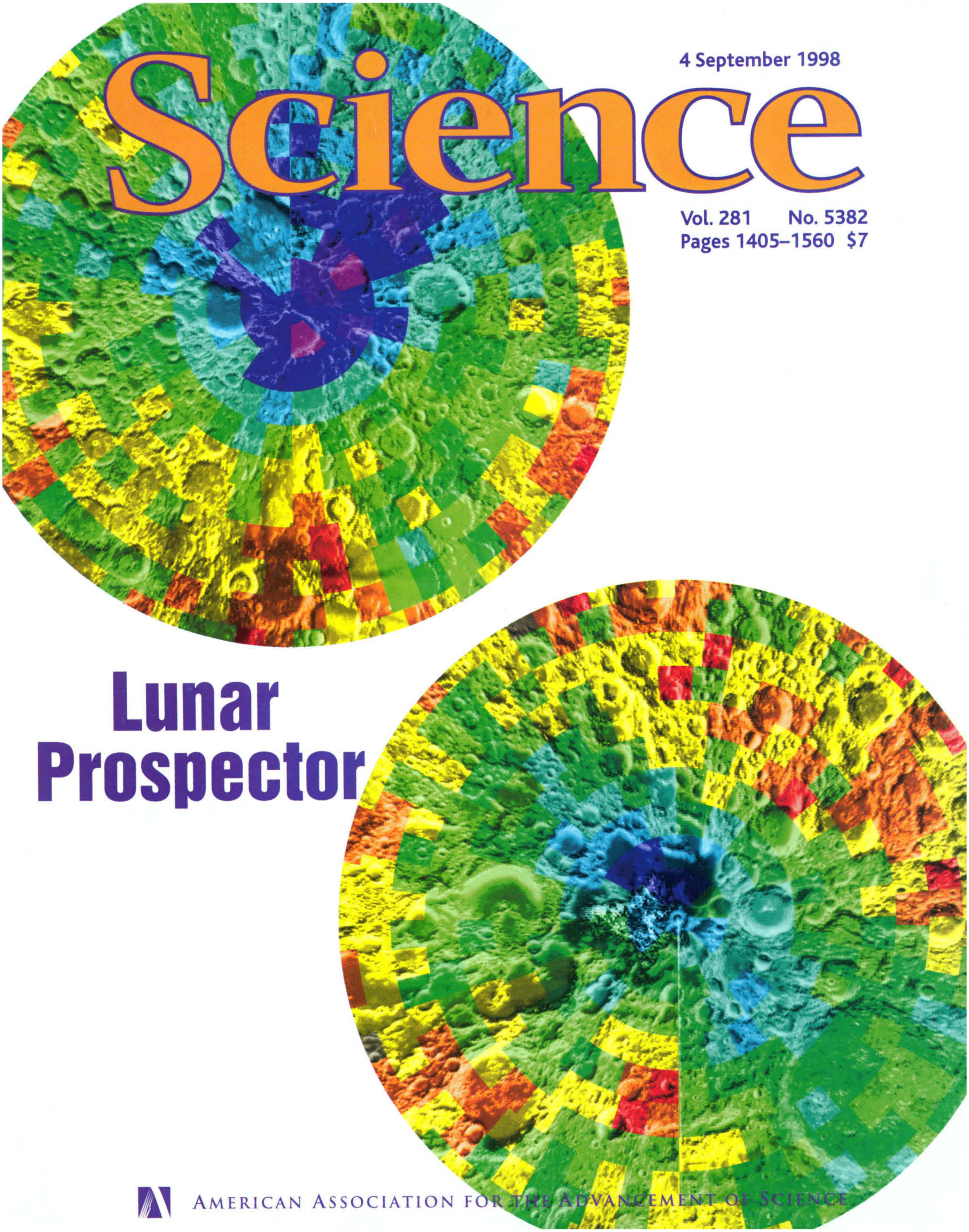
Science

4 September 1998

Vol. 281 No. 5382
Pages 1405–1560 $7



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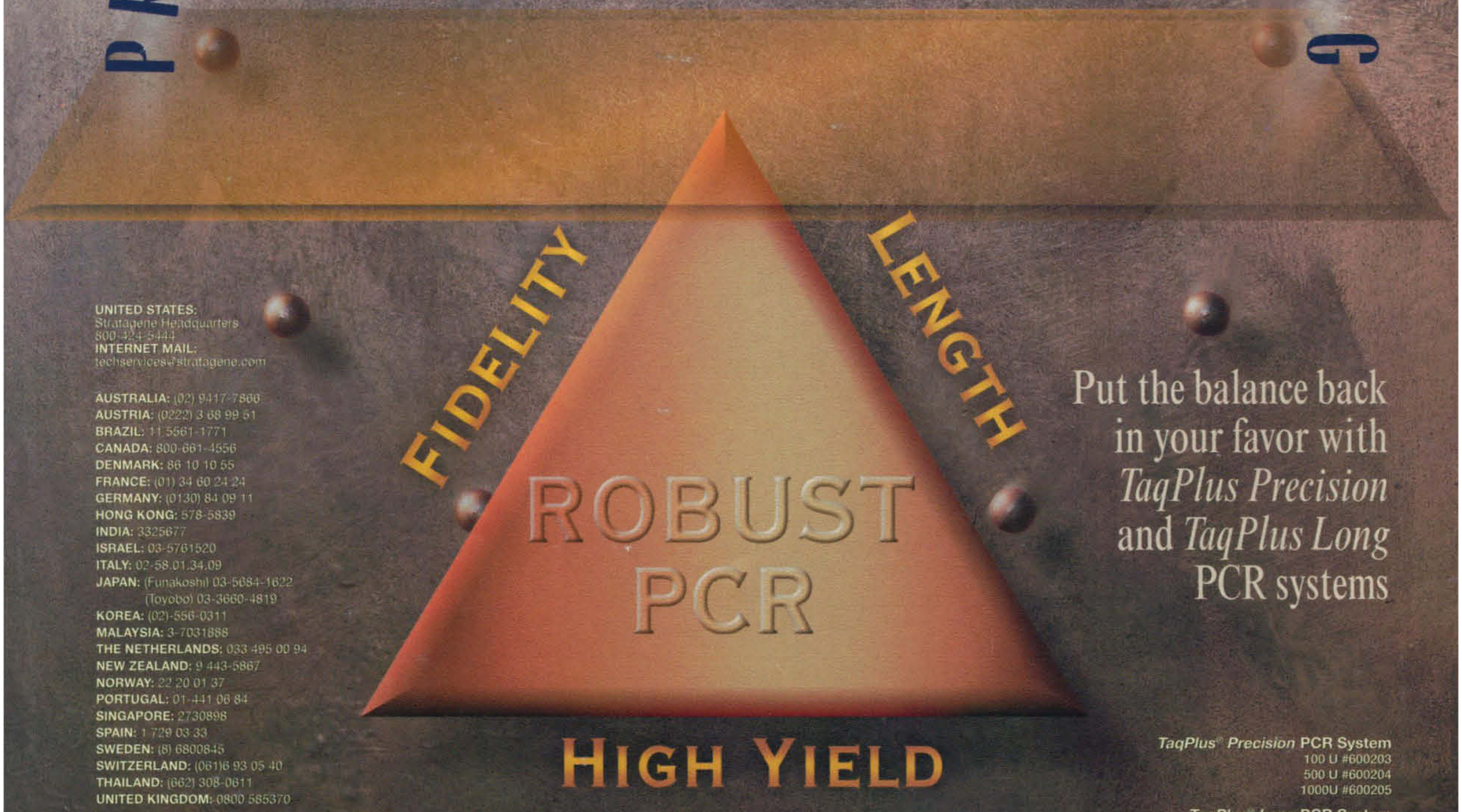

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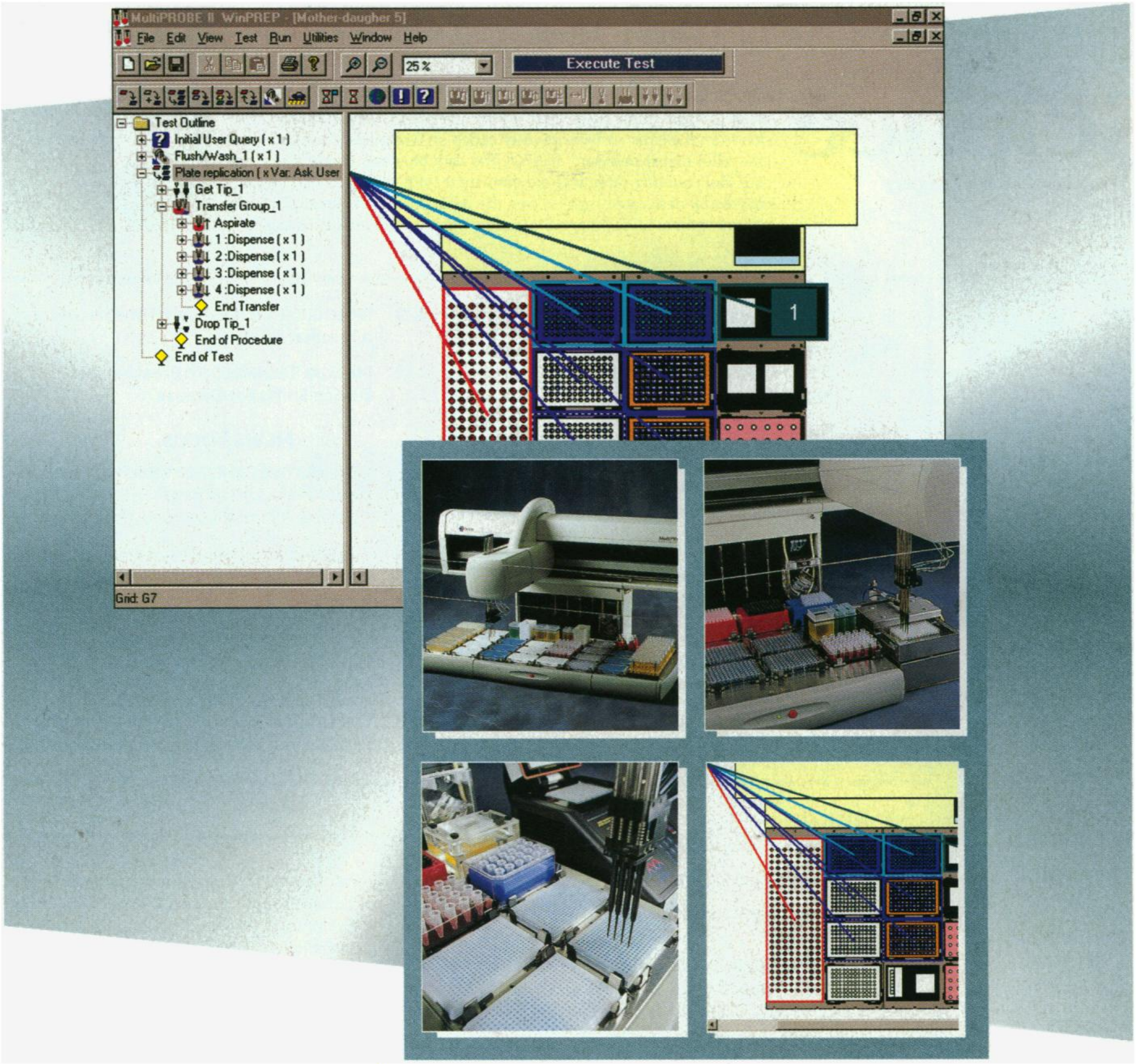

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VOLUME 281 4 SEPTEMBER 1998 NUMBER 5382

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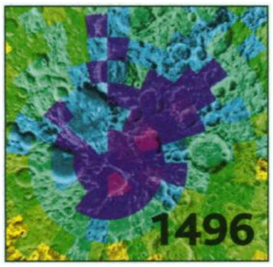
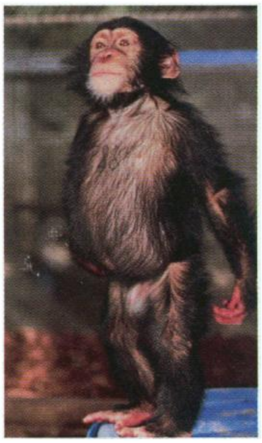
COVER Lunar Prospector evidence for water ice at the north (top) and south (bottom) lunar poles. Data on the rate of epithermal neutron emission from the lunar surface are color coded on two maps (overlaid by surface relief maps) poleward of ±70°. The dark blue and purple areas indicate low counting rates and are consistent with hydrogen-rich deposits covered by desiccated regolith. See the related Lunar Prospector Reports beginning on p. 1475. [Image: S. Maurice, Observatoire Midi-Pyrénées]





1432

The difference between chimps and humans

NEWS

NEWS OF THE WEEK

NEWS FOCUS

DEPARTMENTS

RESEARCH

LUNAR PROSPECTOR REPORTS

REPORTS

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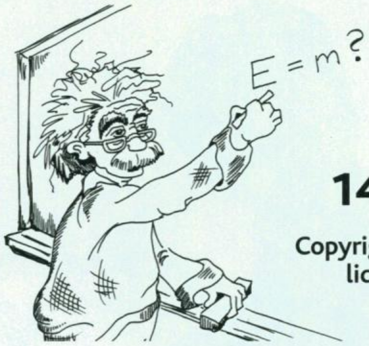

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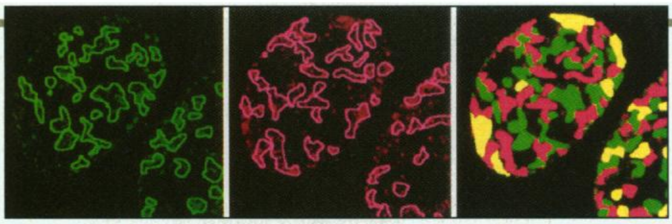
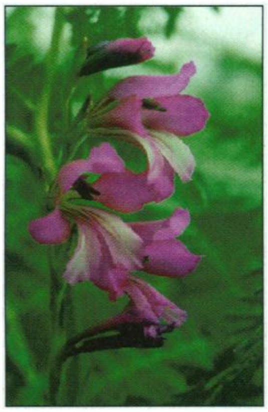


1502

Nuclear organization

TECHNICAL COMMENTS



1513

Patterns of abundance of rare species

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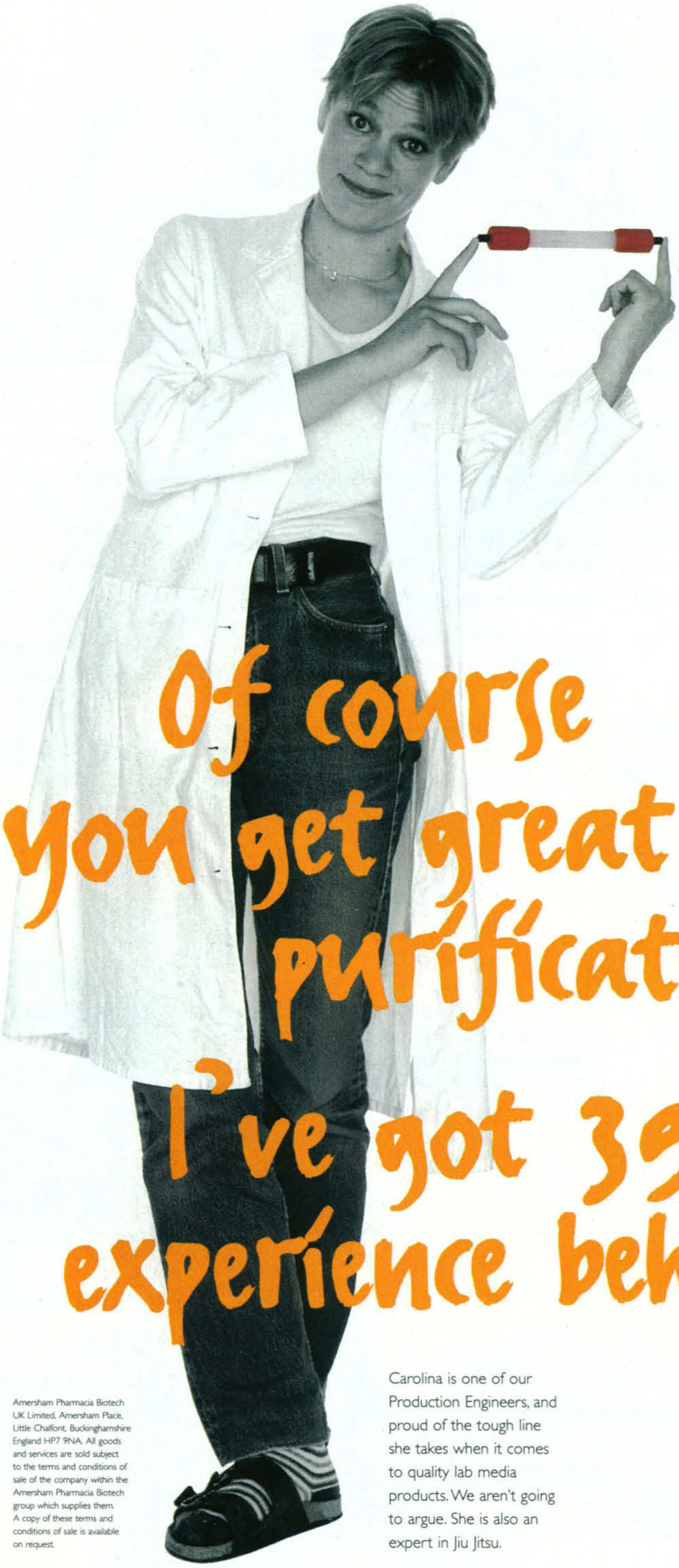8-98 MMC

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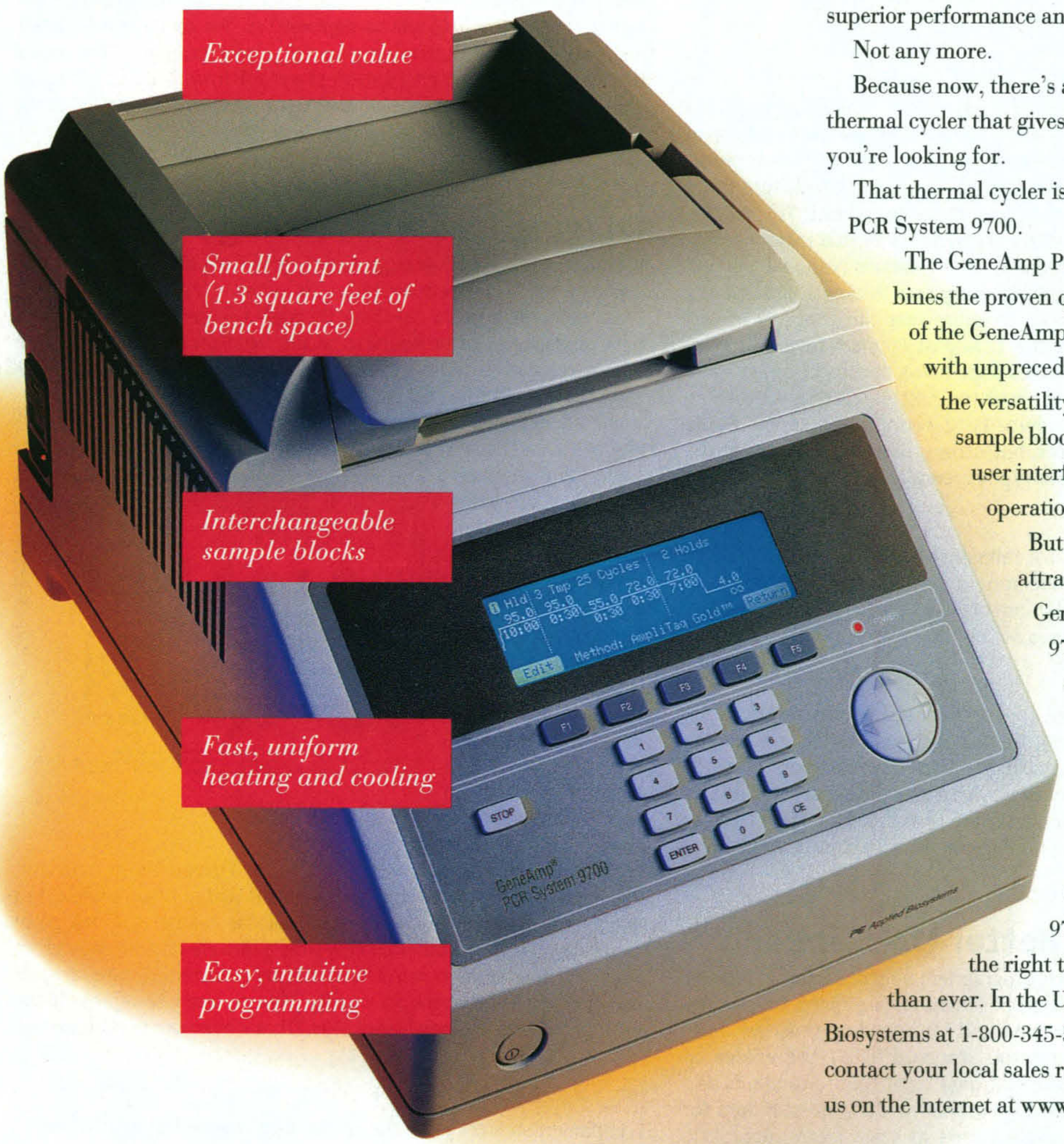
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THIS WEEK IN *SCIENCE*

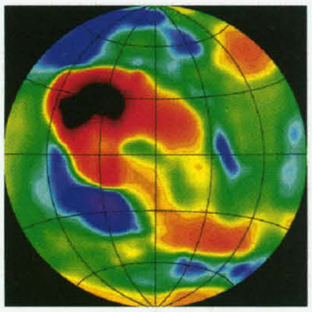
edited by BROOKS HANSON

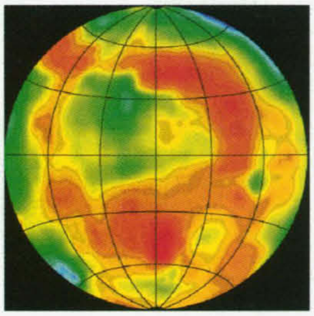
PROSPECTING THE MOON

The moon is the only other planetary body for which we have rock samples from known locations, thanks to the Apollo missions. Extending these into an understanding of the origin and evolution of the moon requires global mapping of the surface composition of the moon and measurements of its gravity and magnetic field to infer its internal structure. Such global information is now being provided by Lunar Prospector, which has been mapping the moon since January, as indicated in a series of seven reports beginning with an overview by Binder on p. 1475.

The moon is thought to have formed about 4.5 billion years ago when a Mars-sized bolide impacted into a proto-Earth and ejected material into orbit around our planet. This material then re-accreted into the moon. Volcanic activity was extensive for about 2 billion years and then waned as the moon cooled. Today, the moon is inactive and is considered to be a quiescent body with a surface unaltered by internal processes, such as convection, which drives plate tectonics on Earth. Throughout its history the moon has been bombarded by bolides that have produced large to small impact craters on the moon. Some of the largest impacts may have excavated material from great depth.

Lunar Prospector is an inexpensive satellite with three spectrometers, a magnetometer, an electron reflectometer, and a Doppler gravity experiment. It is in the midst of a global mapping campaign in a low-altitude polar orbit around the moon. The Doppler gravity experiment analyzes subtle changes in the spacecraft's orbit due to variations in the interior structure of the moon. Analysis of the gravity data (Konopliv *et al.*, p. 1476; see the news story by Irion) suggests that the moon has a small iron-rich core. Thus, sufficient iron must have been included in the moon as a result of the giant impact to form this core, perhaps from an iron-rich terrestrial mantle or the Earth's early core. The magnetometer and electron reflectometer measurements (Lin *et al.*, p. 1480) show that the lunar crust locally harbors relatively intense magnetic fields (contrary to many previous hypotheses) on the opposite side from the Imbrium and Serenitatis impact basins. Thus, some impacts may have induced crustal magnetization on the opposite side from the impact. The magnetic field intensity on the opposite side of the Imbrium impact basin is strong enough to deflect the solar wind and create a tiny magnetosphere.





The gamma ray, alpha particle, and neutron spectrometers are using fluxes derived from particle interactions produced by cosmic rays and solar wind plasma on the lunar surface to map the global distribution of elements that make up the lunar crustal surface. Here initial global maps of Fe, Ti, Th, and K abundances are presented from analysis of the gamma ray (Lawrence *et al.*, p. 1484) and neutron spectrometers (Feldman *et al.*, p. 1489). These global maps show that the major impact basins, such as South Pole Aitken and Imbrium are chemically distinct from the lunar highlands (areas of higher topography, mainly composed of basaltic lava flows). The Fe and Ti distribution maps inferred from the Clementine satellite spectral reflectance data are generally consistent with the Lunar Prospector maps (Elphic *et al.*, p. 1493). Finally, analysis of the abundance of hydrogen derived from neutron spectrometer data (Feldman *et al.*, p. 1496) indicates that water ice may be present at both lunar poles, consistent with the hint of water ice in craters at the south pole from Clementine radar data.

A SINGLE SOURCE

Zintl compounds, which consist of polyatomic post-transition metal anions and alkali or alkaline earth metal cations, are well known in chemistry, but the synthesis of single component materials generally requires very high temperatures and specialized techniques. Beswick *et al.* (p. 1500) describe a low-temperature solution synthesis of a Zintl compound from a single precursor molecule, which allows high stoichiometric control under mild conditions. Other heterometallic phases may also be accessible through this synthetic strategy.

REGULATION THROUGH DIFFERENT CALCIUM STORES

The transcription factor CREB (cyclic AMP response element–binding protein) helps regulate gene expression, but the response of CREB and other transcription factors to extracellular environmental signals and intracellular signals is not clear. CREB was named for its activation in response to increased concentrations of cyclic adenosine monophosphate, but it is also activated in response to increased intracellular concentrations of Ca^{2+}. Chawla *et al.* (p. 1505) report that in response to increased concentrations of cytoplasmic Ca^{2+}, CREB becomes phosphorylated and binds to the CREB-binding protein (CBP), a transcriptional coactivator protein. However, increased transcriptional activity of CREB-CBP complex also required an increase in the concentration of Ca^{2+} within the nucleus. Transcriptional activity of the COOH-terminal domain of CBP was dependent on the concentration of nuclear Ca^{2+} and the activity of the Ca^{2+}/calmodulin–dependent protein kinase IV. The results indicate that recruitment of the coactivator and transcriptional activation are separable events that depend on Ca^{2+} concentrations in distinct cellular compartments and that CBP may itself be regulated by changes in the nuclear concentration of Ca^{2+}.

CONVERGING PATHWAYS TO CANCER

Mutations in the adenomatous polyposis coli (*APC*) tumor suppressor gene are present in the majority of colorectal cancers. There has been much interest in identifying the target genes that are regulated by the APC signaling pathway and whose expression is aberrantly activated in tumor cells when APC is defective. He *et al.* (p. 1509) show that one of APC's downstream targets is the proto-oncogene *MYC*. This convergence of the APC and MYC oncogenic pathways may explain why MYC is often overexpressed in colorectal cancers in the absence of gene rearrangement or amplification (see the news story by Pennisi).

TAKING TURNS AT THE GENOME

Transcription and DNA replication both need access to the genome. Wei *et al.* (p. 1502; see the Perspective by Cook) show, using microscopic fluorescent imaging

CONTINUED ON PAGE 1415

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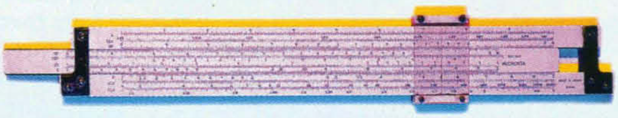

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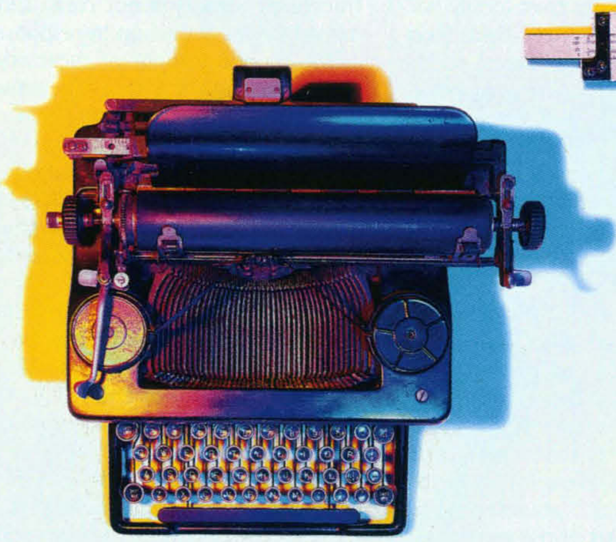

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THIS WEEK IN *SCIENCE*

CONTINUED FROM PAGE 1413

techniques, how this access problem is sorted out. In mammalian cells, sites of active transcription and active DNA replication sort out into large but different domains that must move through the genome through the course of S phase in the cell cycle. It seems that, at least in higher order structures, transcription and replication take turns.

CONSERVATION TO SCALE

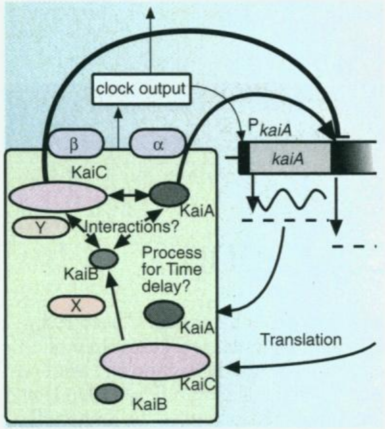
Many conservation decisions require information on a fine spatial scale, for example, the size of populations or the number of local populations. Unfortunately, much of the available data is available only at coarser scales, such as in range maps. A method that would permit the extrapolation of broad distribution information on species down to finer scales could be of great practical value; such a method is described by Kunin (p. 1513). By converting a range of abundance measures to a scale-invariant index, species abundance at fine scales can be estimated accurately, potentially allowing conservation managers to set priorities more accurately.

UNDER THE INFLUENCE OF CYCLIC NUCLEOTIDES

Developing neurons in search of their targets follow a variety of cues along the way. These cues can include soluble signaling factors as well as membrane-anchored factors; and the growth cone's response can be to lean toward or away from each signal. Song *et al.* (p. 1515; see the Perspective by Caroni) have shown through in vitro studies that the response of growth cones to certain signals can be modulated by added cyclic nucleotides. By altering the amount of cyclic nucleotide in the neuron, its growth cone response to a given signal can be tuned from repellent to attractive.

PROKARYOTIC CLOCKS

Circadian clocks in eukaryotes—from plants to man—have received much attention recently, but a class of prokaryotes, the cyanobacteria, also need to regulate their metabolism in tune with the day-night cycle. Ishiura *et al.* (p. 1519; see the news story by Barinaga) describe a cluster of genes from a cyanobacterium that is sufficient to establish and maintain a circadian loop through a cycle of gene expression and feedback inhibition by protein products of the genes. They name the gene cluster *kai*ABC after the Japanese word for cycle.



TECHNICAL COMMENT SUMMARIES

Measuring Patterns in Population Fluctuations

The full text of these comments can be seen at www.sciencemag.org/cgi/content/full/281/5382/1415a

E. Ranta *et al.* studied (Reports, 28 Nov. 1997, p. 1621) "long-term data of the Canadian lynx from eight Canadian provinces" and found that they displayed "large-scale synchrony in population fluctuations." Ranta *et al.* concluded that their observations were "in agreement with predictions of a spatially-linked population model and support contemporary population ecology theory."

B. Cooke comments that similarities between patterns in the lynx data and the "spatiotemporal patterns" produced by the simulation model used by Ranta *et al.* "appear to be superficial and exaggerated by their analytical methods." He states that "a cross-correlation coefficient is a meaningful measure of synchrony only when the population data are stationary" and that it "seems an inaccurate measure of synchrony for populations that cycle in phase and then suddenly snap out of phase."

In response, Ranta *et al.* agree that "nonstationarity is certainly an aspect to be taken into account" and state that the lynx data and the simulation results are stationary. Their reanalysis of the data "so that this linear trend [nonstationarity in the 15-year sliding-window analysis] is removed ... shows that synchrony of fluctuation over time remains, although some details change." Also, "the use of a time window larger than 15 years, or moving the window in increments larger than 1 year, does not change [their] conclusions."

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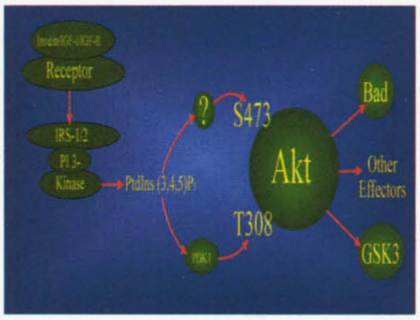

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- phospho-Akt1
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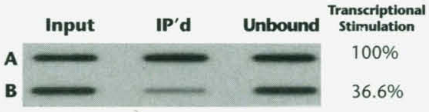

HAT-deficient yeast cells were transfected with wt (A) or mutant (B) HAT constructs, and chromatin was immunoprecipitated with anti-acetyl Histone H4 antiserum. Slot-blots of immunoprecipitated, input, or unbound material were probed with the promoter of a reporter gene, whose expression was monitored in a parallel experiment.

Antibodies/Peptides

- Ac-Lys12-Histone H4
- Ac-Lys8-Histone H4

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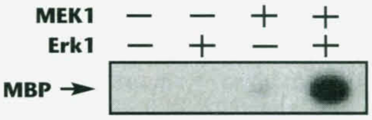

Erk2 was activated by MEK1, and assayed by MBP phosphorylation.

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- Lck
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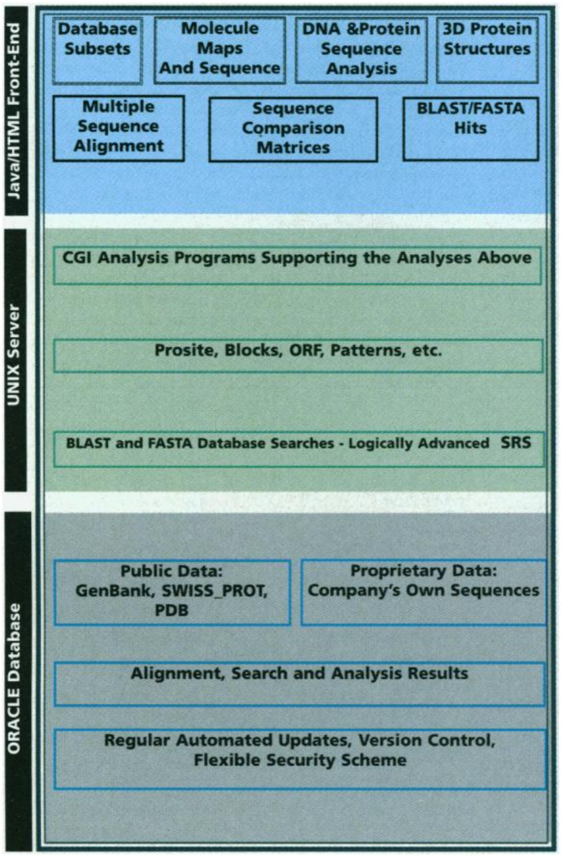
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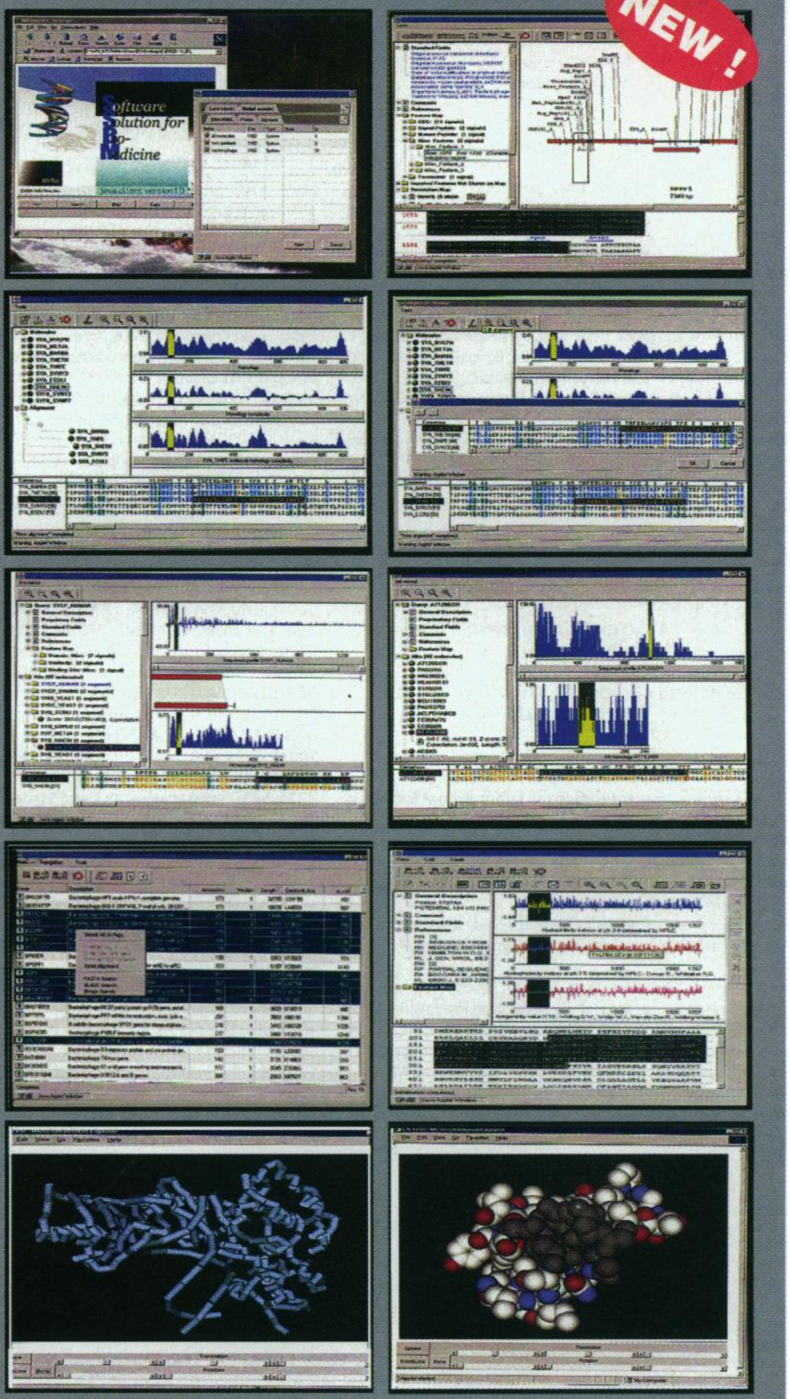
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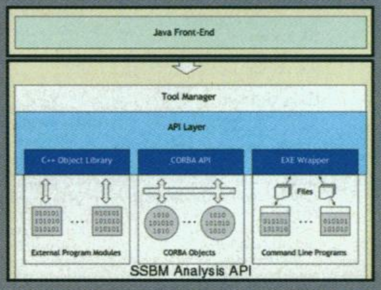
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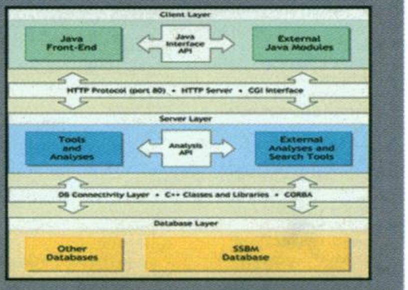
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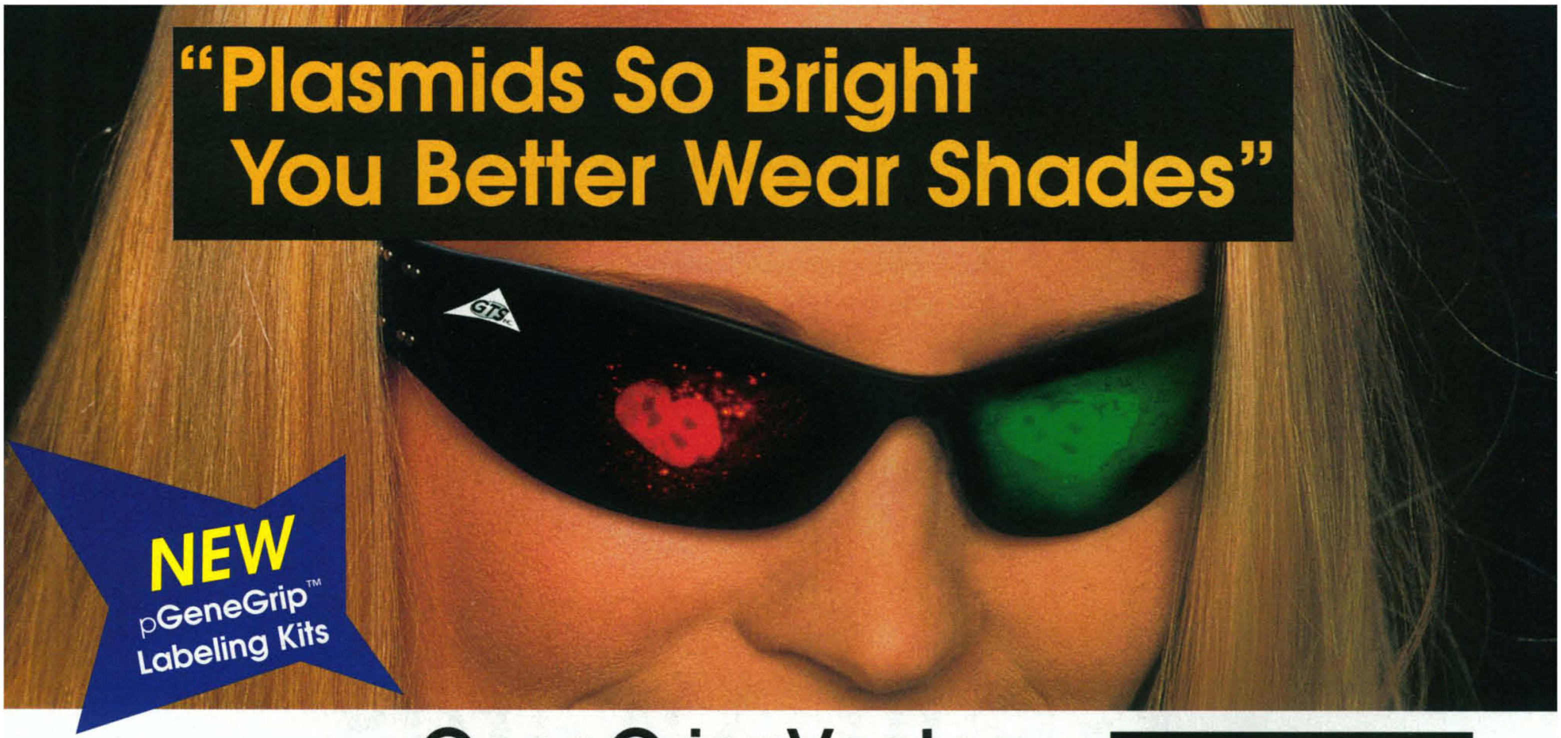

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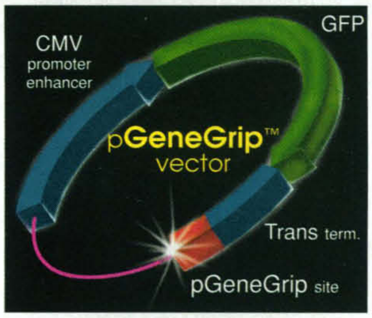

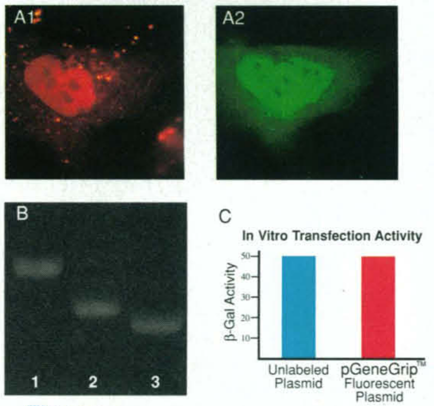

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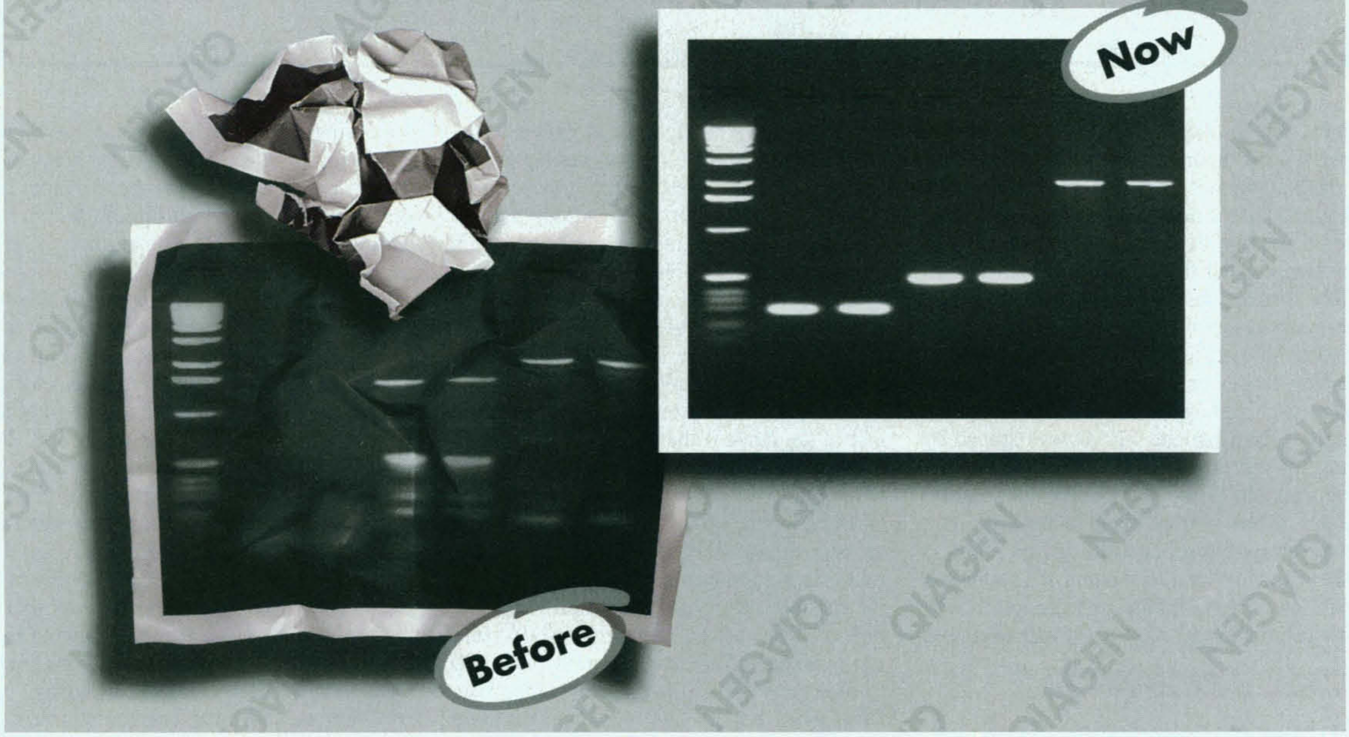

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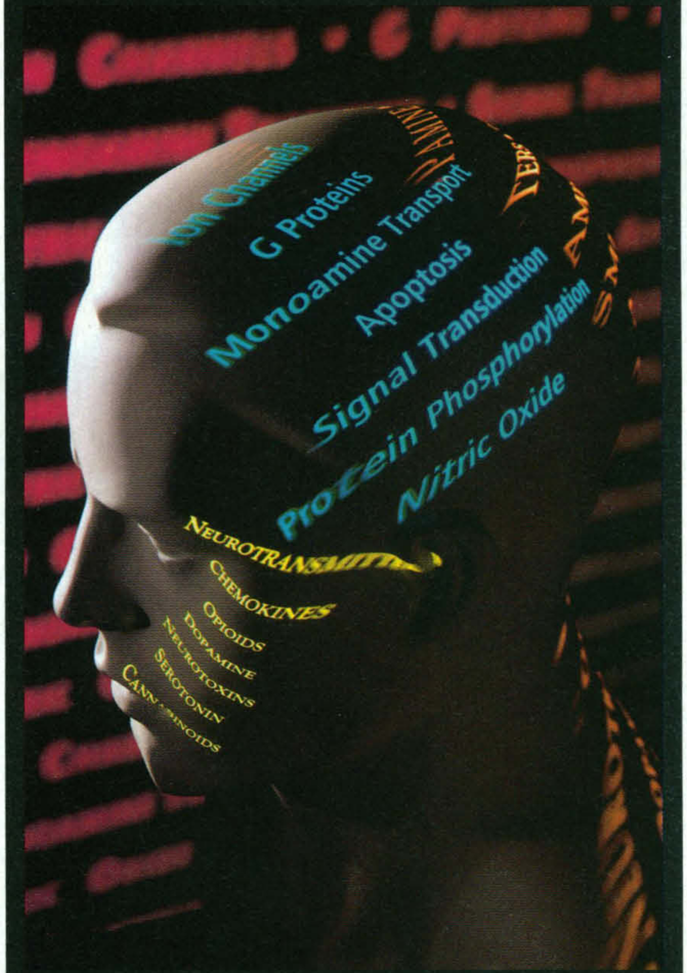

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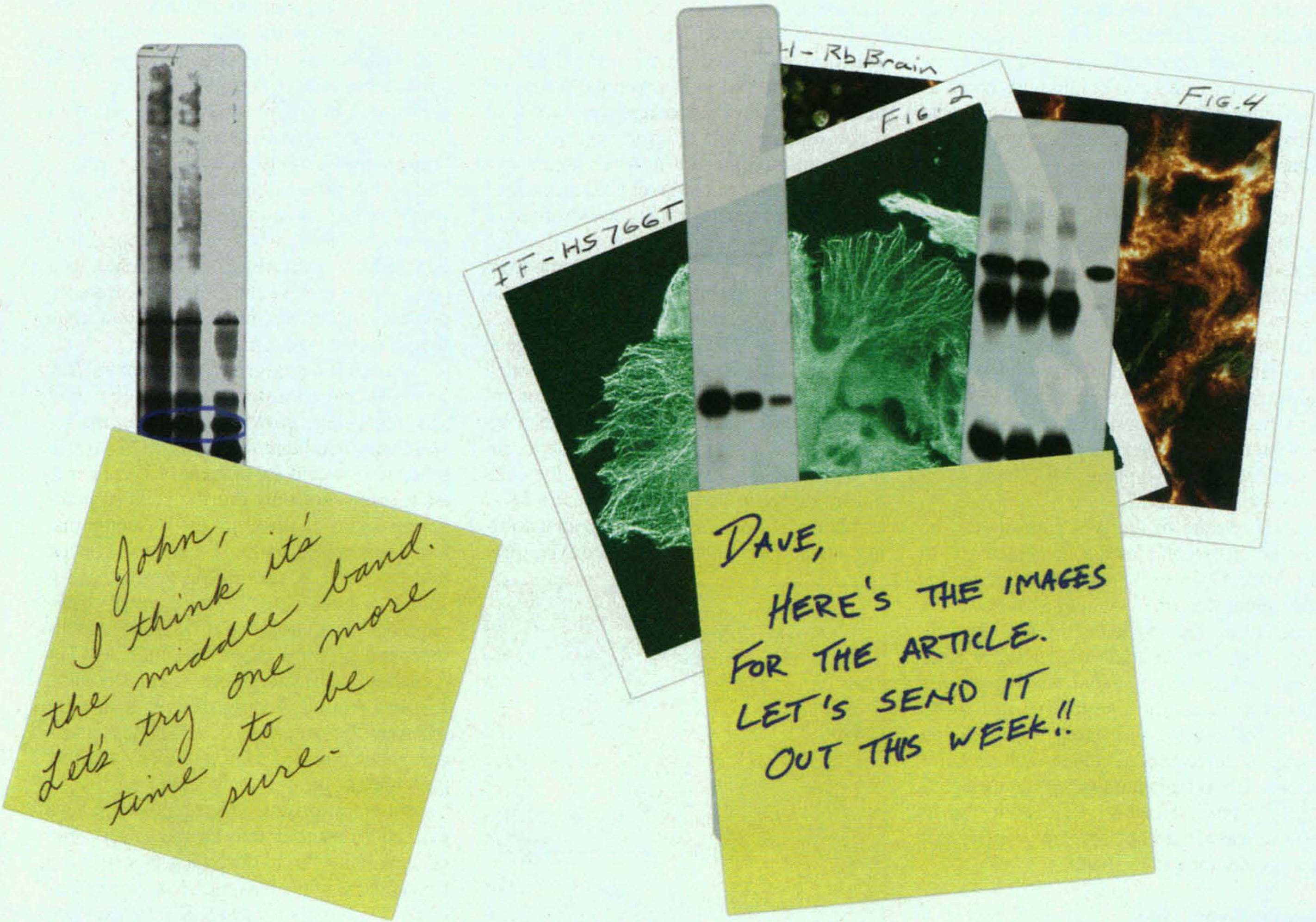
John,
I think it's
the middle band.
Let's try one more
time to be
sure.
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FIG. 2
-Rb Brain
FIG. 4
DAVE,
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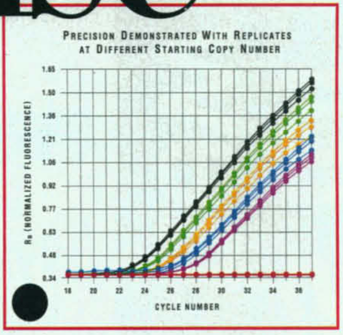

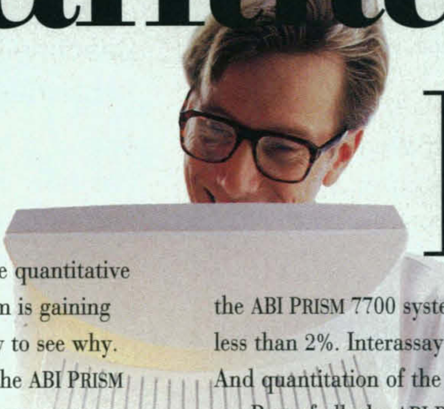

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1. Heid, Christian A., et al. 1996. Real Time Quantitative PCR. Genome Research 6: 986-994. from Molecular Endocrinology
2. Gibson, Ursula E.M., et al. 1996. A Novel Method for Real Time Quantitative RT-PCR. Genome Research 6: 995-1001

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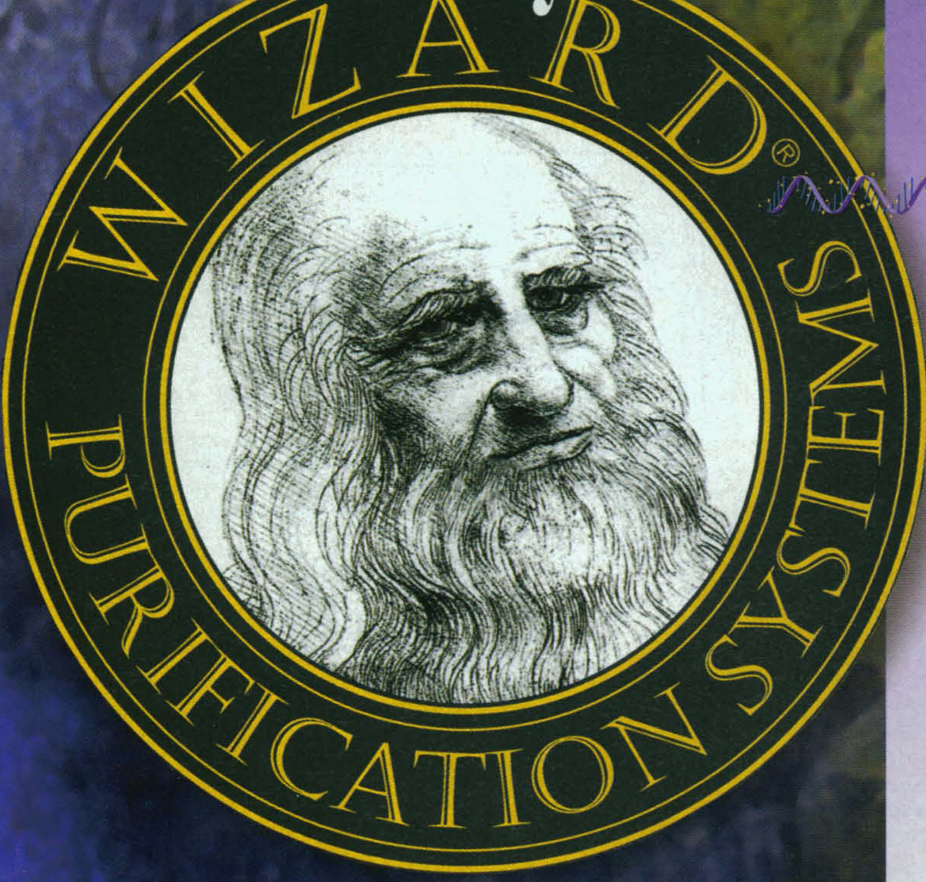

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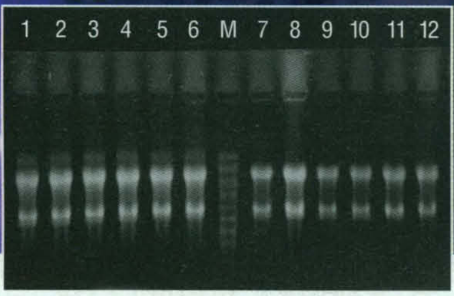

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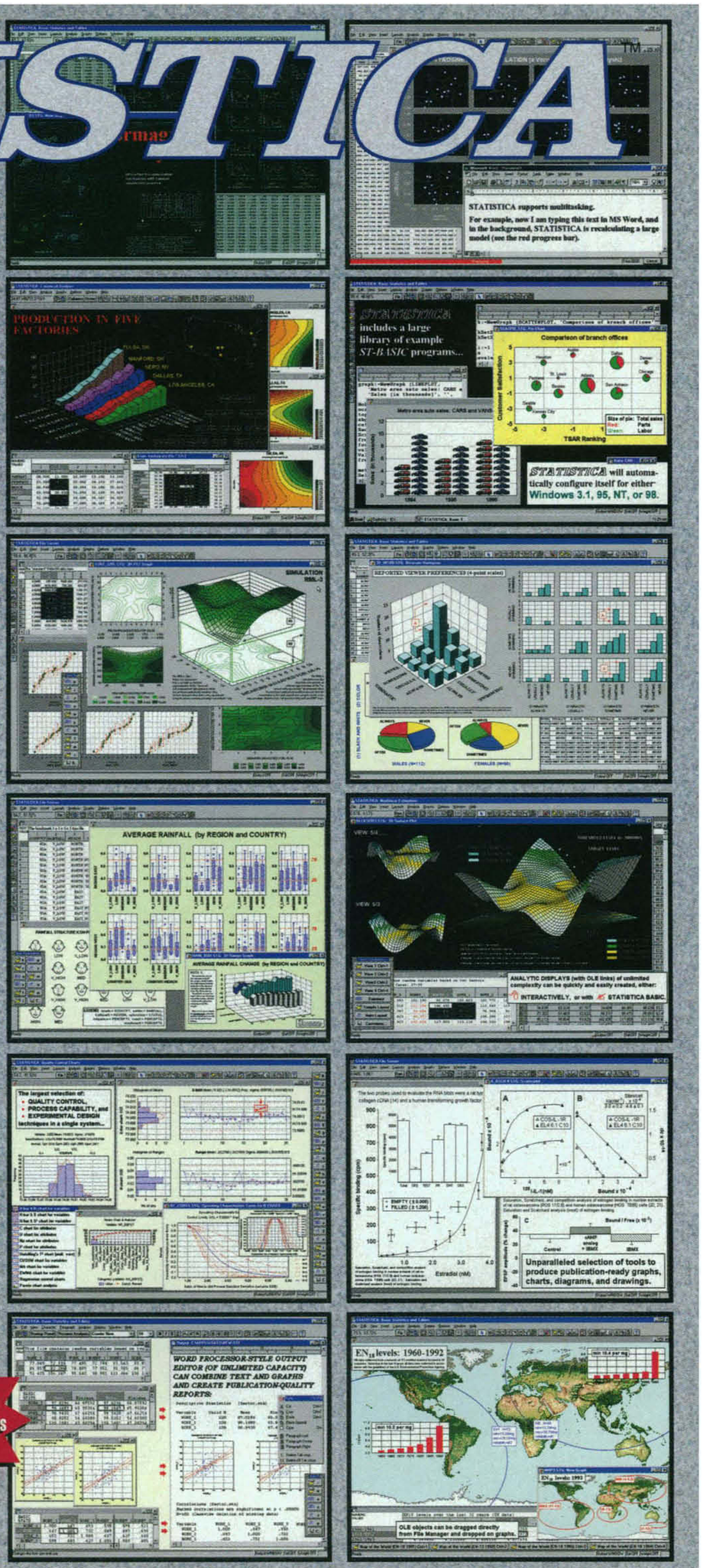

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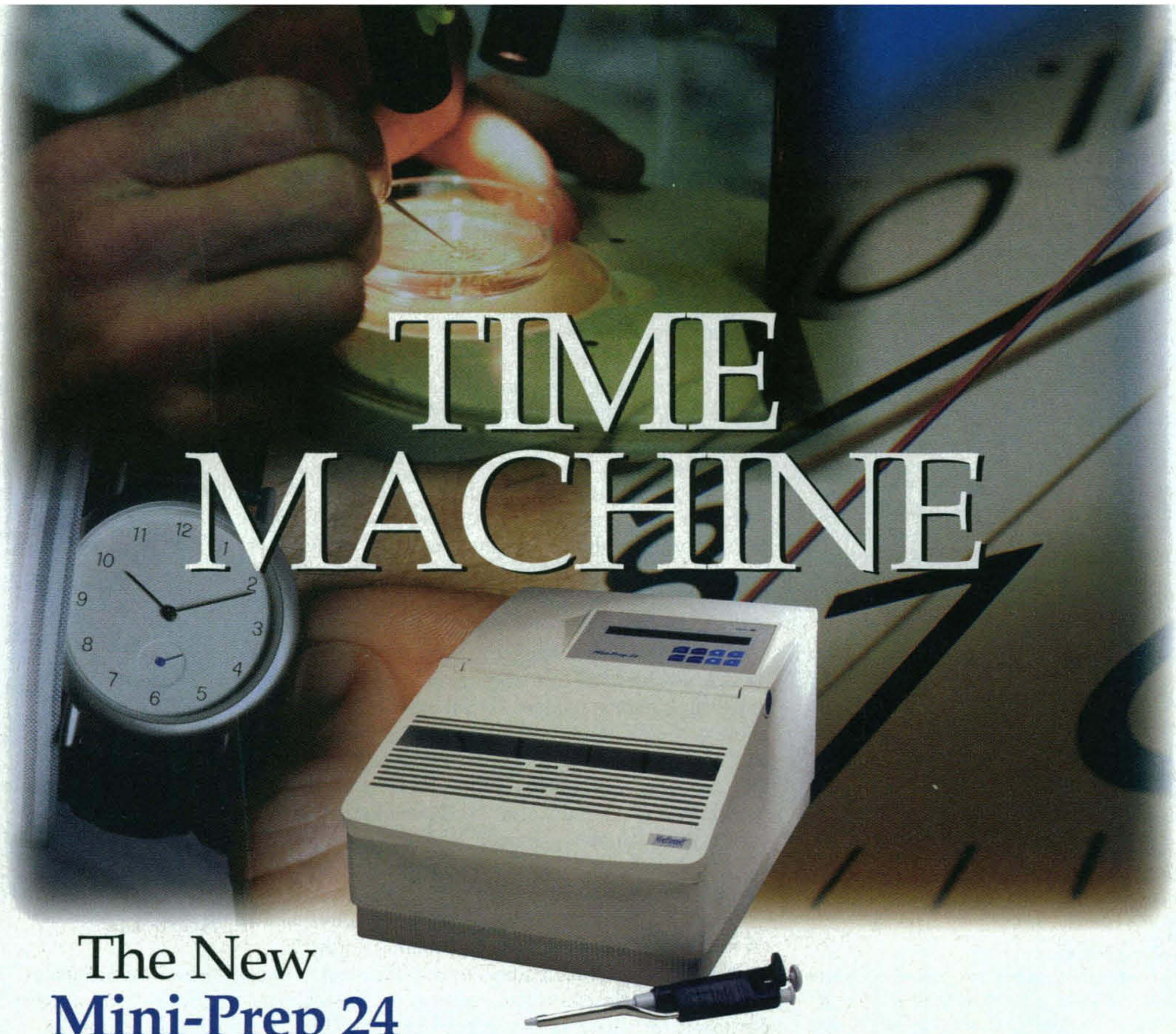
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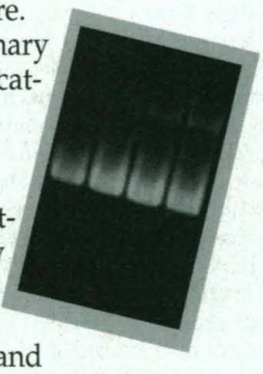

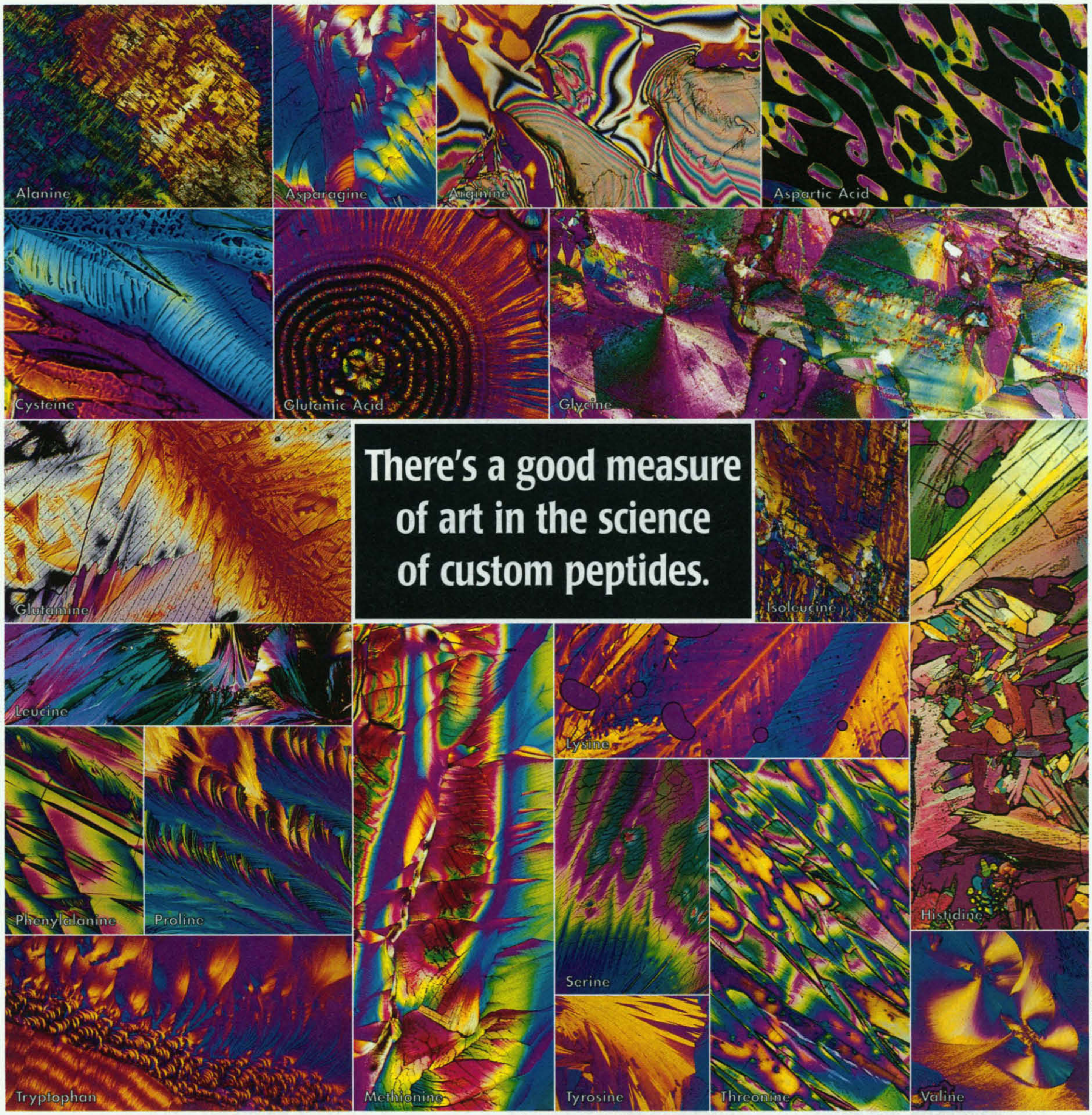

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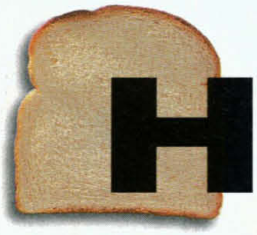

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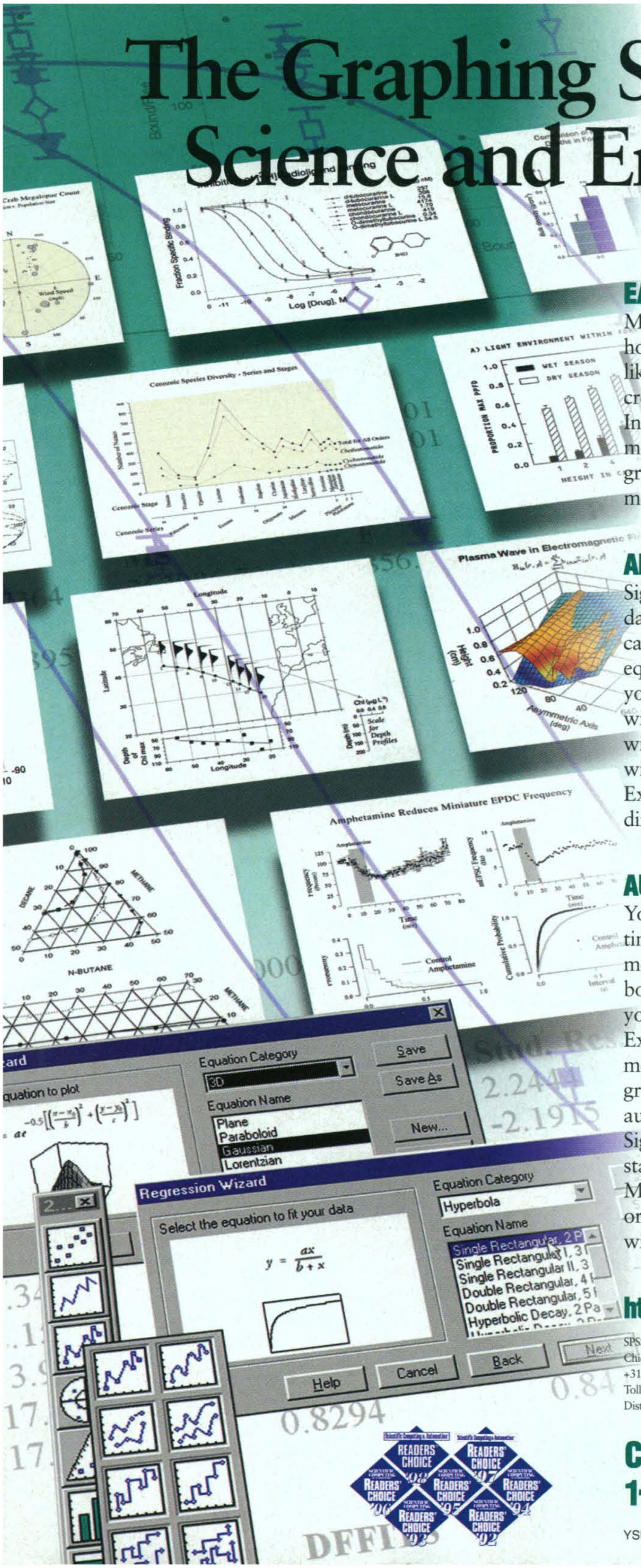

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