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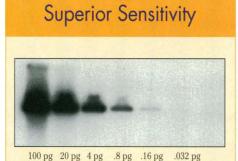
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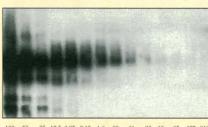
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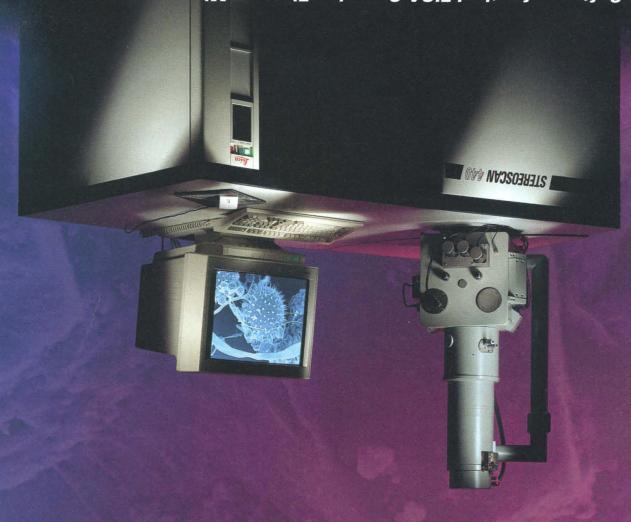
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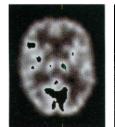
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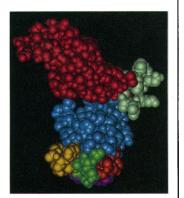








1896 The biology of learning disabilities



1906 & 1984 T cell receptor β chain

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RESEARCH ARTICLE

Architectures of Class-Defining and 1958 Specific Domains of Glutamyl-tRNA Synthetase O. Nureki, D. G. Vassylyev, K. Katayanagi, T. Shimizu, S.-i. Sekine, T. Kigawa, T. Miyazawa, S. Yokoyama, K. Morikawa

RTMENTS

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COVER

recognized features of the glassy state. See page

1939. Amorphous materials and glasses are the focus of a special section on Materials Science, which begins

on page 1918. [Images: P. H. Poole, Dalhousie Univer-

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sity, Halifax, Nova Scotia]

Chen-Kiang

Designed Peptide

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Converting Enzyme

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Receptors: Modulation by Mg2+ and

for Formation of STAT-Promoter Complexes X. Zhang, J. Blenis, H.-C. Li, C. Schindler, S.

Molecular dynamics representations of two low-temperature amorphous states of water, which are characterized by different, incompatible short-range orderings of the molecules. The white spheres represent hydrogen and the red spheres oxygen. Polyamorphism, important in biopolymers, is one of the most recently

| A Topographic View of Supercooled Liquids and Glass Formation F. H. Stillinger | 1935 |
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REPORTS

| Spatially Resolved Visible Luminescence of Self-Assembled Semiconductor Quantum Dots R. Leon, P. M. Petroff, D. Leonard, S. Fafard | 1966 |
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| Design and Application of Electron- Transporting Organic Materials M. Strukelj, F. Papadimitrakopoulos, T Miller, L. J. Rothberg | 1969 . М. |
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| Atmospheric Methyl Bromide (CH ₃ Br) from Agricultural Soil Fumigations K. Yagi, J. Williams, NY. Wang, R. J. Cicero | 1979 |
| Signatures of the Martian Atmosphere in Glass of the Zagami Meteorite K. Marti, J. S. Kim, A. N. Thakur, T. J. M K. Keil | 1981 cCoy, |
| Crystal Structure of the β Chain of a T Cell Antigen Receptor G. A. Bentley, G. Boulot, K. Karjalainen, Mariuzza | 1984 R. A. |

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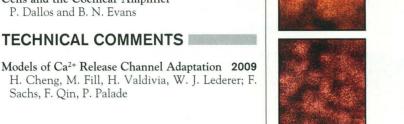
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966 Illuminating quantum dots













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1883



1987

1990

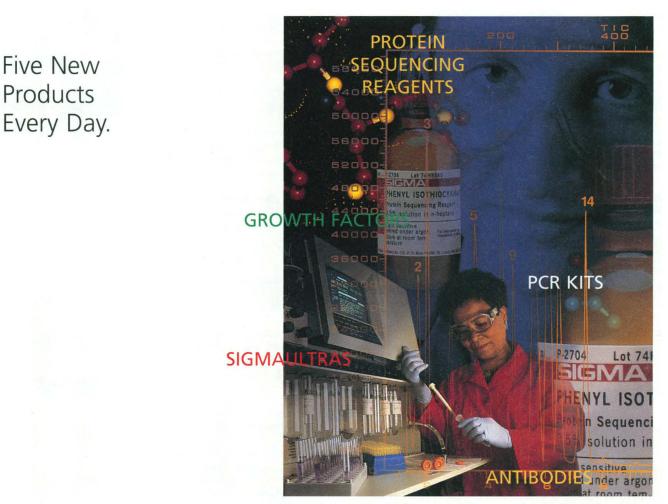
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THIS WEEK IN SCIENCE

edited by DAVID LINDLEY

Alike but not alike

Faithful translation of genetic information relies on the specificity with which the 20 aminoacyl-tRNA synthetases recognize and join their amino acids to tRNA. Nureki et al. (p. 1958) have resolved the crystal structure of glutamyl synthetase (GluRS) from the thermophilic archaebacterium Thermus thermophilus. The amino-terminal half of this GluRS resembles that of the Escherichia coli glutaminyl-tRNA synthetase (GlnRS), the similarities occurring in domains that participate in the recognition of the D and acceptor stems of the glutamyltRNA. In contrast, the carboxylterminal half has a β -barrel structure in GlnRS but for GluRS has an α -helical structure, which was found to be important in anticodon recognition.

Stepping lightly

Quantum dots are small structures in which electrons can be confined in three dimensions much as they are in atoms: The electrons reside in discrete energy levels, and transitions between levels can lead to emission of light. Leon et al. (p. 1966) report the epitaxial fabrication and imaging of indium-aluminum-arsenide dots that luminesce at red wavelengths around 6600 angstroms. Spectroscopic analysis shows the discrete density of states of the quantum dots. Next steps may include fabrication of ordered 2D and 3D arrays of the tiny emitters.

Inner direction

Recent seismic data have suggested that Earth's solid iron inner core is seismically anisotropic. The origin and nature of the anisotropy—presumably re-

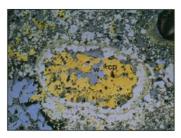
A partly open, partly shut case

The calcium release channels (ryanodine receptors, RyRs) on the sarcoplasmic reticulum open in response to an increased external concentration of Ca^{2+} , but then close or inactivate as they adapt to the higher concentration. The cycle repeats whenever Ca^{2+} concentration is increased. Cheng *et al.* (p. 2009) and Sachs *et al.* (p. 2010) offer models to explain these adaptative properties, while Valdivia *et al.* (p. 1997) provide new evidence for their physiological relevance. They show that the temporal pattern of cardiac RyR adaptation in vitro can approximate what occurs in vivo, and that phosphorylation of the RyR alters both its sensitivity to Ca^{2+} and its adaptation kinetics. Other signals within the cell can modulate the properties of the RyR, influencing the timing of Ca^{2+} release.

lated to preferential orientation of iron crystals—is unclear. Stixrude and Cohen (p. 1972) predict from theoretical arguments elastic constants for iron at the density of the inner core, and use these constants in models that account for the seismic anisotropy of the core. In a news story, Kerr (p. 1910) discusses how these results may relate to models of the geodynamo.

Formed by worms

The black smoker vents along mid-ocean ridges mark areas of active venting of hot hydrothermal fluids and extensive sulfide mineralization. Nutrients at these sites support a distinctive marine community, in-



cluding tube worms, and Cook and Stakes (p. 1975) show, through oriented drill cores into active vents, that the biologic tube structures exert a strong influence on the way mineralization proceeds at the vents.

Trapped atmosphere

Meteorites of the SNC (shergottite-nakhlite-chassignite) class are thought to be fragments of the surface of Mars. Marti et al. (p. 1981) found pockets of shock-melted glass in the shergottite meteorite Zagami, and determine that isotopic ratios of nitrogen and noble gases in them resemble ratios found by the Viking spacecraft for the martian atmosphere. In combination with earlier findings in another shergottite, these results point toward a systematic martian signature in all the SNC meteorites.

Recognizing structure

T cell receptors (TCRs) recognize antigens in the form of peptides bound to major histocompatibility complex (MHC) molecules. The crystal structure of a TCR β chain reported by Bentley et al. (p. 1984; see also news by O'Brien, p. 1906) offers some clues into how this recognition occurs. Conformational restrictions in the complementarity-determining regions (CDRs) on the variable part of the β chain appear to support models whereby the CDRs make contact with α -helical parts of the MHC molecules, and tight linkage between the constant and variable regions indicate a fairly rigid structure that might facilitate signal transduction by responding to structural changes initiated by the TCR binding to the peptide-MHC complex.

1

ICE minus

Interleukin-1 β (IL-1 β), a key cytokine in inflammatory response, is generated from an inactive precursor by IL-1B converting enzyme (ICE). Kuida et al. (p. 2000) created mice lacking the gene for ICE expression. The mice developed normally, but their monocytes failed to release IL-1 β when stimulated by the bacterial endotoxin lipopolysaccharide. Thymocytes from the mice were triggered into apoptosis by ionizing radiation and glucocorticoid, but stimulation by Fas antigen failed to induce the normal apoptotic response. These findings support the idea that apoptosis proceeds through many pathways.

Hearing the high notes

In the mammalian ear, outer hair cells respond to acoustic stimuli and transmit signals to auditory centers in the brain. Only a small number of the outer hair cells are activated by a particular frequency, and the response is amplified and sharpened by cochlear amplification, in which the hair cell shape changes in response to signals of the appropriate frequency. Dallos and Evans (p. 2006) propose a model in which cochlear amplification at high frequencies is attributed to extracellular potential gradients across the hair cell, explaining how shapechange behavior persists at high frequencies despite severe attenuation of the response by the cell membrane.

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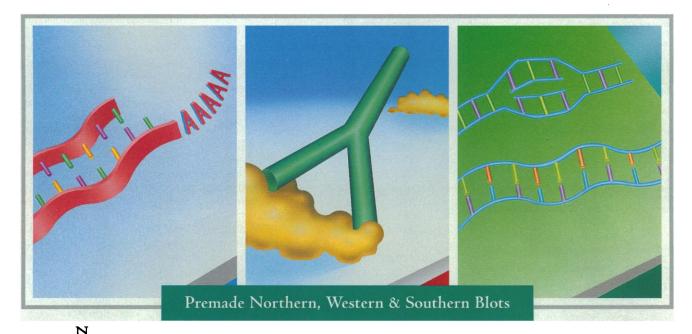


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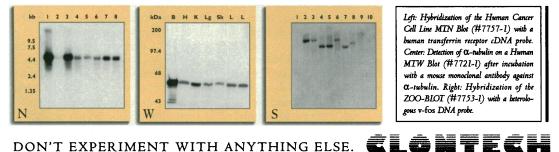
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Separate, quantify, or sequence carbohydrates in one day with Glyko FACE[®] technology

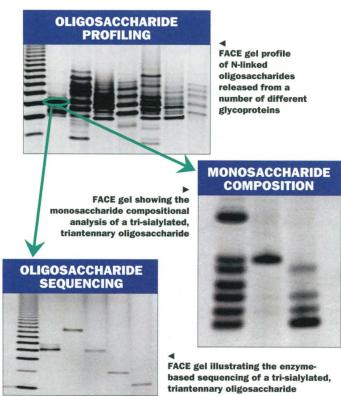
If you're working with DNA or protein, you're ready to work with carbohydrates

Glyko's FACE (Fluorophore Assisted Carbohydrate Electrophoresis) technology, makes it possible for you to work with and analyze complex carbohydrates using the same technique you already use every day in your laboratory: polyacrylamide gel electrophoresis.

Now, in less than one day, you can perform profiling, composition, or sequencing experiments such as the ones shown here, using FACE chemistry kits.

Color-coded FACE kits make carbohydrate analysis easy and reliable

FACE kits are color-coded and are designed to provide a complete approach to carbohydrate analysis...starting



with the enzymatic or chemical release from the glycoconjugate to the separation, isolation, or sequencing of oligosaccharides.

Everything you need is included: enzymes or release chemicals, fluorescent-labeling reagents, electrophoresis

The FACE Imager and FACE Analytical Software give you the ability to analyze, quantify, and document the results of N-linked and O-linked oligosaccharide profiling, monosaccharide composition, and sequencing gels standards, controls, running buffers, precast polyacrylamide gels, and complete



Glyko FACE kits are available for:

- N-linked Oligosaccharide Profiling Kit
- N-linked Capillary Electrophoresis Profiling Kit
- O-linked Oligosaccharide Profiling Kit
- O-linked Capillary Electrophoresis Profiling Kit
 N-linked Oligosaccharide
- Sequencing Kit
 Monosaccharide Composition
- Kit
- Glycosphingolipid Analysis Kit
 Glycosaminoglycan Identification Kit

Sequence your oligosaccharides with Glyko recombinant glycosidases

Glyko offers the most complete line of recombinant glycosidases available, each cloned to be free of other glycosidases, protease activity, and carbohydrates:

- PNGase F: releases Asn-linked oligosaccharides
- Endo H: releases Asn-linked high mannose and hybrid-type oligosaccharides
- O-Glycosidase I: releases Ser/Thr linked Gal-GalNAc
- Enzymative Deglycosalation Kit: releases oligosaccharides from glycoproteins
- NANase I: releases α2-3 N-acetylneuraminic acid
- NANase II: releases 0.2-3,6 N-acetylneuraminic acid
- NANase III: releases α2-3,6,8 Nacetylneuraminic acid
- Neuraminic Acid Linkage Analysis Kit: NANase I, II, and III
- HEXase I: releases β1-2,4,6 N-acetylglucosamine
- MANase I: releases al-2,3,6 mannose
- FUCase I: releases 0.1-6 fucose
- HEPase I: recombinant heparinase I

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Glyko provides complete CARBOHYDRATE ANALYTIC SERVICES if you have only an occasional need for carbohydrate analysis, or lack the personnel to perform the analyses you require.

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Mathematica

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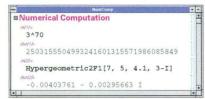
"The importance of the program cannot be overlooked"

- New York Times

Basic function: Integrated environment for numerical, symbolic, graphical computation, interactive programming.

Users: Scientists, engineers, mathematicians, programmers, financial analysts, students. Includes all 50 largest U.S. universities.

Numerical computation: Arbitrary-precision arithmetic, complex numbers, special functions (hypergeometric, elliptic, etc.), combinatorial and integer functions. Matrix operations, root finding, function fitting, Fourier transforms, numerical integration, numerical solution of differential equations, function minimization, linear programming.

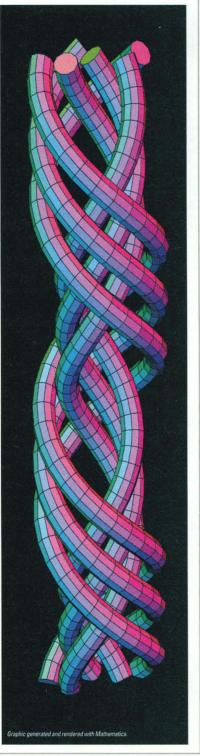


Symbolic computation: Equation solving, symbolic integration, differentiation, power series, limits. Algebraic operations, polynomial expansion, factorization, simplification. Operations on matrices, tensors, lists, strings,

| Symbo | lic Computation | Computation |
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Graphics and sound: 2D, 3D plots of functions, data, geometrical objects. Contour, density plots. 3D rendering with intersecting surfaces, lighting models, symbolic descriptions. Color PostScript output, combining and labeling, publication quality graphics, animation (most versions). Sound from waveforms and data (most versions).

Programming: High-level, interactive, symbolic language. Procedural and functional programming constructs. Transformation rules and pattern



matching. Fully compatible on all platforms. No built-in limitations on computation size.

| 12 | Programousjana – me | è |
|----|---|---|
| 0 | ■Programming | |
| h | log[1] = 0 | |
| 8 | log[E] = 1 | |
| В | log[x y] := log[x] + log[y] | |
| 8 | $\log[x ^n] := n \log[x]$ | |
| B | $\log'[x_1] = 1/x$ (* derivative *) | |
| 1 | log/: InverseFunction[log] = exp | |
| 8 | log/: Series[log[x], {x , 1, n }] := | |
| 1 | $Sum[-(-1)^k (x-1)^k/k, \{k, 1, n\}] +$ | |
| 8 | O[x, 1] ^(n+1) | |
| 1¢ | | - |

External interface: Input of data (numbers, records, text) from files, programs. Output in TeX, C, Fortran, PostScript. Calling of external programs and functions. General MathLink® interprocess communication mechanism.

User interface: Electronic book interactive documents mixing text, graphics, animations, calculations. Graphics, animation, sound interapplication compatibility. Style sheets, hierarchical outlining. Computation kernel can run on remote computer (most versions).

Additional material: Journals, newsletters, more than 80 books. Add-on packages, free Math-Source[®] electronic resource.

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Multiprobe Fluorescence Technique Finds Increasing Application in Research

Fluorescence in situ Hybridization (FISH), first introduced in the late 1970's, has played an important role in identifying chromosomes, detecting chromosomal abnormalities, and determining the number, size and location of specific DNA sequences in mammalian cells. Today, thanks to advances in probe technology and fluorescence microscopes, FISH is becoming increasingly important as a research tool and may eventually become a standard clinical diagnostic technique in areas such as cytogenetics, prenatal diagnosis and tumor biology.

As biomedical researchers continue to discover more and more human diseases with their causes rooted in genetic abnormalities, Fluorescence *in situ* Hybridization (FISH) has become an increasingly important tool for the analysis of genetic cellular characteristics. This highly sensitive technique is fast, easy to interpret, and yields statistically relevant data. It can be used to identify both normal and abnormal chromosomes and to determine the presence and location of specific genomic sequences with unprecedented detail and clarity.

In FISH, the hybridization reaction biochemically targets gene sequences so their location and size can be determined using fluorescence microscopy. DNA from a chromosome-specific probe is labeled by chemically modifying it to insert a reporter molecule that can be

observed via fluorescence. The labeled DNA is then hybridized to metaphase chromosomes or interphase nuclei for which chromosome-specific staining is desired. The technique is sufficiently sensitive to detect and characterize both numerical and structural aberrations, making it valuable for detection of a number of genetic disorders.

Multicolor probes permit simultaneous analyses

The FISH technique depends on the availability of probes that bind specifically to regions of genetic or cytogenetic interest. It is a powerful research tool because multicolor probe labeling permits simultaneous use of several different probes inside a single cell, allowing the researcher to analyze multiple genetic sequences and check for several genetic disorders at the same time

In clinical studies, multicolor FISH analyses have shown striking differences in chromosome frequency in interphase cells from solid tumors, both from the same tumor and from tumors of different patients. Several of these studies are focused on relating tumor aggressiveness to specific chromosomal sequences to improve tumor prognosis beyond what is possible today.

New technology for new techniques

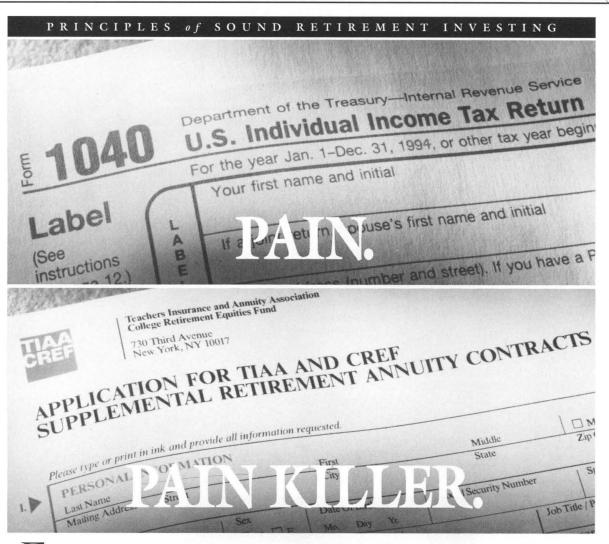
As FISH and other direct probe techniques have emerged, the need for more sophisticated fluorescence microscope systems has increased dramatically. Since individual sites on a chromosome are so minute, high numerical aperture, high transmission objectives are needed to image them. And simultaneous use of 2, 3 or 4 fluorescent probes necessitates multiple filters to image multiple sites.

In response to these needs, Nikon has introduced the new Quadfluor Epi-Fluorescence Illumination System, along with a series of higher numerical aperture objectives with higher transmission characteristics.

The new CF Plan Fluor objectives feature new optical cements and high transmission coatings to permit broader wavelength ranges (UV --- Deep Red) and brighter images that are color aberration free with extremely high contrast and low background autofluorescence. The Quadfluor Illuminator offers expanded filter cube capacity and enhanced filter designs with even better signal to noise ratio performance. It accepts up to four filter cubes at once to separate different signals, or a multiband filter cube to image several fluorochromes simultaneously. The filters can be rapidly switched via an extremely smooth yet very precise linear slider, allowing excellent image registration and making the Quadfluor Illuminator ideal for today's multi-probe techniques.

For more information on Nikon's new Quadfluor Epi-Fluorescence Illumination System, call Nikon at (516) 547-8567, fax us at (516) 547-0306 or contact us on the Internet at nikonbio@aol.com.

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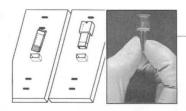
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PRODUCTS & MATERIALS



DNA Recovery from Gels

GeneCapsule is a single-use device for rapid recovery of DNA from gels with as little as 90 s hands-on time. It makes use of the principle of electroelution and requires no additional equipment. The user simply picks up the DNA band with Gene-Capsule and replaces it on the top of the gel. The recovered DNA is ready for ligation, restriction enzyme digestion, sequencing, amplification, random priming, nick translation, and other enzymatic reactions. Geno Technology. Circle 139.

Combined Radioisotope Detector

A new tandem detector can be used for both beta and gamma isotopes. With one electronics and software package, the researcher can now quantitate ³H, ¹⁴C, ³²P, ³⁵S, ⁴⁵Ca, ¹²⁵I, ¹³¹I, ⁹⁹mTc, ¹¹¹In, ¹⁸Fl, ⁵¹Cr, ¹¹C, and many other beta, gamma, and positron isotopes. **IN/US Systems. Circle 140.**

Mutation Detection Agarose

MetaPhor XR agarose, which forms flexible gels for high resolution of small DNA conformers of <1 kb, is useful in mutation detection. This agarose, compatible with most horizontal and vertical electrophoretic equipment, combines the convenience and ease of agarose with the resolving power of polyacrylamide. FMC BioProducts. Circle 141.

Rapid DNA Ligation Kit

10

The Rapid DNA Ligation Kit can ligate blunt-ended or stickyended DNA fragments in 5 min at room temperature, reducing the cloning and transformation procedure to 1 day and eliminating the need for special water baths. Extensive function tests and quality control procedures performed on each lot of kits guarantee optimal transformation efficiencies and ensure the validity of results. **Boehringer Mannheim. Circle 142.**

Hot Start PCR Beads

HotWax Mg²⁺ Beads are designed to make hot start polymerase chain reaction (PCR) easier, faster, and more efficient. The specially prepared wax beads contain MgCl₂, which is released into the reaction when the wax bead melts during the first denaturation step. This simple system eliminates many of the manipulations required for a manual hot start. In addition, the melted bead forms an evaporation barrier making an oil overlay unnecessary. **Invitrogen. Circle 143.**

Streptavidin-Coated Plate

A streptavidin-coated, thin-wall polycarbonate plate for use in thermocyclers makes possible the simultaneous amplification and capture of the amplified product. The captured product can then be quantitated in a simple hybridization step. The immobilized strand can also be used as a template for sequencing. These plates make use of a special grade of streptavidin that is stable at the high temperatures of thermocyclers. The streptavidin is covalently attached to the surface through a proprietary chemistry that provides exceptional uniformity, extended shelf life, and maximum stability during high stringency washes. The plates are available to fit most thermocyclers. Xenopore. Circle 144.

Sequence Assembly Software

AutoAssembler software automatically performs labor-intensive DNA sequence assembly tasks. Designed for Macintosh computers, AutoAssembler features automatic, batch-mode sequence clean-up and feature identification, automatic assembly of sequences, and easy viewing and editing of results. Designed for researchers performing smallto medium-size sequencing projects, the software can be easily upgraded for large-scale projects. **Perkin-Elmer. Circle 145.**

Lead Generation Software

Fast Clustering software can reduce the need for random screening of candidates for new drugs and conserve sample stocks. Many pharmaceutical organizations store vast quantities of structural data in chemical databases, including compounds available for testing. Through a novel algorithm, Fast Clustering can group databases in excess of 50,000 structures into subsets of similar compounds. Representative members of these subsets are then easily extracted to provide a further subset reflecting the diversity of the database screening. The algorithm groups molecules in the three-dimensional database based on the similarity of their pharmacophores. Chemical Design. Circle 146.

Micro Perfusion System

The Horizontal Myograph has been redesigned to create a versatile, simple, and economical precision system for measuring developed tension in very small tissue rings and strips. The modu-

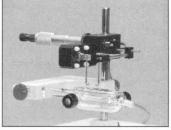
SCIENCE • VOL. 267 • 31 MARCH 1995

support post while still having several axes of adjustment. The myograph assembly can be used easily with dissecting and ińverted microscopes. The minimal spatial arrangement leaves ample area for other instruments such as

lar design allows the microman-

ipulator, transducer, and tissue

segment to be mounted from one



electrodes to measure action potential. Kent Scientific. Circle 147.

Literature

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FragmeNT Analysis Software is a four-page brochure on this program for analyzing one-dimensional DNA and protein gel electrophoresis patterns. The brochure is illustrated with screen graphics that show how the software performs lane and band finding; size, mass, and isoelectric point calculation; and other restriction fragment length polymorphism analysis. Molecular Dynamics. Circle 148.

SynChroNotes is a technical newsletter. The most recent edition contains an article, "Hydrophobic Interaction—The 'Other' Hydrophobic Chromatography." Synchrom. Circle 149.

The Informed Choice for Protein Labelling and Detection is a 36-page catalog highlighting an extensive range of products, both radioactive and nonradioactive. Sections include Western blotting, total protein detection, and immunocytochemistry; cellular protein labeling; post-translational modification; and in vitro translation systems. Amersham International. Circle 150.

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