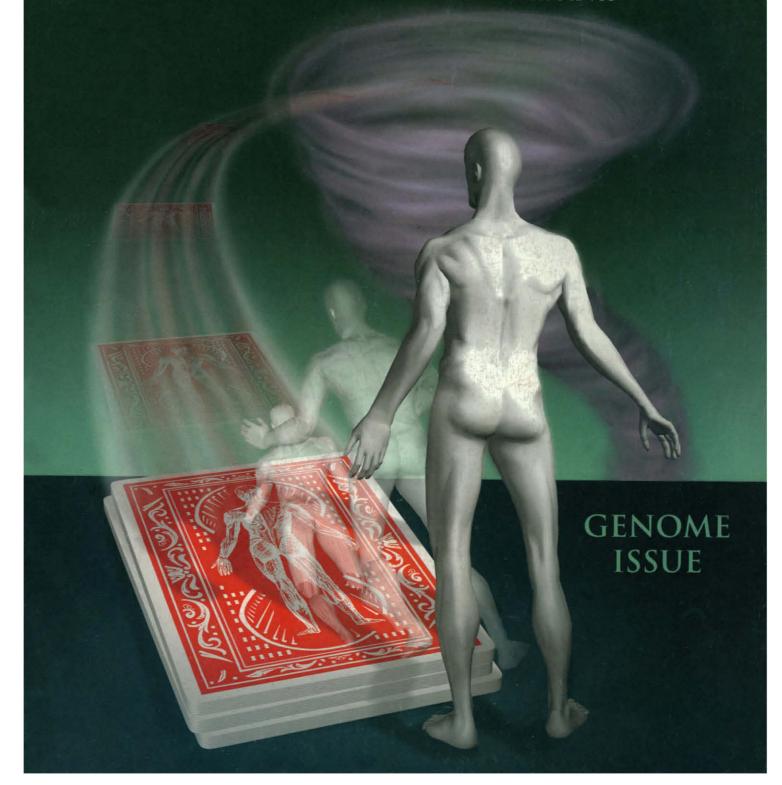
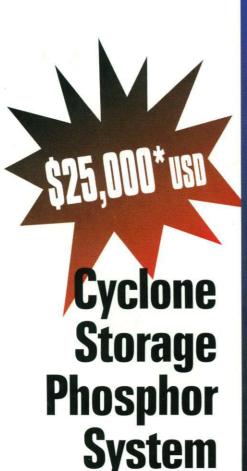
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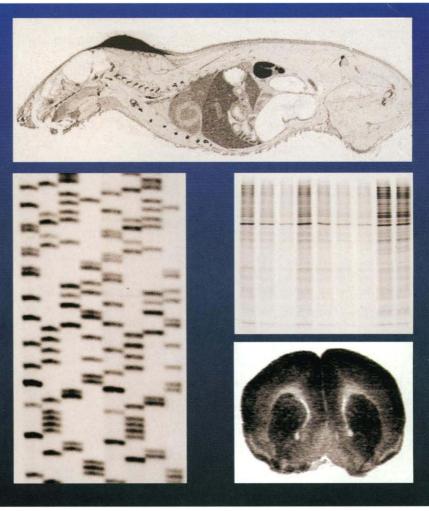
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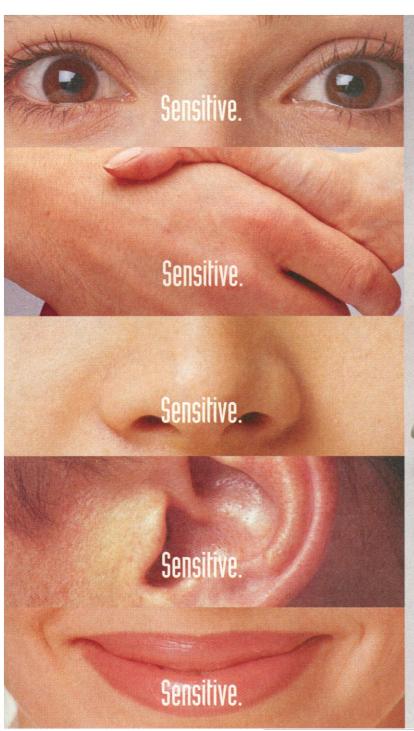
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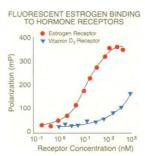
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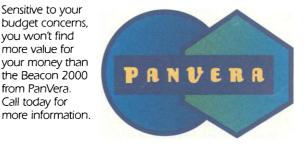
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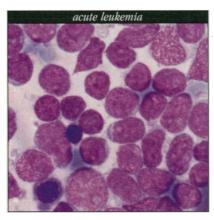
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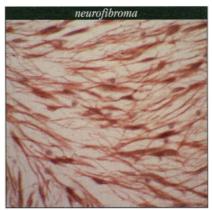


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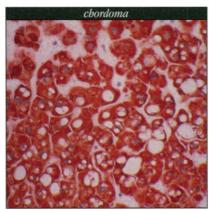
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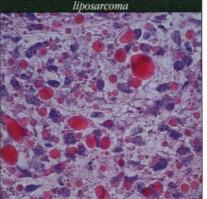
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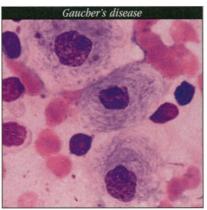
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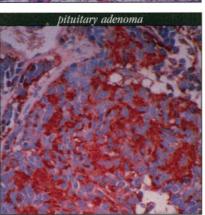
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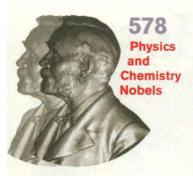
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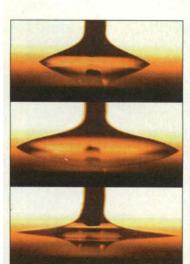
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Increasingly, genes are not being considered in isolation, but as part of functional or evolutionary systems. The tornadoes on the cover and the special chart in this issue were used to symbolize the powerful, sometimes random, forces that generate gene families from indi-

vidual building blocks. A special section beginning on page 601, News stories (pages 564, 568, and 569), an Editorial (page 555), and Reports (pages 675 and 680) illustrate the evolving nature of the genome project. [Illustration: Steven Keller]



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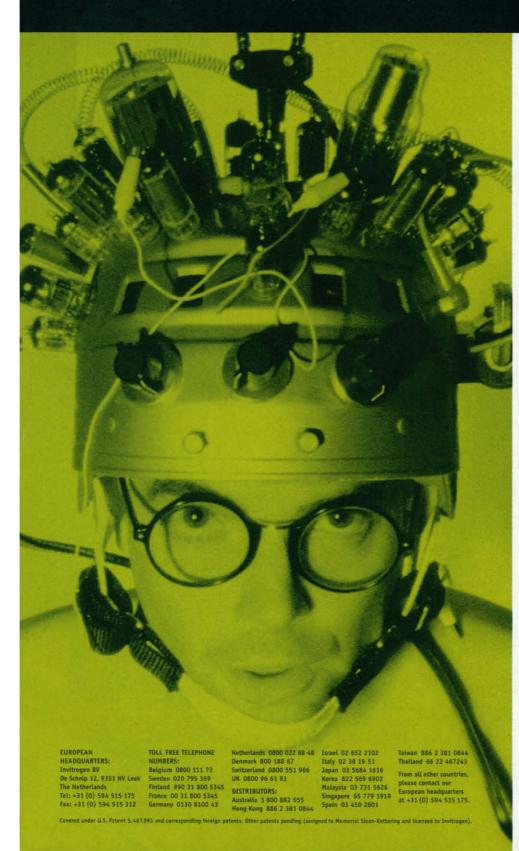
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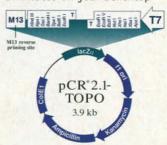


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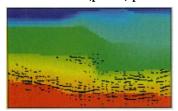
edited by PHIL SZUROMI

Not so slippery drops

Superfluid helium-4 is hard to contain since it wets nearly all surfaces and flows freely without dissipation. Ross et al. (p. 664) show that on uniform cesium surfaces, however, superfluid helium-4 will form isolated droplets. The contact angle with the surface shows hysteresis depending on flow direction, and the droplets pin to the surface, refusing to flow down an incline.

A coupled plate

Although it is known that oceanic crust is spreading and subducted crust is being pulled down due to mantle convection, the coupling between crust and mantle is poorly understood. Along strike-slip faults such as the San Andreas, where plates slide past each other, the connection between the crust and mantle is not even well defined. Henstock et al. (p. 650) provide



a velocity model based on a seismic experiment near the Mendocino Triple Junction in northern California that shows a narrow, vertical zone of deformation throughout the crust along the San Andreas fault. Strikeslip faulting appears to extend through the crust into the upper mantle, coupling deformation to mantle dynamics.

Tube in a tube

Carbon nanotubes are finding numerous applications and, together with their boron nitride counterparts, show great potential in nanoscale electronic applications. Heterojunctions of carbon and boron nitride nanotubes can be envisioned because

A molecular basis for ethanol sensitivity

People and animals differ in their sensitivity to the intoxicating and addictive properties of ethanol, but the molecular basis for this variation has not been known. Miyakawa et al. (p. 698; see the news story by Pennisi, p. 573) show that mice missing one of the nonreceptor tyrosine kinases, Fyn, are hypersensitive to ethanol. They also lack the usual ethanol-induced phosphorylation of the *N*-methyl-D-aspartate (NMDA) subtype of the glutamate receptor (a likely mediator of ethanol's intoxicating effects) and show no ethanol tolerance, as monitored by measuring ethanol's ability to inhibit NMDA current. The ability of Fyn to phosphorylate the NMDA receptor is likely a determinant of an individual's response to ethanol.

of their different electronic properties. Suenaga *et al.* (p. 653) have now succeeded in realizing such a combined structure in nanotubes forming structures of carbon, boron nitride, and in some cases further carbon layers. A strong phase separation between the carbon and the boron nitride layers is observed.

Birds in hand?

One characteristic used to suggest that birds arose from theropod dinosaurs is hand morphology. The theropod hand is generally thought to preserve digits I, II, and III. Burke and Feduccia (p. 666; see the Perspective by Hinchliffe, p. 589) examined the hands and feet of developing embryos of birds, alligators, and turtles and show that their hands develop to preserve digits II, III, and IV. This pattern is in apparent conflict with the identification of the first digit in Archaeopteryx.

Relaxation in water

Mid-infrared spectra of water can reveal the orientational dynamics of the OH groups of water, and by using fast laser pulses, the dynamics of the vibrational and orientational relaxation can be resolved for specific subensembles of water molecules. Woutersen et al. (p. 658) found that there are two distinct time scales for orientational re-

laxation in the liquid. While weakly hydrogen-bonded water molecules may relax through both the fast and the slow relaxation process, strongly hydrogen-bonded molecules can only relax via the slow process.

Getting to the infected site

After an infection, T cells that are specific for the infectious agent enter the inflamed site. Part of this extravasation process involves cell surface adhesion molecules in the integrin and selectin families. In an in vivo study, DeGrendele et al. (p. 672) now show that when T cells were activated through their T cell receptors in the regional lymph nodes, CD44 on their surface was activated to bind to its ligand hyaluronate (HA) and acquired the capacity to roll. These activated cells next moved into the blood stream, and their entry into inflamed tissue required both CD44 and HA. Thus CD44 is a key player in the movement of cells into an inflammatory site.

Why a Y?

Although most chromosomes appear to contain a diverse set of genes, Lahn and Page (p. 675) have tested the theory that the Y chromosome may contain a functional organization. A systematic search of the Y chromo-

some (specifically the nonrecombining part, which includes 95% of the chromosome) revealed 12 novel genes or families of genes. These genes fell into only two classes: Housekeeping genes that are also expressed on the X chromosome and genes expressed specifically in the testis. In this way, comparable expression of housekeeping genes in males and females and the pressure to enhance male reproductive fitness are maintained.

Population losses

How many populations, demographically or genetically distinguishable groups, are there on Earth, and how rapidly are they being lost? Hughes et al. (p. 689; see the Perspective by Myers, p. 597) estimate, on the basis of published studies of population differentiation for a variety of taxa and distribution maps for different species, that there are several billion populations globally. Using the rate of tropical deforestation as a surrogate for habitat loss, and assuming that population loss parallels habitat destruction, they calculate that around 16 million individual populations are disappearing each year.

Surprising survival

The effect of mass extinction can be enormous in terms of species loss, but what is the effect on the preservation of the history of life? In a mathematical analysis, Nee and May (p. 692; see the Perspective by Myers, p. 597) show that even with an extinction event that removes at random 95% of all species, the bulk (80%) of evolutionary history will be maintained in the surviving 5%. The study may help focus conservation policy for dealing with the current anthropogenic biotic crisis, even though the importance assigned to species is usually not related to their evolutionary history.

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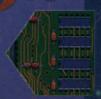
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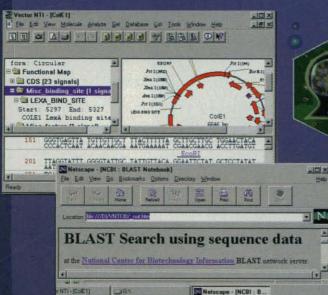
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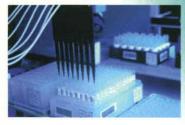
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SL.1NFLS	norm. fetal liver/spleen
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SL.2NbHP8-9W	norm. 8-9 week placenta
SL.2NbHMSP	norm. multiple sclerosis plaques
SL.NbHH19W	norm. fetal heart
SL.NbHSF	norm. senescent fibroblast
SL.b2HP	non-norm. full-term placenta
SL.b4,5HB55Y	non-norm. adult brain
SL.bHOT	non-norm. ovary tumor
SL.bHM	non-norm. melanocyte
SL.bHP8-9W	non-norm. 8-9 week placenta
SL.HMSP	non-norm. multiple sclerosis plaques
SL.HH19W	non-norm. 19 week fetal heart
SL.HBst	non-norm. breast
SL.bHSF	non-norm, senescent fibroblasts
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SL.NbME13.5-14.5	norm. mouse embryo, 13.5-14.5 dpc
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SL.NbRP	norm. rat placenta
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- 1. Soares, et al. (1994) Proc. Nat. Acad. Sci. 91 9228-9232.
- 2. Bonaldo, Lennon and Soares (1996) Genome Res. 6 791-806.

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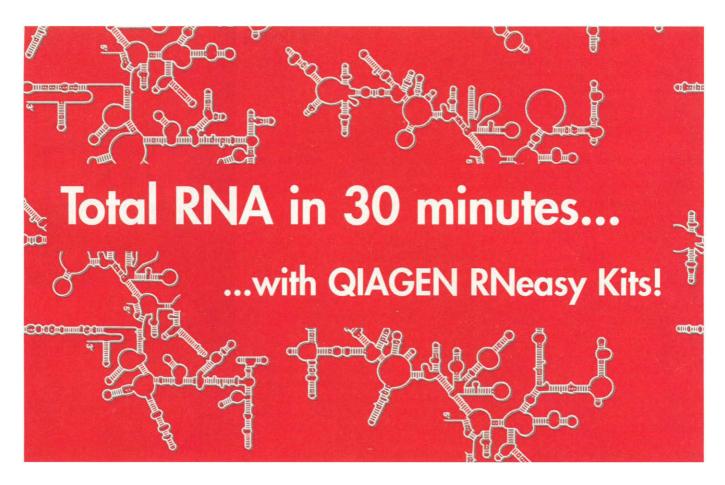
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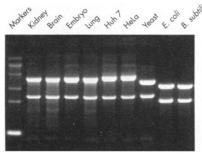
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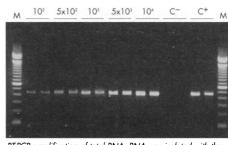


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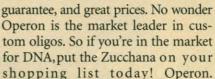
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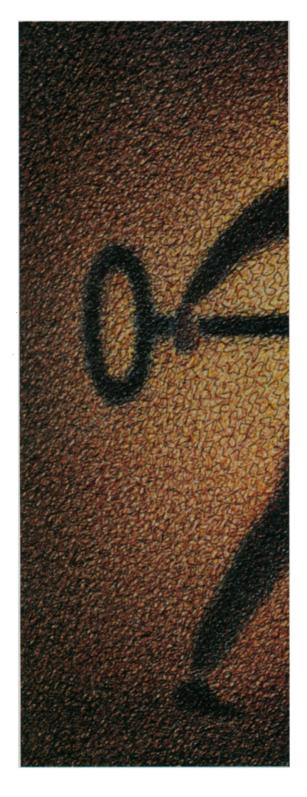
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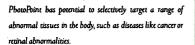
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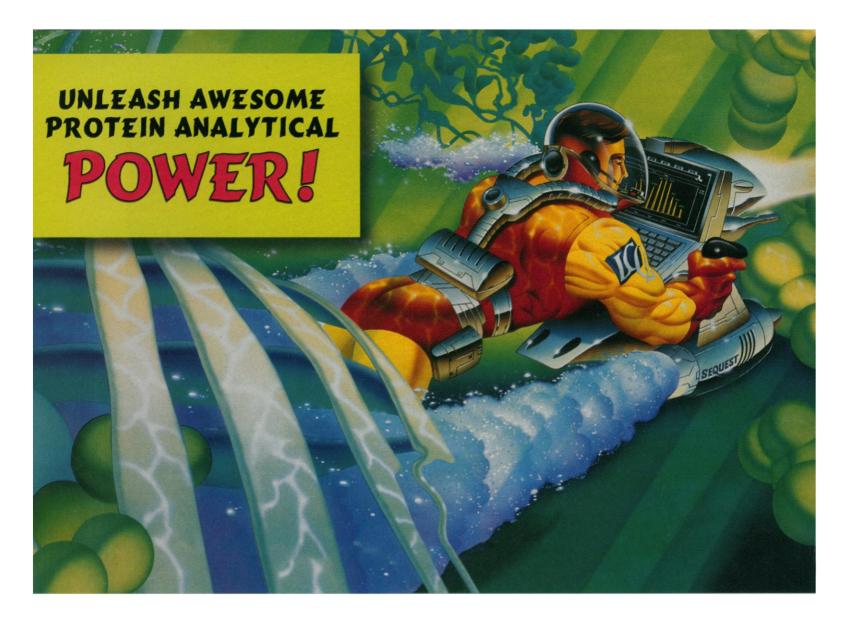
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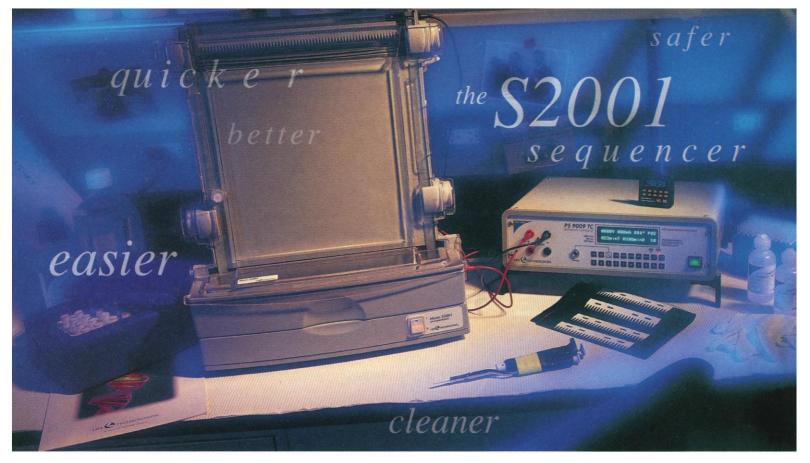
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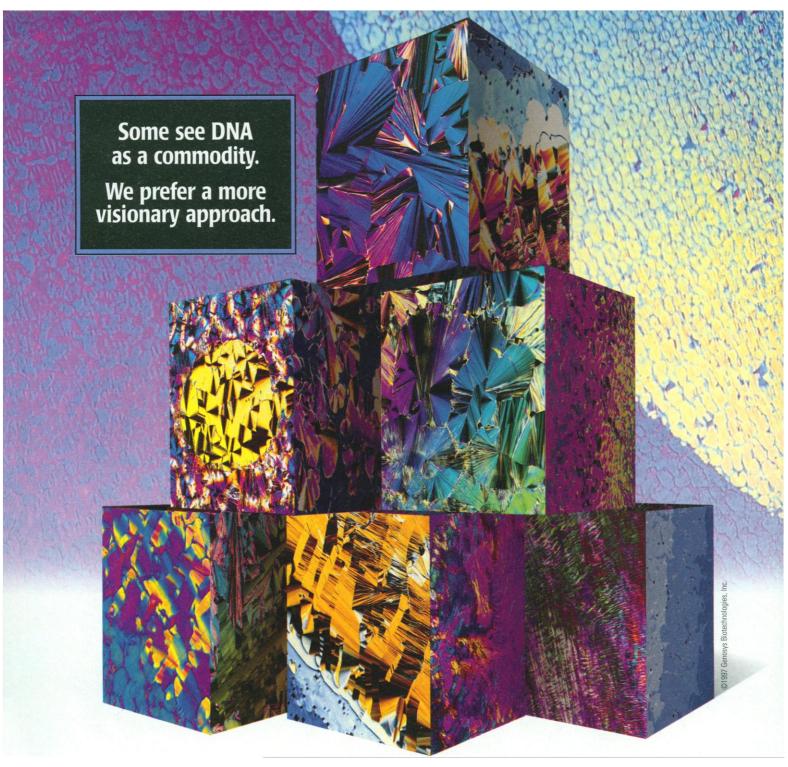
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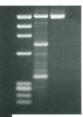
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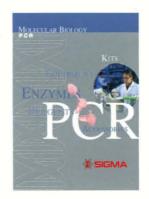
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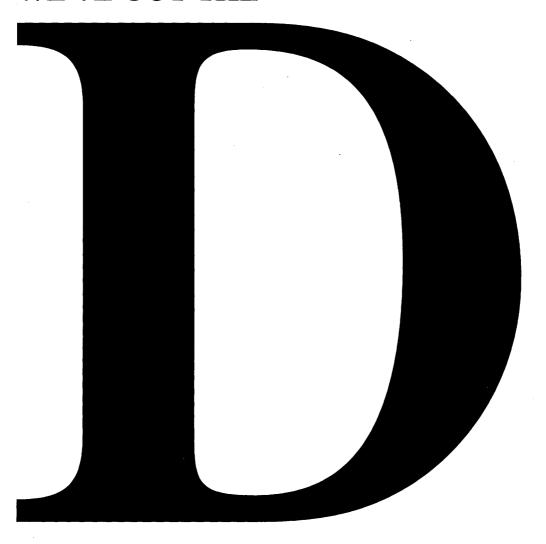
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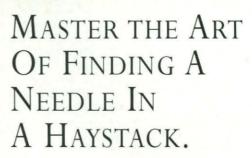
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Science

Genome Maps

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The GENEBRIDGE 4 and Stanford G3 Radiation Hybrid panels can be used to place members of gene families on the human transcript map. By using the same radiation hybrid panels as were used to make the transcript map you can map your new family members. With the map position you have access to the I.M.A.G.E. Consortium (LLNL) cDNA clones and CEPH YACs that have been mapped to the same region, as well as GENEPAIRSTM. Your primers can also be used to screen our BAC DNA pools to find clones containing the genomic form of the transcript. The BAC and YAC clones may be used to

screen high density membranes for additional cDNA and/or genomic clones in the region.

The Stanford G3 RH Panel is a medium resolution, 10,000 rad panel consisting of 83 clones and two controls. An e-mail server, operated by the Stanford Human Genome Center, will attempt to link your marker to framework markers they have already assayed. Current details may be obtained from http://shgc-www.stanford.edu.

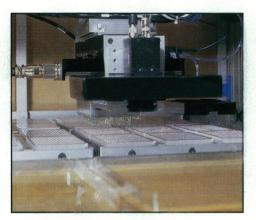
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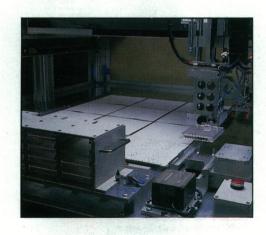
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When new family members are identified by using computer programs, individual clones are often available. Currently, over 1,000,000 5' and 3' sequences are deposited into public databases and are searchable for any information such as putative gene function using the dBest/GenBank query (http://www.ncbi.nlm.nih.gov/Web/Search/index.html). When ordering cDNA clones, please keep in mind that the clone ID # is the number assigned by I.M.A.G.E. Consortium, not the NCBI number or the Genbank accession number.



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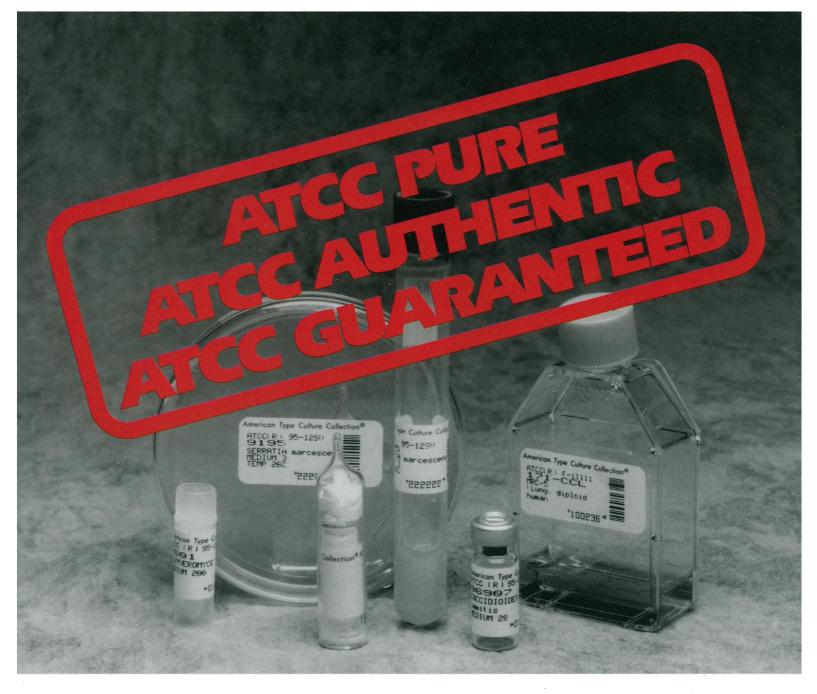
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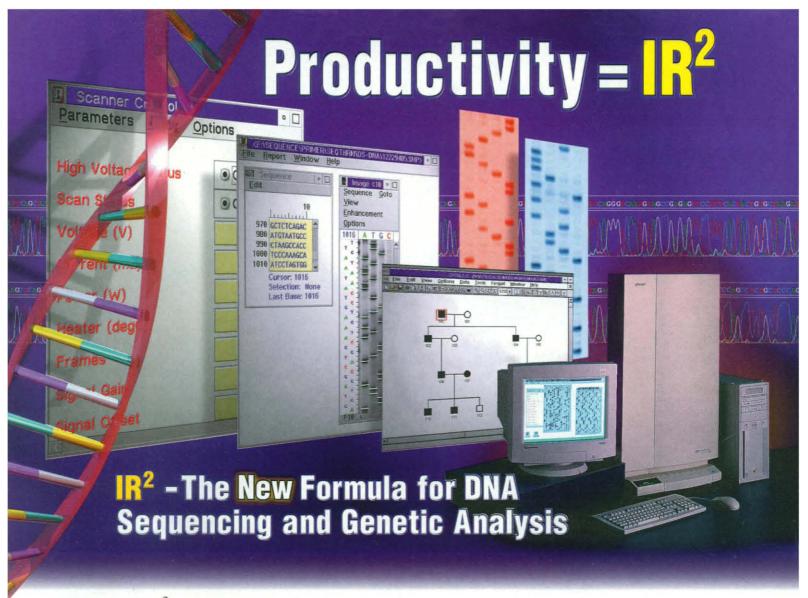
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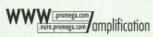
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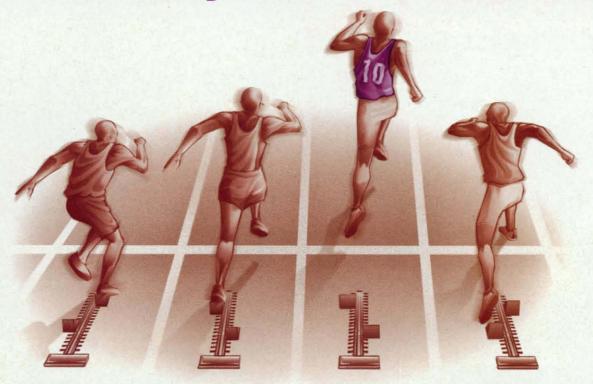
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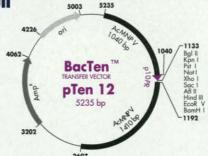
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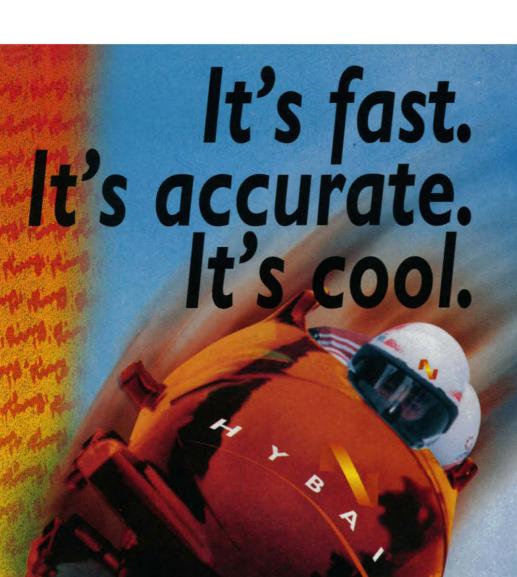
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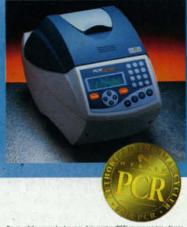
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