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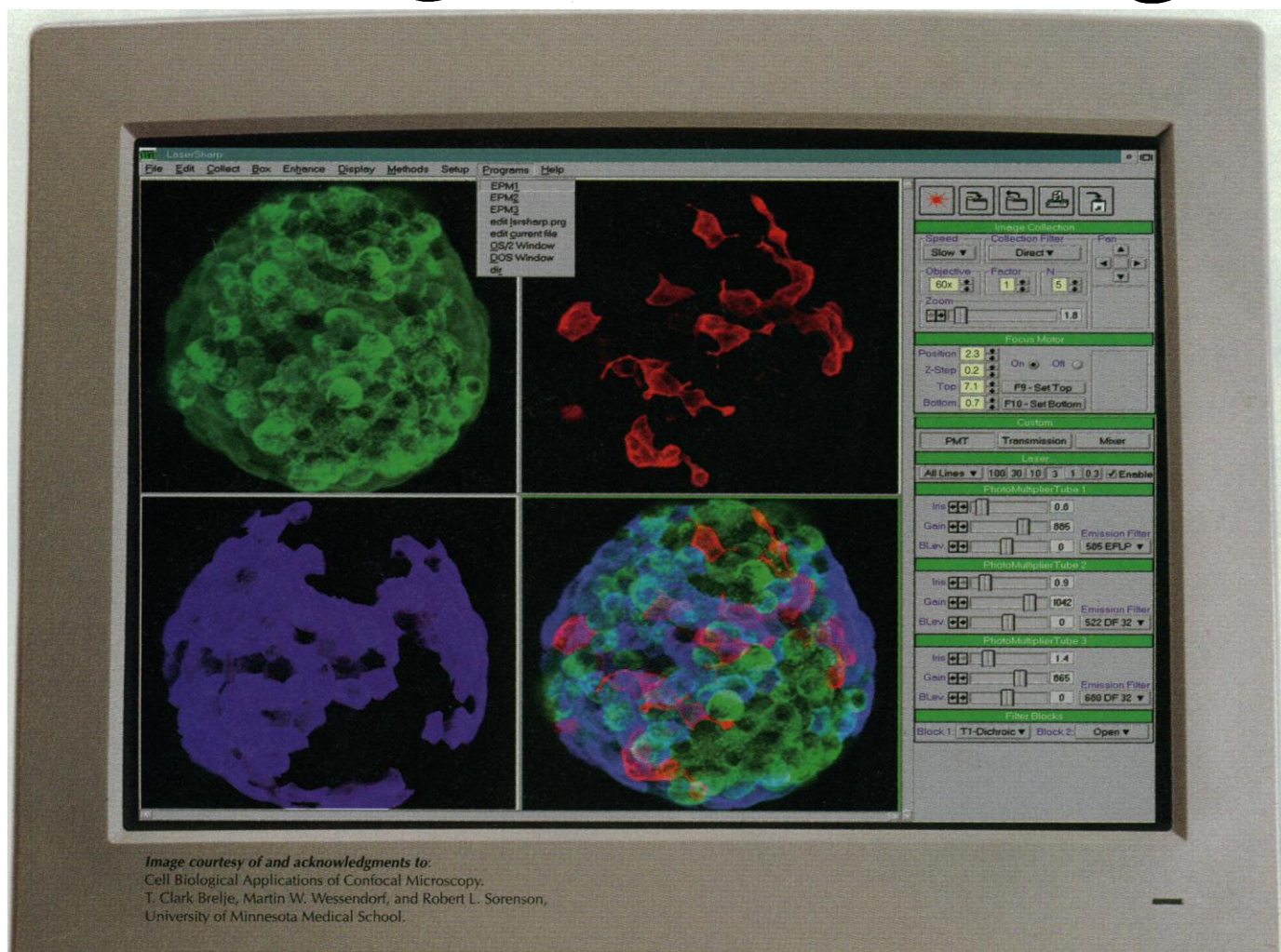
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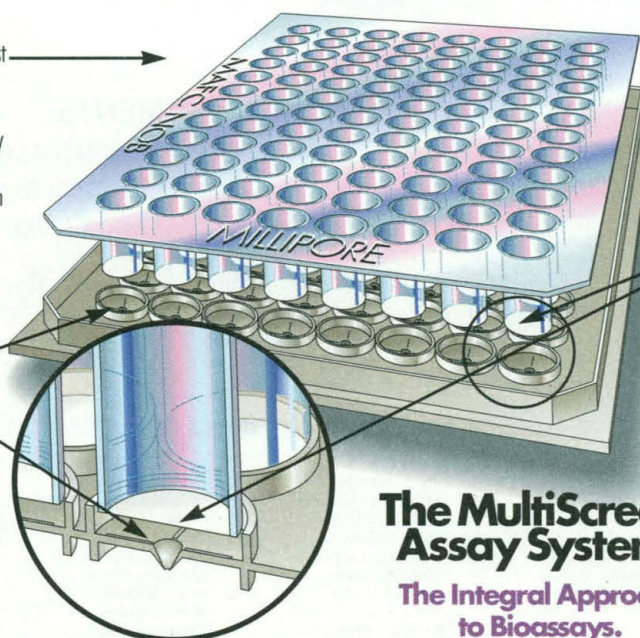
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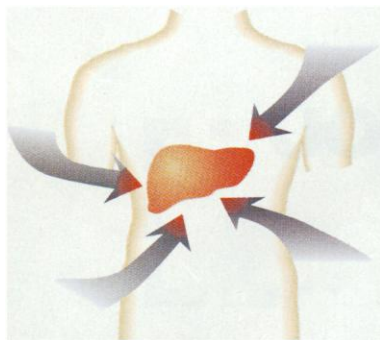
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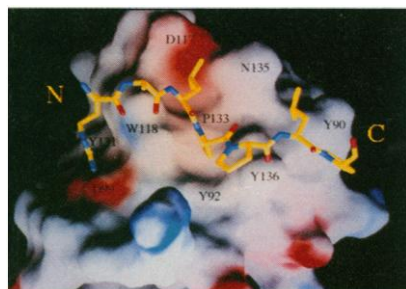
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The lavishly appointed pavilion at the International Institute for Advanced Studies, the flagship of the fledgling Kansai Science City, is intended to be a meeting ground for scholars from around the world. But its emptiness since it opened 17 months ago symbolizes

the unfulfilled dreams of the Japanese science establishment. The new structures that are shaping science in Japan are the focus of this year's special issue on Science in Asia. See the special section beginning on page 1169. [Photo: Caroline Parsons/Sygma]



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When a current flows through a conductor, a transverse magnetic field will set up a field perpendicular to the current, which has a characteristic resistance. The Hall effect, as this phenomenon is known, takes on an unusual quantum mechanical behavior in solids at low temperatures and high magnetic fields—the transverse electrical resistance vanishes for many values of the field strength, and for other values the resistance is simply a function of Planck's constant and the electron charge, times either an integer or a fraction. These phenomena result from highly correlated electron interactions. As Jain points out in a review of two-dimensional electron physics (p. 1199), electrons can form weakly interacting quasi-particles called composite fermions that differ from free electrons.

Pre-T cell receptor

As immature thymocytes develop into T cells, the T cell receptor (TCR) genes undergo a series of rearrangements to express first the TCR β chain and later the TCR α chain. Saint-Ruf *et al.* (p. 1208) have cloned and analyzed a transmembrane protein, the pre-TCR α chain, that is expressed in immature thymocytes before the TCR α chain is expressed. This chain associates with TCR β and CD3 proteins to form a signaling complex that likely plays a role in the survival and expansion of immature T cells.

Growing nanotubes

Carbon nanotubes are synthesized from graphite under arc-discharge conditions. Colbert *et al.* (p. 1218) show that the de-

Recovering DNA from bone fossils

How long and under what conditions can some fragments of DNA survive in fossils? Woodward *et al.* (p. 1229; see news story by Gibbons, p. 1159) report the recovery and amplification of a small piece (174 base pairs) of the mitochondrial cytochrome b gene from two bone fragments that are about 80 million years old. The bones were recovered from an underground coal mine in Utah. DNA was not recovered from the host rocks, but was successfully amplified from nine bone samples.

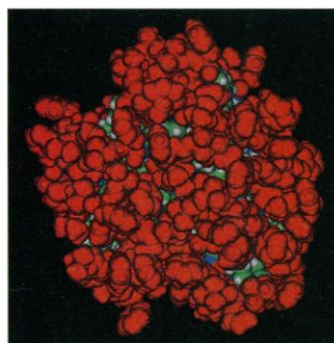
fects that are usually present in these nanotubes are due to sintering and can be reduced by cooling the cathode on which the nanotubes are deposited. A careful analysis of the deposit revealed a honeycomb structure—bundles of well-aligned nanotubes are surrounded by a zone of poorly aligned, tangled nanotubes. The authors propose that the well-aligned bundles of open nanotubes act as field emitters. Field emission produces C⁺ ions, which lengthens the already growing ends of the open nanotubes.

Entangled phase

Liposomes are closed shells of phospholipid bilayers that are finding increased use for the controlled release of compounds, ranging from cosmetics to drugs. Chirovolu *et al.* (p. 1222) have found that certain three-component solutions of a phospholipid, water, and a branched-chain alcohol form a phase consisting of highly entangled, multilayered tubules.

Branched boxes

Highly branched polymers called dendrimers are synthesized in a series of steps that build outward from a central core. Jansen *et al.* (p. 1226) have constructed dendrimers with a flexible inner core capped by a



rigid outer shell of phenylalanine residues. They show that molecules can be trapped in the internal cavities of the inner core if they are present in solution during the final capping step. These guest molecules are trapped in a dendritic box because the dense outer shell drastically slows diffusion.

Making a muscle

The myoD family of basic helix-loop-helix (bHLH) transcription factors can induce a variety of nonmuscle cells to differentiate into multinucleate myotubes. Kaushal *et al.* (p. 1236) found that a member of another family of transcription factors, a MADS box protein, muscle enhancer factor MEF2A, can also induce myogenic development in nonmuscle cells. Many muscle-specific genes contain binding sites for both myoD family and MEF family members. These factors interact cooperatively in order to induce high levels of muscle-specific gene activation. The interac-

tion between these factors requires the MADS domain of MEF2A and the three amino acids required for myogenesis in the muscle bHLH proteins.

Both ways now

Many intracellular proteins contain Src homology 3 (SH3) domains that are involved in protein-protein interactions. Previous structural studies have revealed one type of orientation for this binding, with the peptide backbones oriented in the same direction. Nuclear magnetic resonance solution structures of the c-SH3 domain in complex with two different proline-rich peptide ligands have been obtained by Feng *et al.* (p. 1241). Although both bound ligands form polypyrrolone type II helices, they bind in opposite directions. The authors used these structures and mutational data to develop a general model for SH3 ligand binding.

Defense coordinator

Plants defend against the onslaught of disease in a variety of ways, including synthesizing defensive compounds or collapsing the host cells at the site of infection. Some of the disease response mechanisms work systemically to protect the entire plant. Delaney *et al.* (p. 1247) find that salicylic acid, the precursor of common aspirin, serves as a natural signal in plants to mediate several of the plant's responses to disease. Transgenic plants expressing an enzyme that degrades salicylic acid were unable to resist effectively infections by certain viral, fungal, and bacterial disease agents. Salicylic acid apparently serves as a common element in several of the plant's defense responses.

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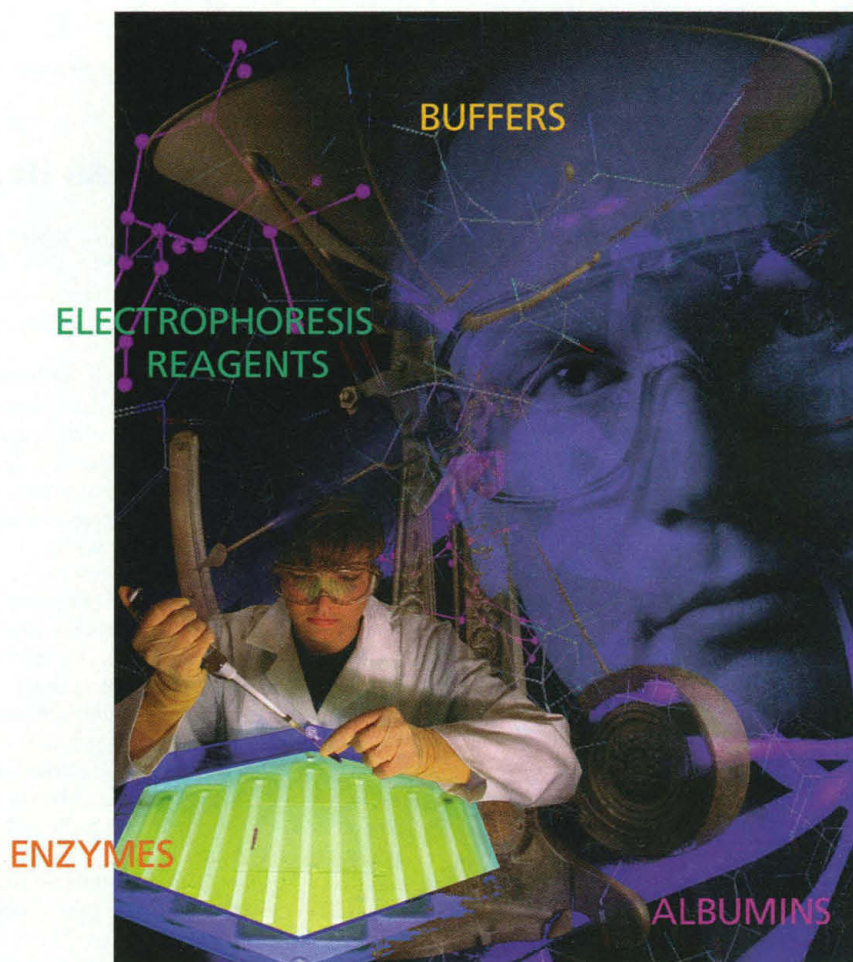
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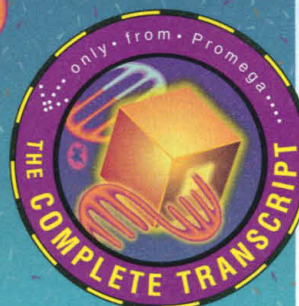
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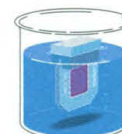
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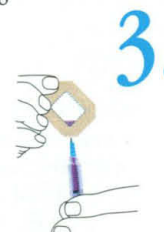
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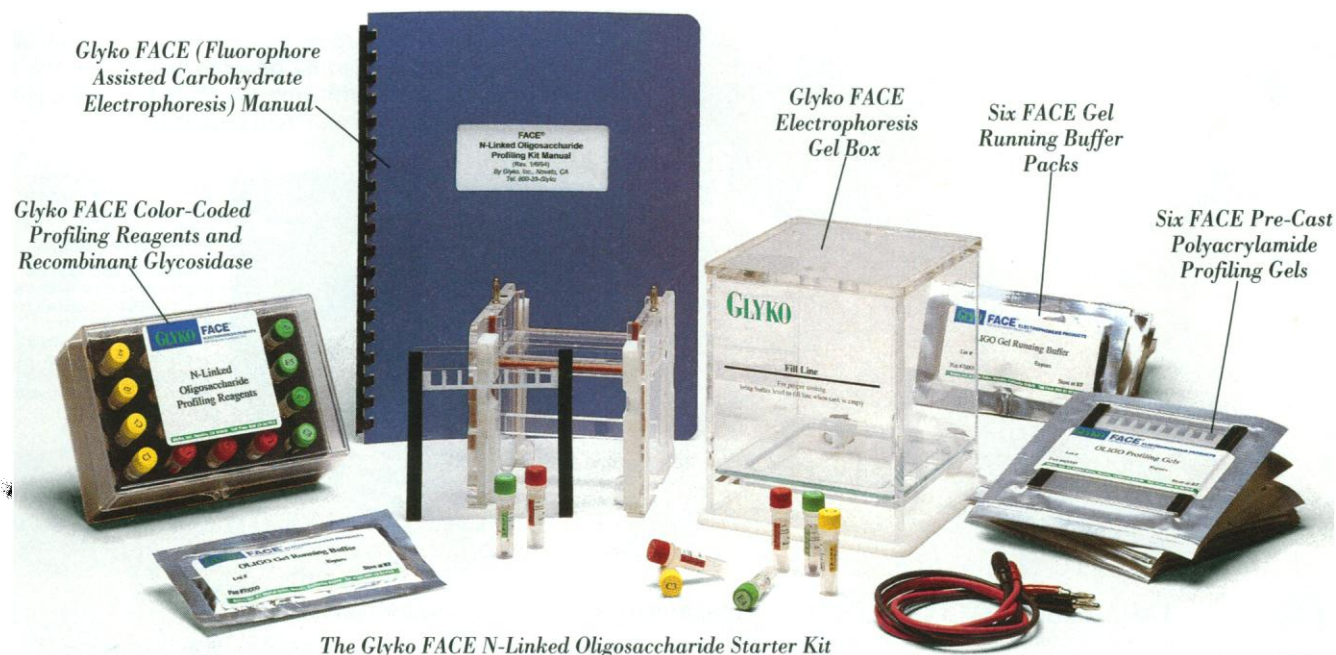
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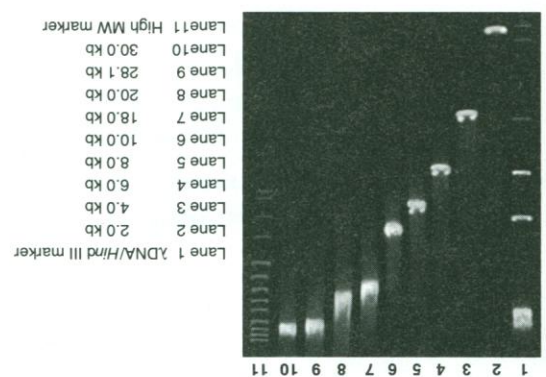
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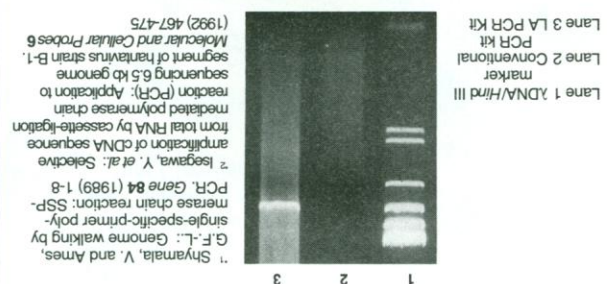
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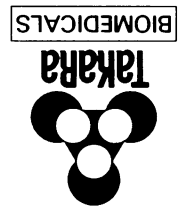


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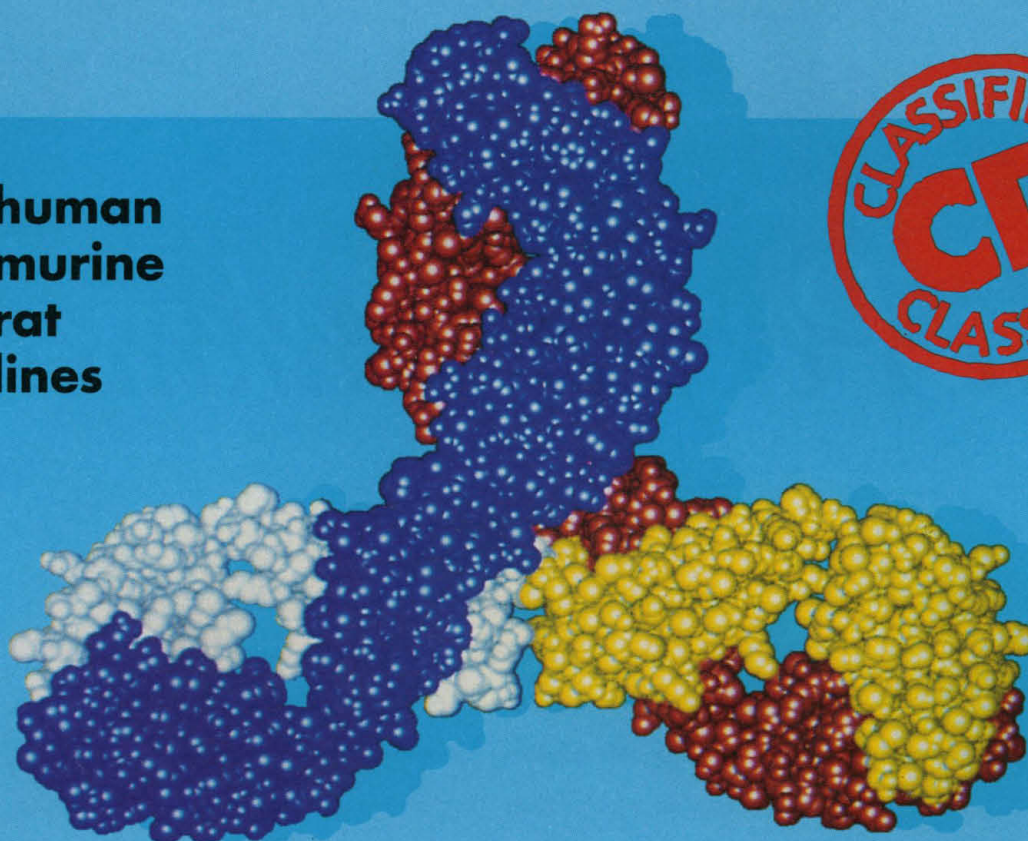
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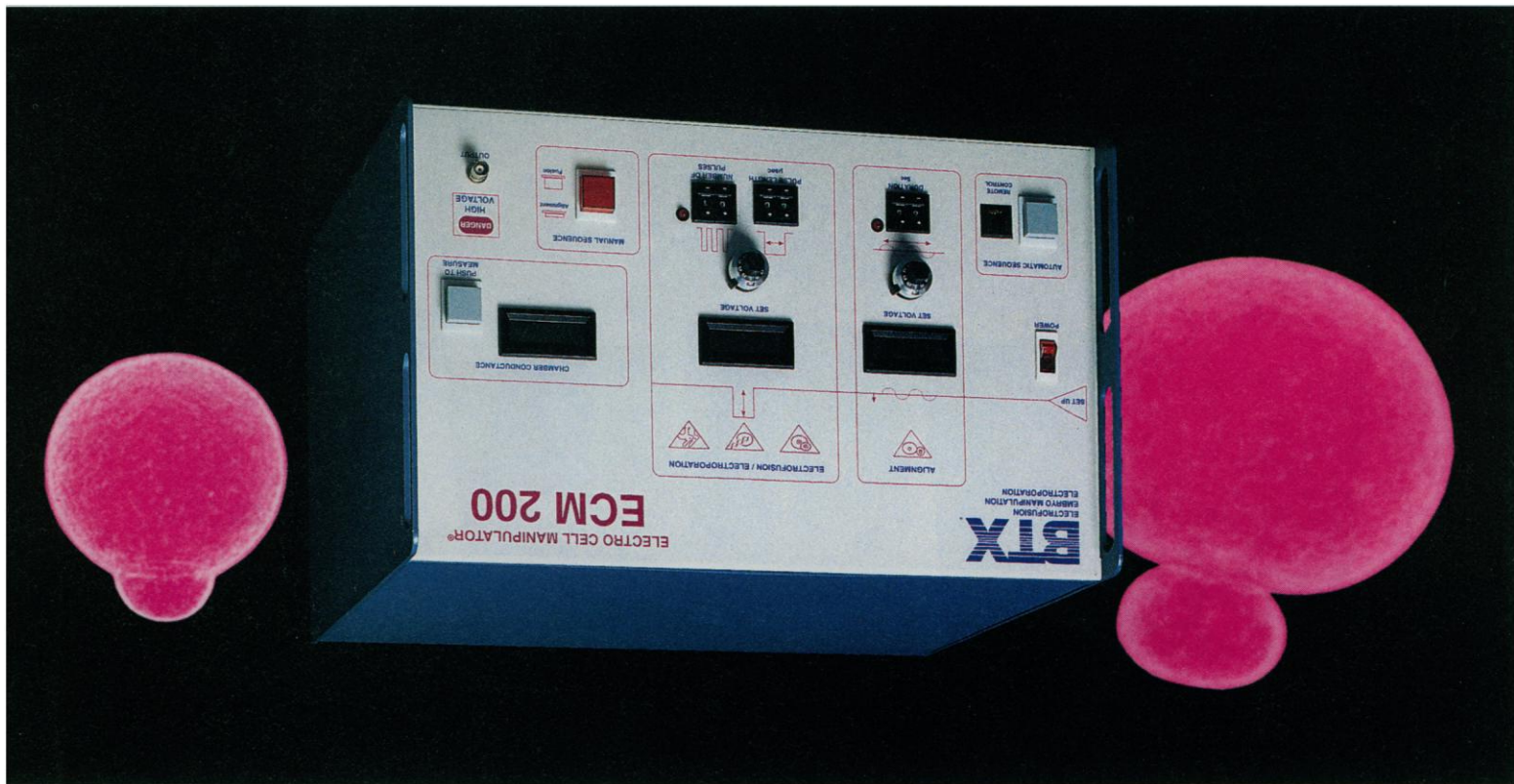
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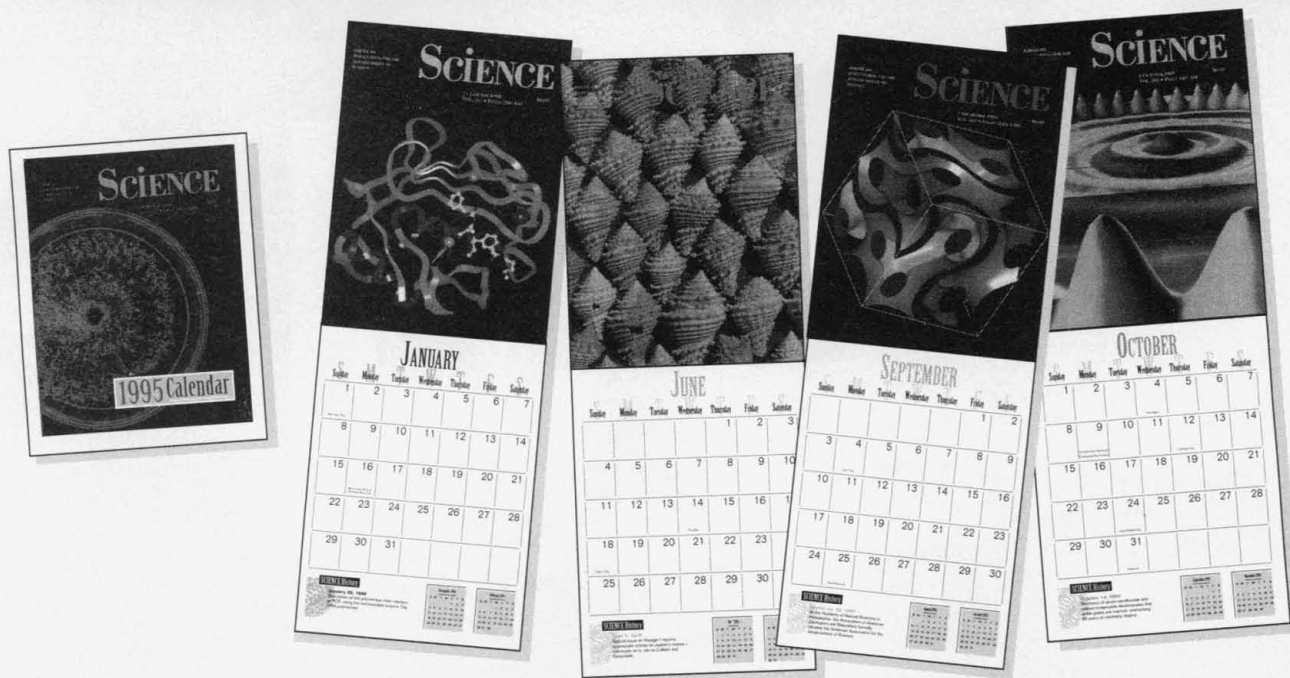
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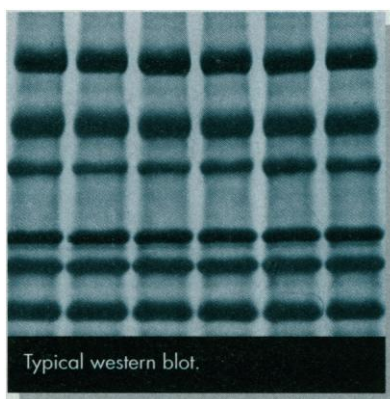
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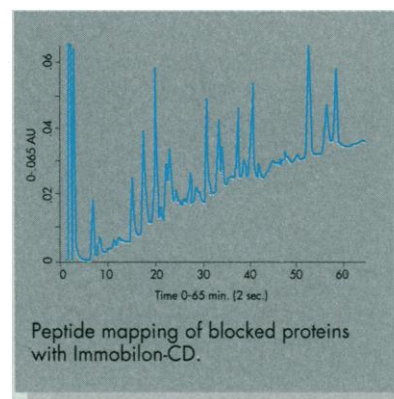
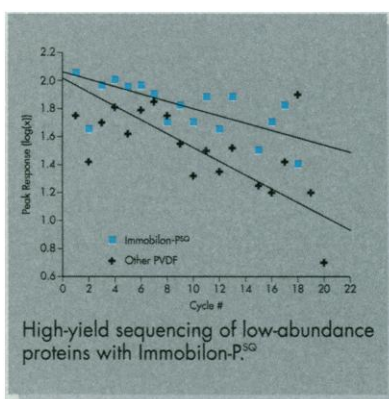
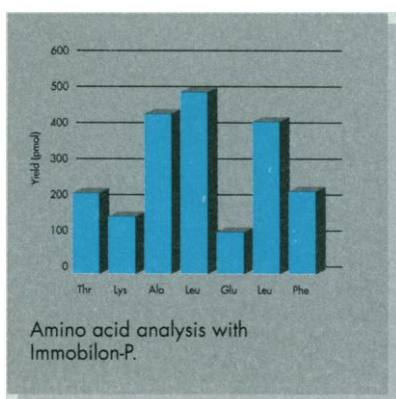
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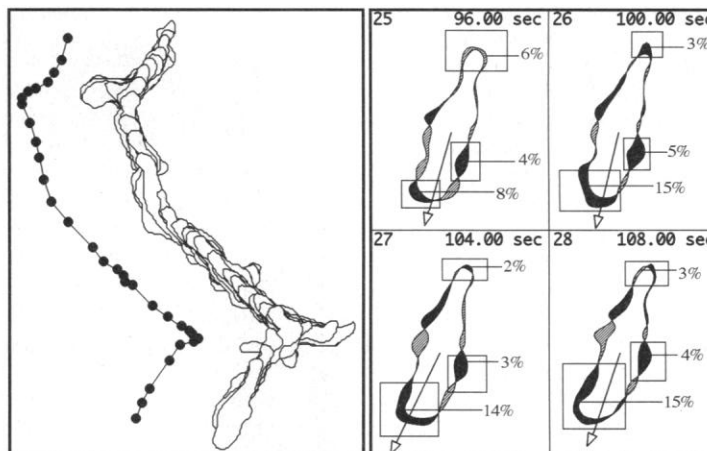
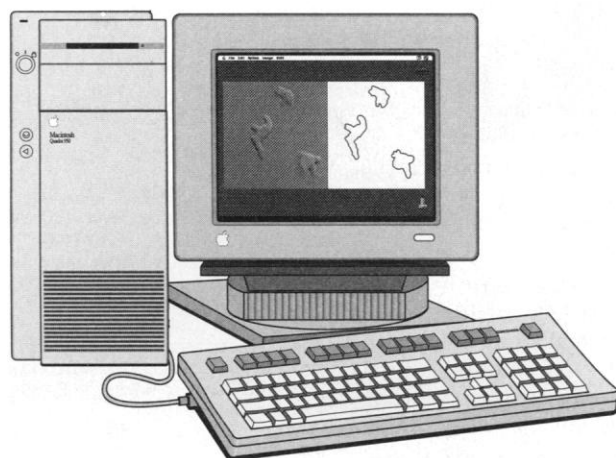
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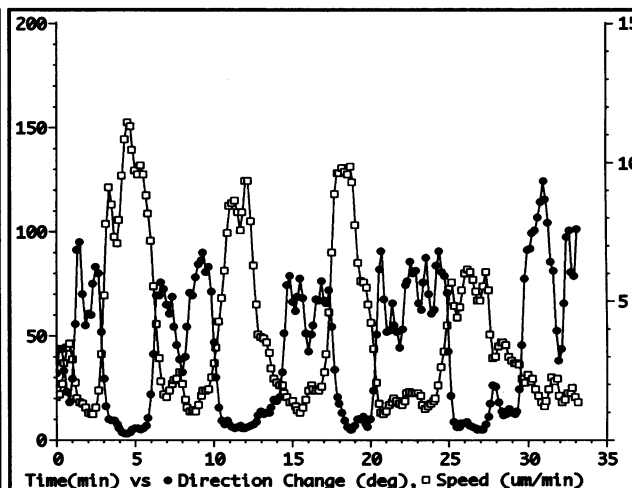


The contour of any video-imaged cell can be digitized into DIAS® and analyzed. In this example, a translocating cell is being outlined. DIAS® maps the x,y coordinates of pixels at the perimeter of the cell in each video frame. This information is used to quantitate cellular translocation and dynamic morphology. The number of quantitative methods for the analysis of movement provided by DIAS® is too large to adequately describe here.

DIAS® displays tracks of the cell's center (centroid) and stacks the outlines of the cell over time. DIAS® generates and displays difference pictures, containing color-coded expansion zones (solid) and contraction zones (hatched) of the moving cell. DIAS® can then automatically animate the paths, stacks and difference pictures for display and analysis side by side with the original movie. The user can window any portion of the cell (e.g., a pseudopod) and quantitate the dynamics of expansion, contraction and changes in contour.

| Frame Time (sec) | Speed (in/sec) | Direct (deg) | Dir Ch (deg) | Accel (in/sqsec) | Persis (in/sec-d) | Area (sq in) | Perim (in) | AvgWid (in) | MaxWid (in) | Convex (deg) | Concave (deg) |
|------------------|----------------|--------------|--------------|------------------|-------------------|--------------|------------|-------------|-------------|--------------|---------------|
| 1 0.000 | 0.325 | -81.313 | 0.000 | 7.369 | 0.325 | 0.116 | 1.828 | 10.079 | 21.375 | 524.003 | 164.003 |
| 2 0.050 | 0.693 | -74.614 | 6.699 | 6.190 | 0.242 | 0.115 | 1.813 | 10.257 | 21.211 | 541.822 | 181.822 |
| 3 0.100 | 0.944 | -74.594 | 0.020 | 0.284 | 0.939 | 0.106 | 1.551 | 9.999 | 19.229 | 528.712 | 168.712 |
| 4 0.150 | 0.722 | -81.912 | 7.317 | -4.453 | 0.238 | 0.109 | 1.586 | 10.325 | 20.022 | 516.235 | 156.235 |
| 5 0.200 | 0.498 | -97.188 | 15.276 | -3.829 | 0.095 | 0.110 | 1.655 | 9.746 | 18.020 | 492.574 | 132.574 |
| 6 0.250 | 0.339 | -75.020 | 22.168 | -0.737 | 0.047 | 0.119 | 1.853 | 9.304 | 18.000 | 533.372 | 173.372 |
| 7 0.300 | 0.425 | -67.938 | 7.082 | 3.490 | 0.143 | 0.124 | 2.149 | 9.104 | 17.029 | 542.479 | 182.479 |
| 8 0.350 | 0.688 | -77.631 | 9.693 | 2.353 | 0.186 | 0.121 | 2.044 | 9.418 | 17.103 | 550.147 | 190.147 |
| 9 0.400 | 0.660 | -75.207 | 2.424 | -2.791 | 0.394 | 0.124 | 1.811 | 9.075 | 14.990 | 562.701 | 202.701 |

| | |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Cell 1, Frames: 1 to 97 Time: 0 to 184.8 sec, Total Elapsed Time: 184.8 sec Total path length: 2.970 in Net path length: 2.552 in Directionality - Total: 0.859241 Upward: -0.858256 Rightward: -0.0411352 Speed (in/sec): 0.598848 +/- 0.308206 Direction (deg): 259.848 +/- 28.6274 Direction Change (deg): 0.954923 +/- 0.104357 Acceleration (in/sq sec): 0.254851 +/- 3.35319 Persistence (in/sec-deg): 0.255022 +/- 0.225761 Area (sq in): 0.142545 +/- 0.0198024 Perimeter (in): 2.09529 +/- 0.25573 Mean Convexity (deg): 395.931 +/- 207.121 | Cells 1-30, Frames: 1 to 97 Time: 0 to 184.8 sec, Total Elapsed Time: 184.8 sec Total path length: 7.246 in Net path length: 5.246 in Directionality - Total: 0.724029 Upward: -0.724027 Rightward: -0.00170255 Speed (in/sec): 0.852628 +/- 0.466008 Direction (deg): 266.441 +/- 38.009 Direction Change (deg): 0.901018 +/- 0.247878 Acceleration (in/sq sec): .38779e-05 +/- 0.0608797 Persistence (in/sec-deg): 0.316854 +/- 0.331365 Area (sq in): 0.165489 +/- 0.023689 Perimeter (in): 2.168953 +/- 0.36594 Mean Convexity (deg): 380.133 +/- 203.263 |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|



DIAS® automatically and rapidly computes more than 40 predefined parameters of motility and dynamic morphology for intervals as short as a thirtieth of a second and for as many as 50 cells in parallel. Data is presented in tabular form, and as summaries for each cell, or any group of cells.

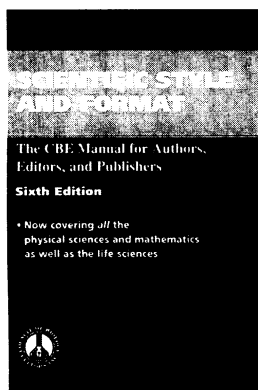
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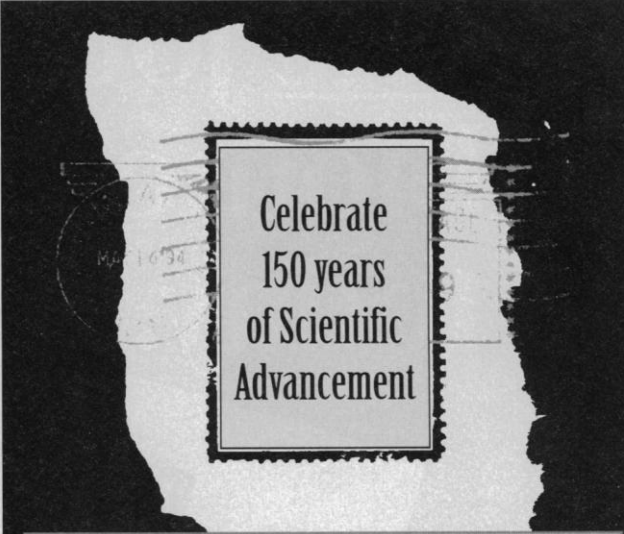
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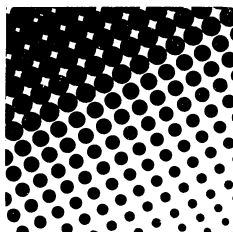
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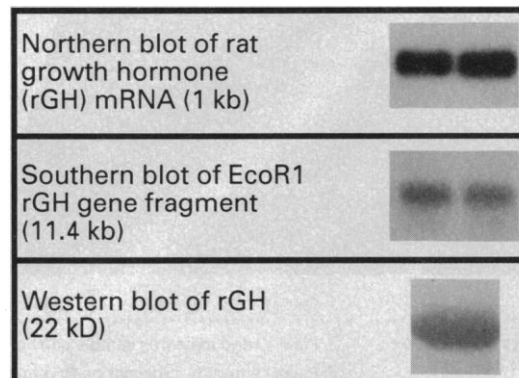
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