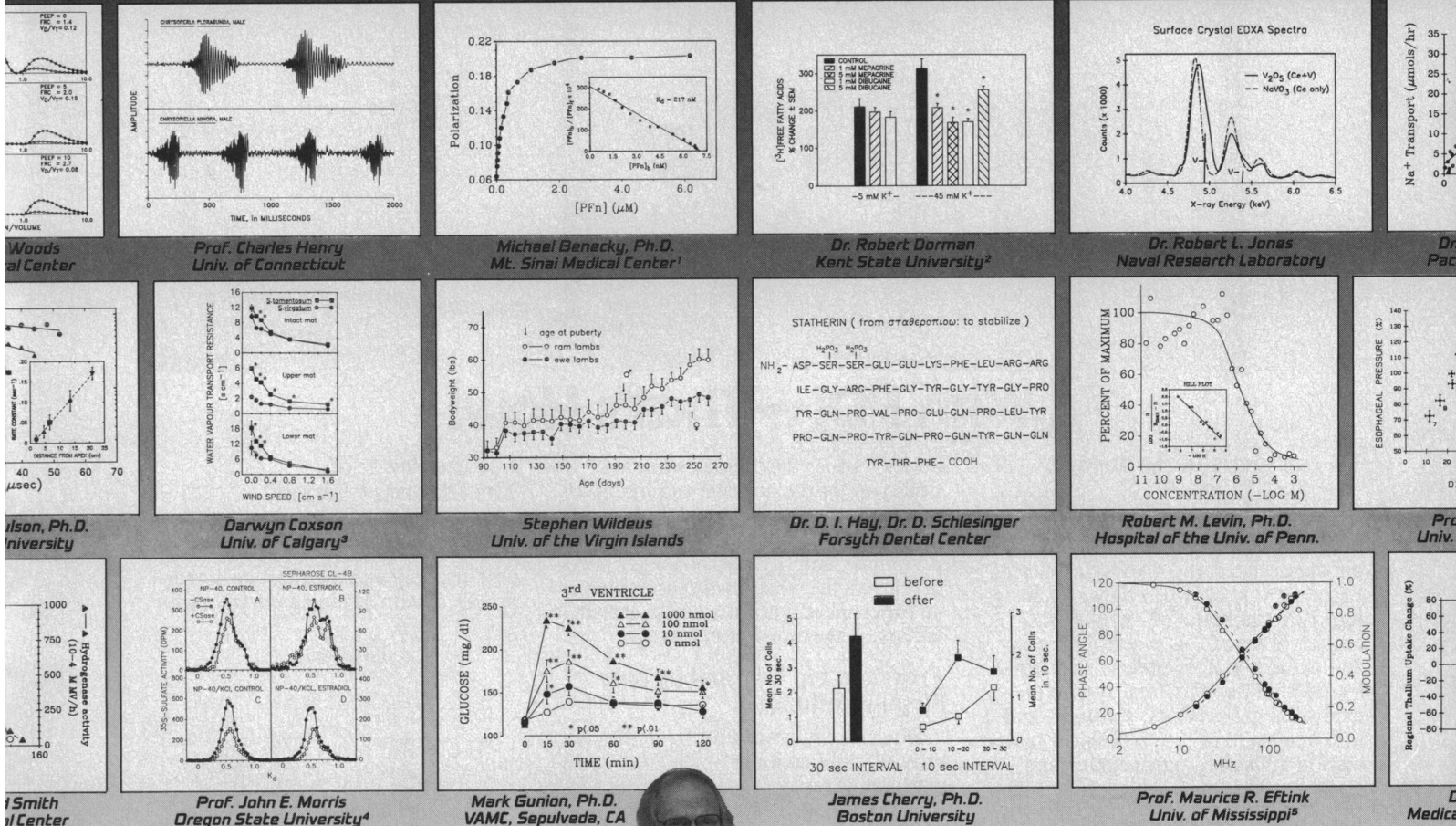
September 10-14, 1989, Bao-Long Hotel, Shanghai, China.

Organizing Committee - C.C. Tan (Honorary Chairman), S.D. Kung (Chairman), C.H.Y. Chu, (Vice Chairman). Program Committees:
Recent Advances in Drosophila Genetics: B. Judd, Chairman; New Approaches to Human Genetics, E.H.Y. Chu, Chairman; Impact of Genetics and Genetic Engineering on Agriculture: R. Wu, Chairman; Microbial Genetics and Molecular Evolution: J.T.F. Wong, Chairman; Local Arrangements: J.L. Xue, Chairman

Program: Mon., Sept. 11: Opening Ceremony & Keynote address:

Howard M. Temin; Plenary Session: Seymour Benzer, Lawrence Bogorad, Yuet Wai Kan; Session I - Drosophila Genetics: Spyros Artavanis-Tsakonas, Yuh Nung Jan, Elliot M. Meyerowitz, Ruth Lehman, Michael Young; Session II - Human Genetics: Savio Woo, David A. Williams, Y. T. Zeng, C. C. Liew, Dean Hamer, Zai-Ping Li, Barbara Hamkalo; Session III - Plant Genetics: Ray Wu, Marc Van Montagu, Roger Beachy, Y. T. Qian, Ning-Sung Yang, Zhang-Liang Chen; Session IV - Microbial Genetics & Molecular Evolution: J. Tze-Fei Wong, Jeffrey Miller, Alastair Matheson, Robert Cedergren, Ke-zhong Tong, Haruo Ozeki; Tues., Sept. 12: Plenary Session: Gerald Fink, Nam Hai Chua, C. Thomas Caskey, Charles Langley; Poster Session; Banquet: C.C. Tan Birthday Celebration; Keynote Address: Joshua Lederberg; Wed., Sept. 13: Plenary Session: David Hogness, Gurdev Khush, James Neel, Rita Colwell; Session I - Drosophila Genetics: L.Y. Jan, Bruce Baker, Michael Ashburner, William Engels, Chung-I Wu, Hampton Carson; Session II - Human Genetics: Ernest H.Y. Chu, Robert Moyzis, Elbert Branscomb, Lap-Chee Tsui, L.C. Sze, Larry Deaven, John J. Wasmuth; Session III - Plant Genetics: Thomas Hodges, A. Hirai, John C. Gray, Shain-dow Kung, Shyam Dube, Alan Teramura, C.C. Chen; Session IV - Microbial Genetics & Molecular Evolution: Edmund C.C. Lin, Frank Maley, Paul E. Sadowski, Paul O.P. Ts'o, Pei-Xuan Guo, Temple F. Smith; Thurs., Sept. 14: Plenary Session & Closing Ceremony: Eric Davidson, Thomas C. Kaufman, Michael Smith, Zu-Jia Sheng. For further information & registration contact: Helen Phillips, Ctr. for Agricultural Biotechnology, University of Maryland, College Park, Maryland 20742, USA, Telephone: (301) 454-6056 or 8312; FAX: (301) 454-8143.

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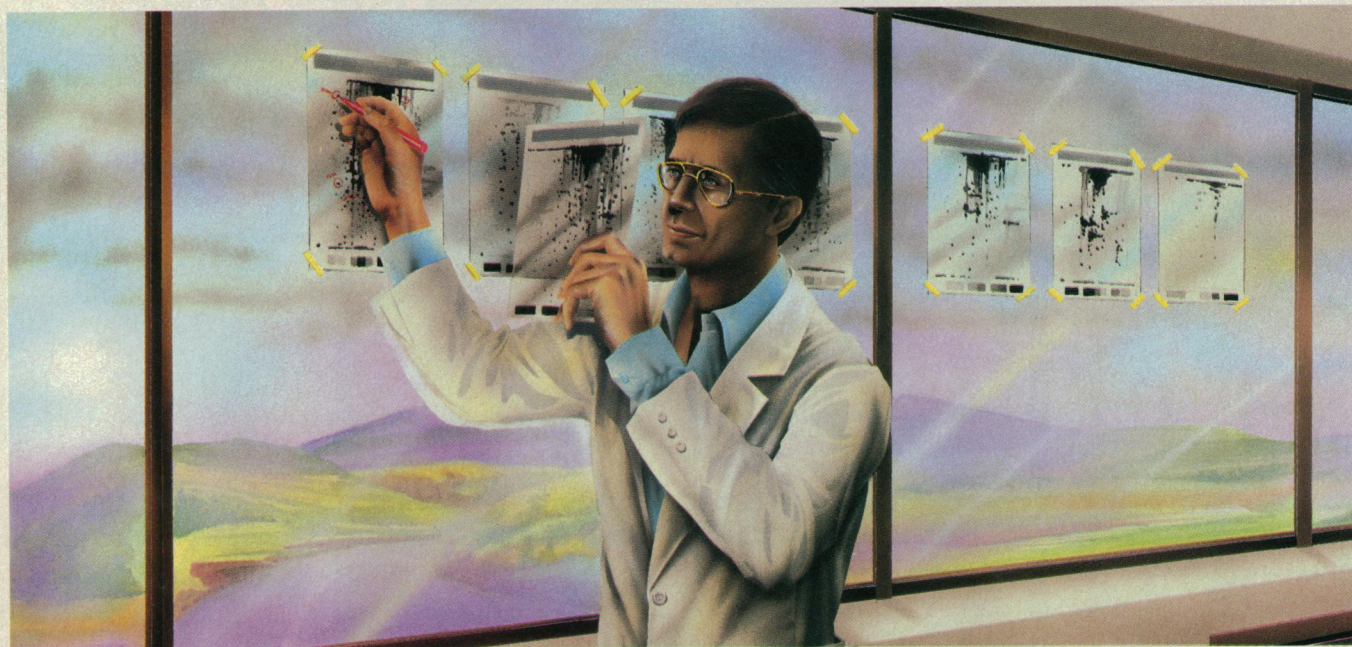
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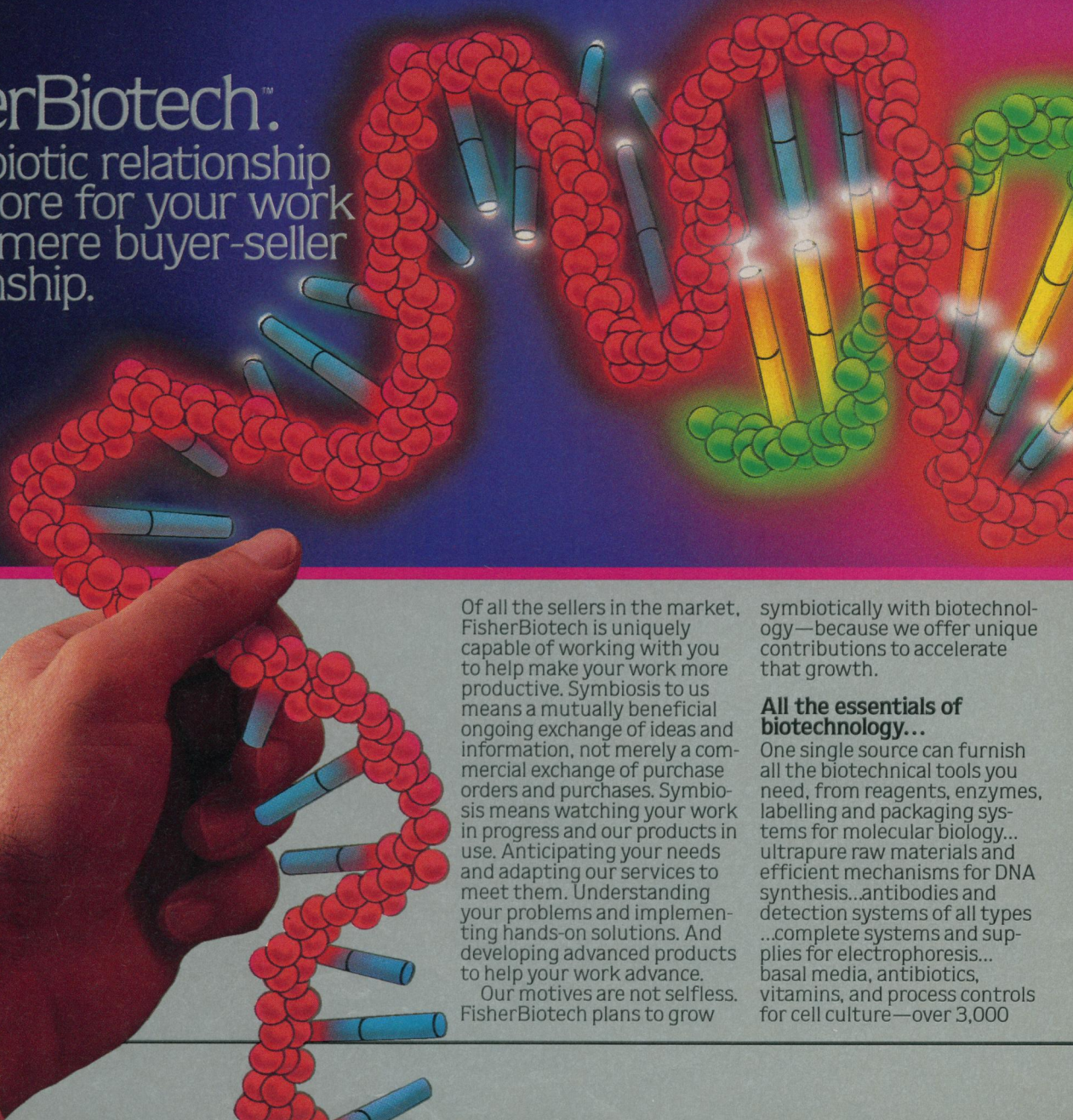
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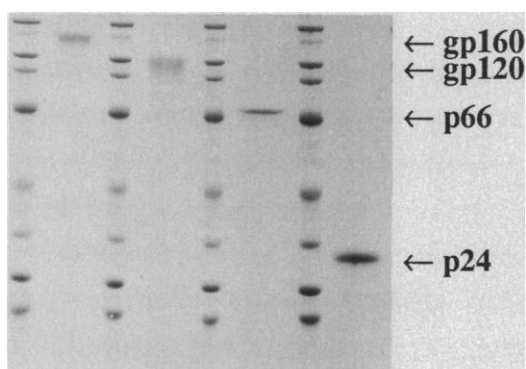
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