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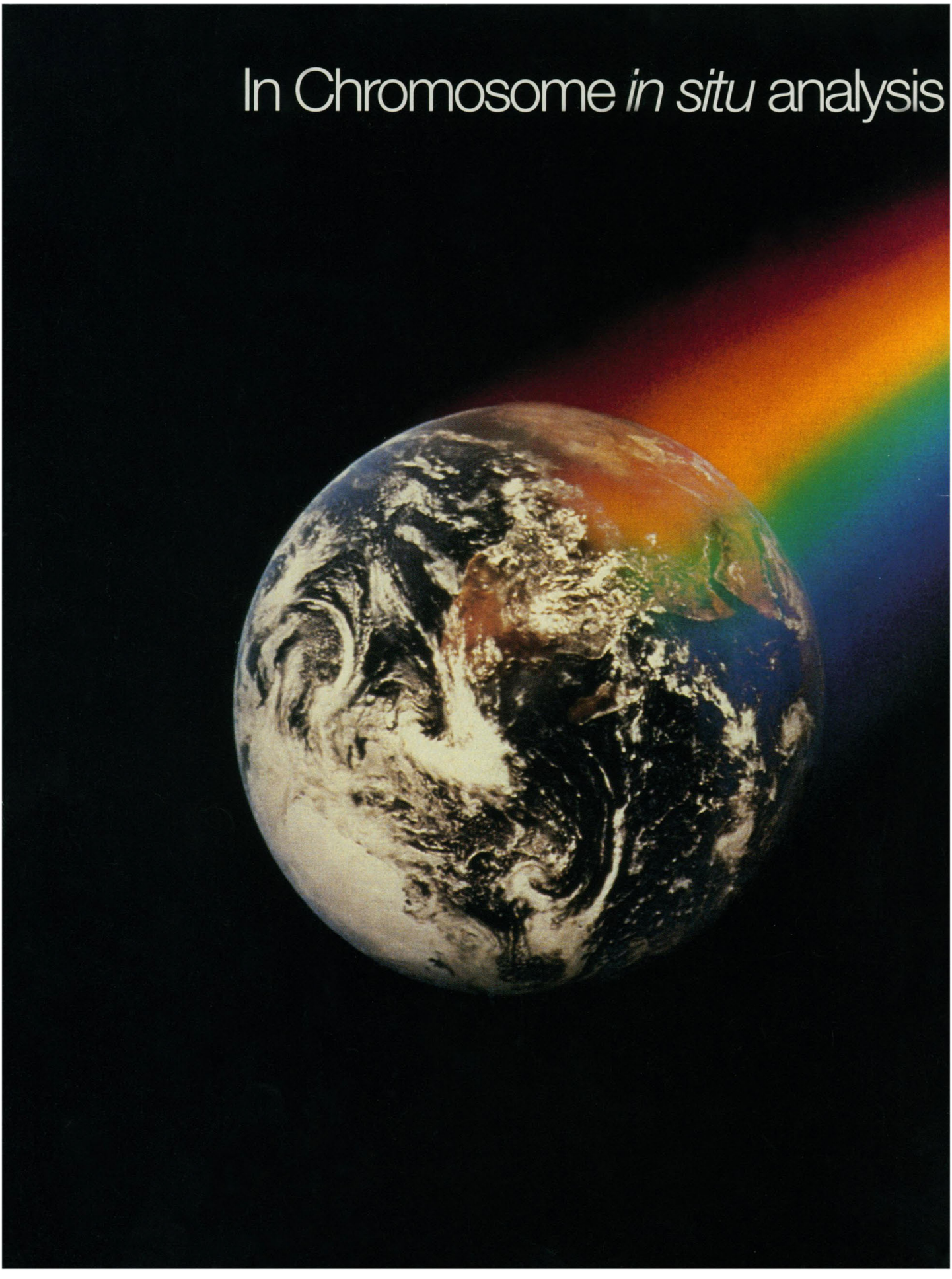
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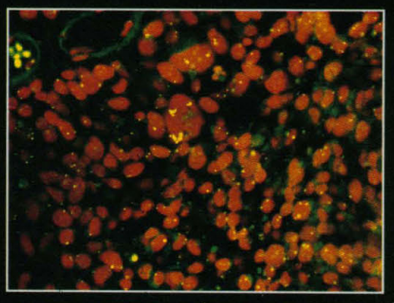

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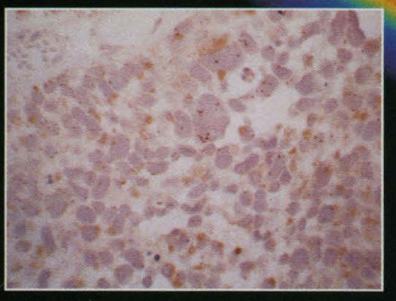
Human X Alpha Satellite Probe



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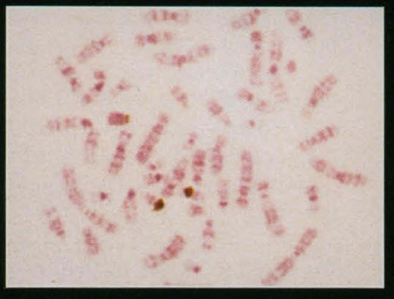

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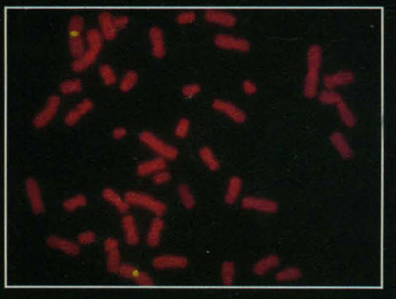

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COVER Ribbon diagram of the conserved catalytic core shared by all known eukaryotic protein kinases. The crystal structure of the catalytic subunit of cyclic adenosine monophosphate–dependent protein kinase provided the template for the core. The amino terminus of the protein (shades of brown) is associated with magnesium adenosine triphosphate binding, and the carboxyl terminus (purple) with peptide binding. Catalysis occurs in the cleft between the two lobes. Insertions at the sites indicated by dots (blue-green, more than 70 residues; violet, more than 25 residues) occur in some members of the protein kinase family. See pages 407 and 414. [Source: S. S. Taylor; illustration by Diana DeFrancesco]

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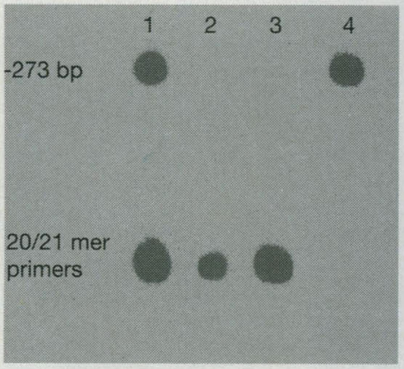

Purification with a QIAGEN / QIAEX >PCR purification < spin kit of a 273 bp fragment amplified from the plastocyanine gene.
A radiolabeled 20/21-mer primer pair was used for the amplification.
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Lanes 2, 3 & 4: Same aliquot purified with the QIAGEN / QIAEX procedure.
Lane 2: Total flow through.
Lane 3: Total wash.
Lane 4: Purified PCR product devoid of any residual primers in a yield of 95 %.

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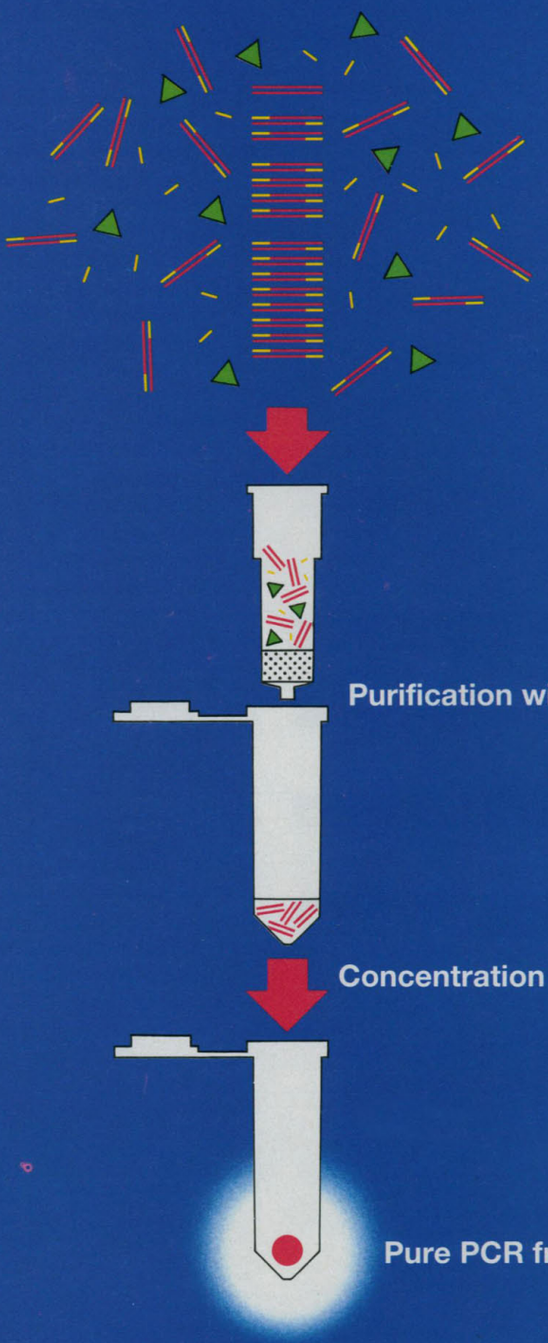

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This Week in

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Magnetoencephalography: losing attraction?

Magnetoencephalography (MEG) may not be all it was once cracked up to be. That's what its greatest detractor, who was initially one of its strongest advocates, is claiming. David Cohen, the founder of this noninvasive and purportedly ultrasensitive procedure for measuring electric activity, is now arguing that the anticipated promise of MEG will not be realized; his disenchantment with MEG and the reaction of others to it are discussed in a story by Crease (page 374). Should MEG technology fall short, it will be a disappointment to both the research and clinical communities and to the companies that have been developing MEG's very expensive equipment.

Catalytic core structure

Some 100 protein kinases are known and they all share a conserved catalytic core. Their function is to phosphorylate and, in so doing, to activate proteins; therefore, these enzymes play a critical part in eukaryotic cell development and growth. Protein kinases typically exist in an inactive state; binding by cyclic adenosine monophosphate (cAMP) activates them. Then regulatory subunits and activated catalytic subunits are released. New information about the three-dimensional structure of the catalytic core of the cAMP-dependent protein kinase and of its interactions with a tightly binding inhibitor is presented in two Research Articles by Knighton *et al.* (pages 407 and 414). The enzyme has two lobes linked by a deep cleft. The smaller lobe has an unusual structure; its glycine-rich loop serves to anchor the phosphate groups of the nucleotide (magnesium adenosine triphosphate). The larger lobe includes the catalytic loop that is essential for peptide binding and catalysis. An understanding of the complex structure-function relations in this enzyme should aid in the design of high-affinity substrates and inhibitors for this and related protein kinases for use in pharmacologic and research applications.

High-pressure chemistry

Iron hydride has been difficult to obtain and study because it forms only at elevated pressures and temperatures. Geophysicists are extremely interested in this compound because of its possible importance in accounting for an enigmatic property of Earth's core—the core is less dense than expected for a body consisting solely of hexagonal close-packed iron. And materials scientists are interested in iron hydride because ferrous metals can be degraded by hydrogen; circumventing this problem has become a persistent technologic challenge. The formation of iron hydride has now been studied in a diamond anvil cell and its crystal structure determined, its pressure-volume relations—the equation of state—explored, and its stability at high pressures evaluated (page 421). Badding *et al.* propose that the hydrogen atoms of iron hydride occupy the octahedral interstices of double hexagonal close-packed iron crystals. Their studies show how hydrogen atoms can destabilize metallic samples and make them brittle. They also indicate that a large hydrogen component in the core of Earth would be consistent with the seismologic studies that show that the core is not dense enough for pure iron.

Fluidity of fate

When, in development, is a cell's fate irreversibly set and what molecules and interactions contribute to cellular fate determinations? Nelson and Weisblat have used the leech embryo system, a relatively simple and manipulable one, to examine these questions (page 435). At the embryo's fourth cleavage stage, a single cell called D′ divides into DM and DNOPQ cells, the progenitors of the mesodermal and ectodermal lines of cells, respectively. DM is situated near the embryo's vegetal pole; DNOPQ is nearer the animal pole; both inherit a mixture of teloplasm—yolk-deficient cytoplasm containing mitochondria, endoplasmic reticulum, and RNA—from the two poles. Teloplasm could be removed from one pole or the other shortly after it formed, and the effect of its absence on cell fate assessed. Embryos that had received only animal teloplasm developed normally for many stages; those having only vegetal teloplasm did not; in the latter, the progenitor of ectodermal cells switched and instead produced mesodermal cells. Manipulations of this sort, involving teloplasm, cells, and other factors, are helping to clarify what are the necessary and sufficient ingredients for fate determinations.

Carbohydrate recognition

Many of the natural antigens of pathogens and the surface molecules on tumor cells are carbohydrates, yet relatively little is known about the interactions of carbohydrates with the body's defensive antibody molecules. Cygler *et al.* have determined the crystal structure of a complex of a bacterial carbohydrate antigen with the binding domain (the Fab fragment) of the antibody molecule that specifically recognizes it (page 442). The O-antigen of serogroup B *Salmonella*, a pathogenic group of organisms responsible for gastrointestinal infections, was studied. The O-antigen contains four sugars arranged in repeating units. It is anchored to the outer membrane of the bacteria. The interactions of antibody and antigen involve a hydrophobic pocket of the antibody that is dominated by aromatic amino acids and that includes a buried water molecule; the water molecule coordinates hydrogen bonding and enhances the surface interactions of carbohydrate and antibody; at their interface these two assume highly complementary shapes. The novel forms of hydrogen bonding that have been found may be something that could be exploited by bioengineers attempting to produce tighter binding antibody molecules. ■ RUTH LEVY GUYER

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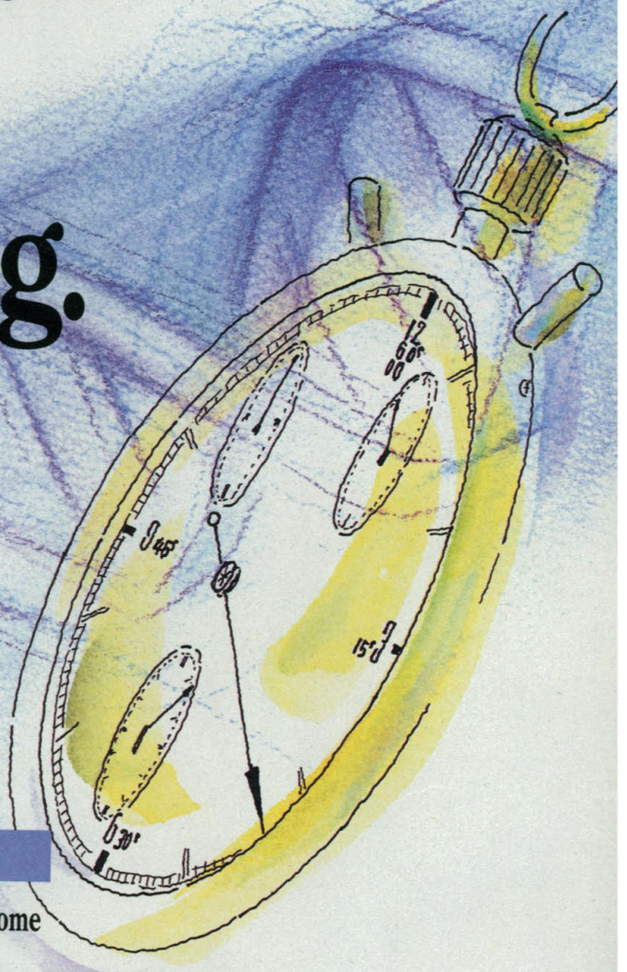

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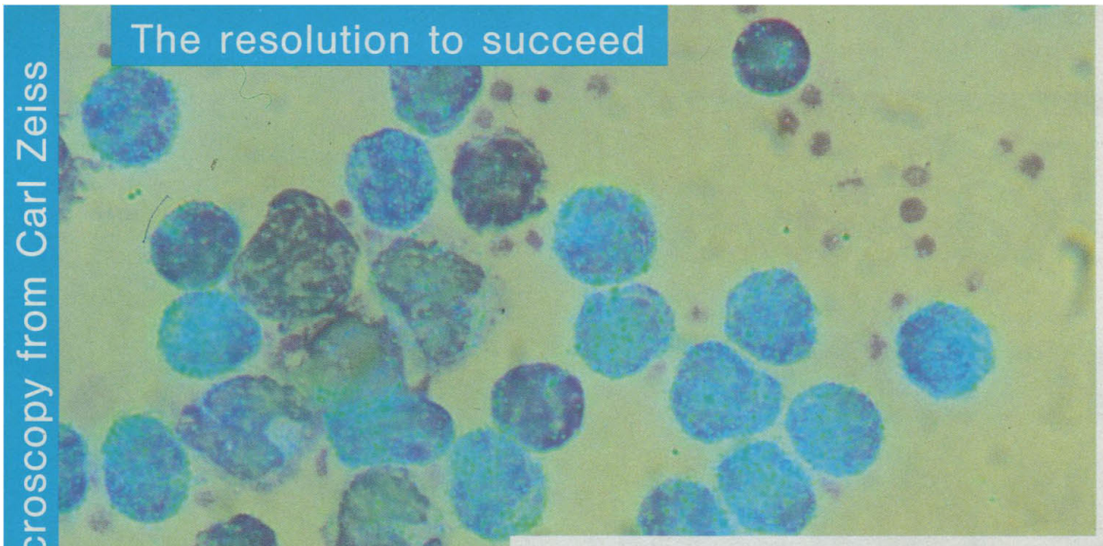

Selective IGSS surface antigen labelling of human leucocytes; May-Grünwald/Giemsa counterstaining

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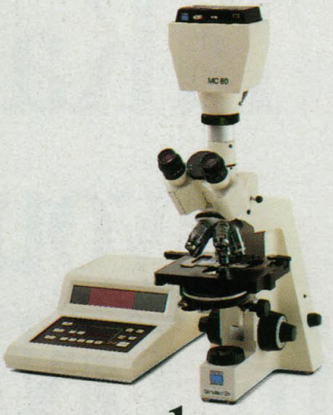

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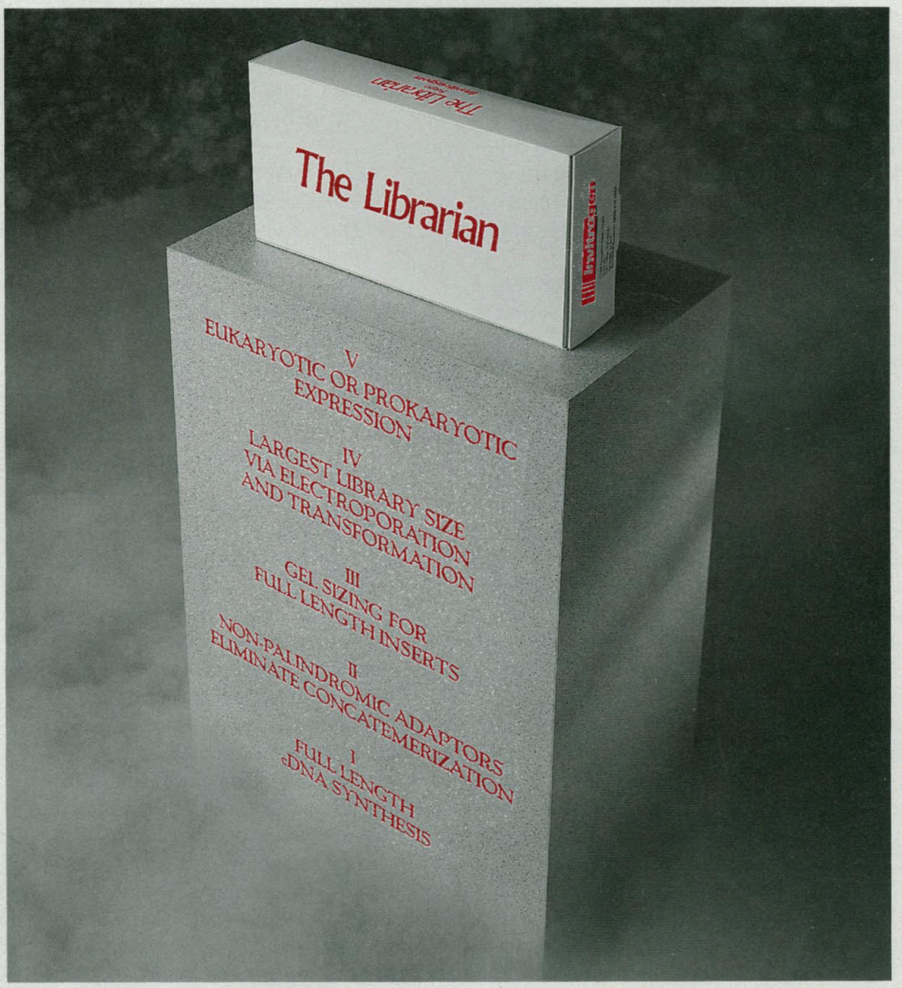
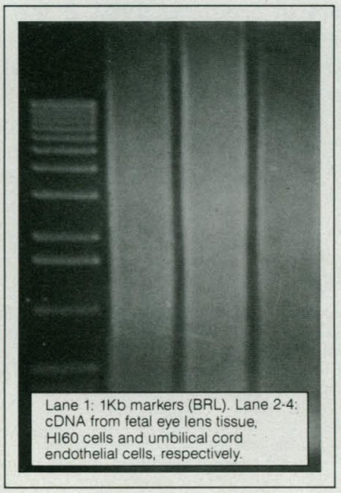


Lane 1. Lane 2. Lane 3. Lane 4.



Lane 1: 1Kb markers (BRL). Lane 2-4: cDNA from fetal eye lens tissue, HI60 cells and umbilical cord endothelial cells, respectively.

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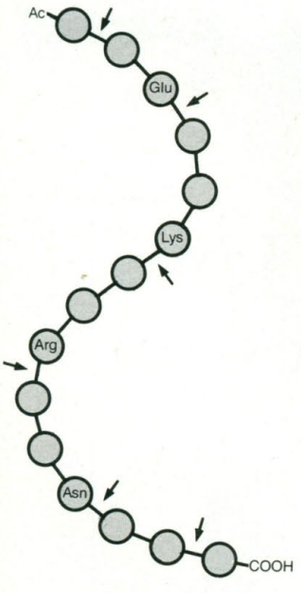

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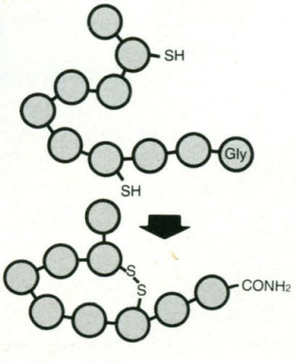

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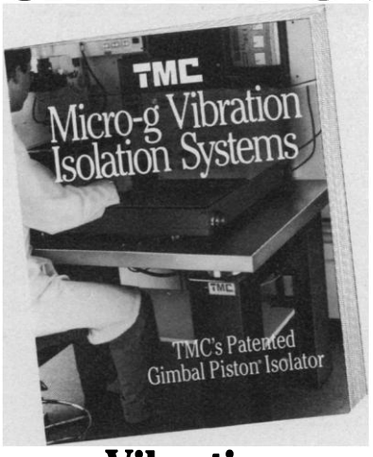

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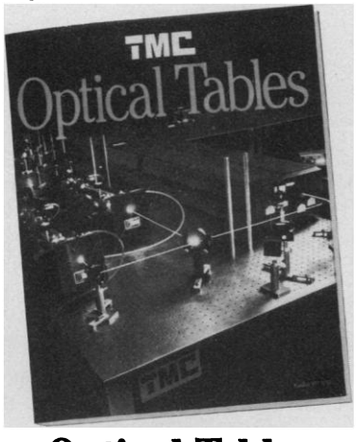

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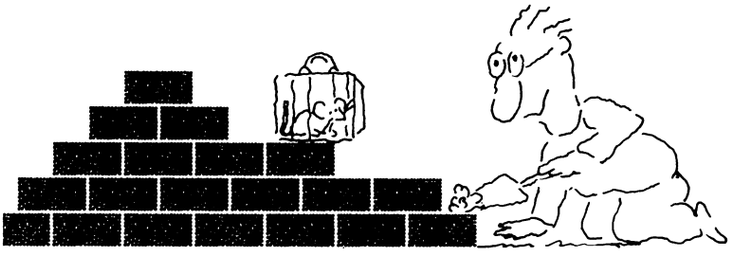

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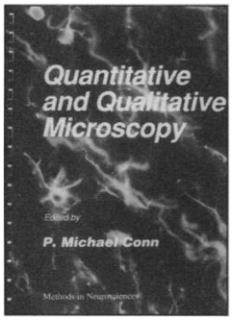

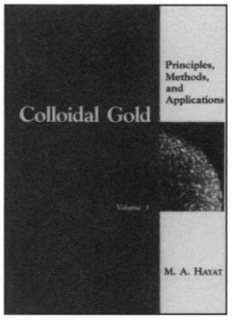

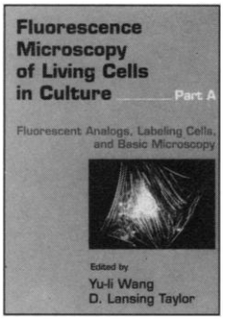

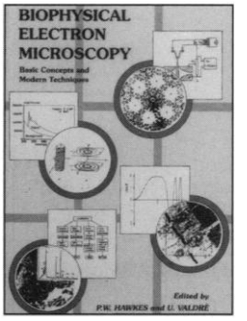

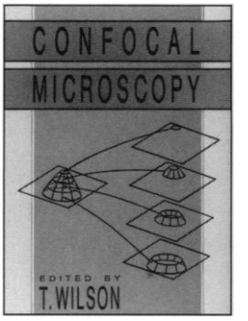

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