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SCIENCE

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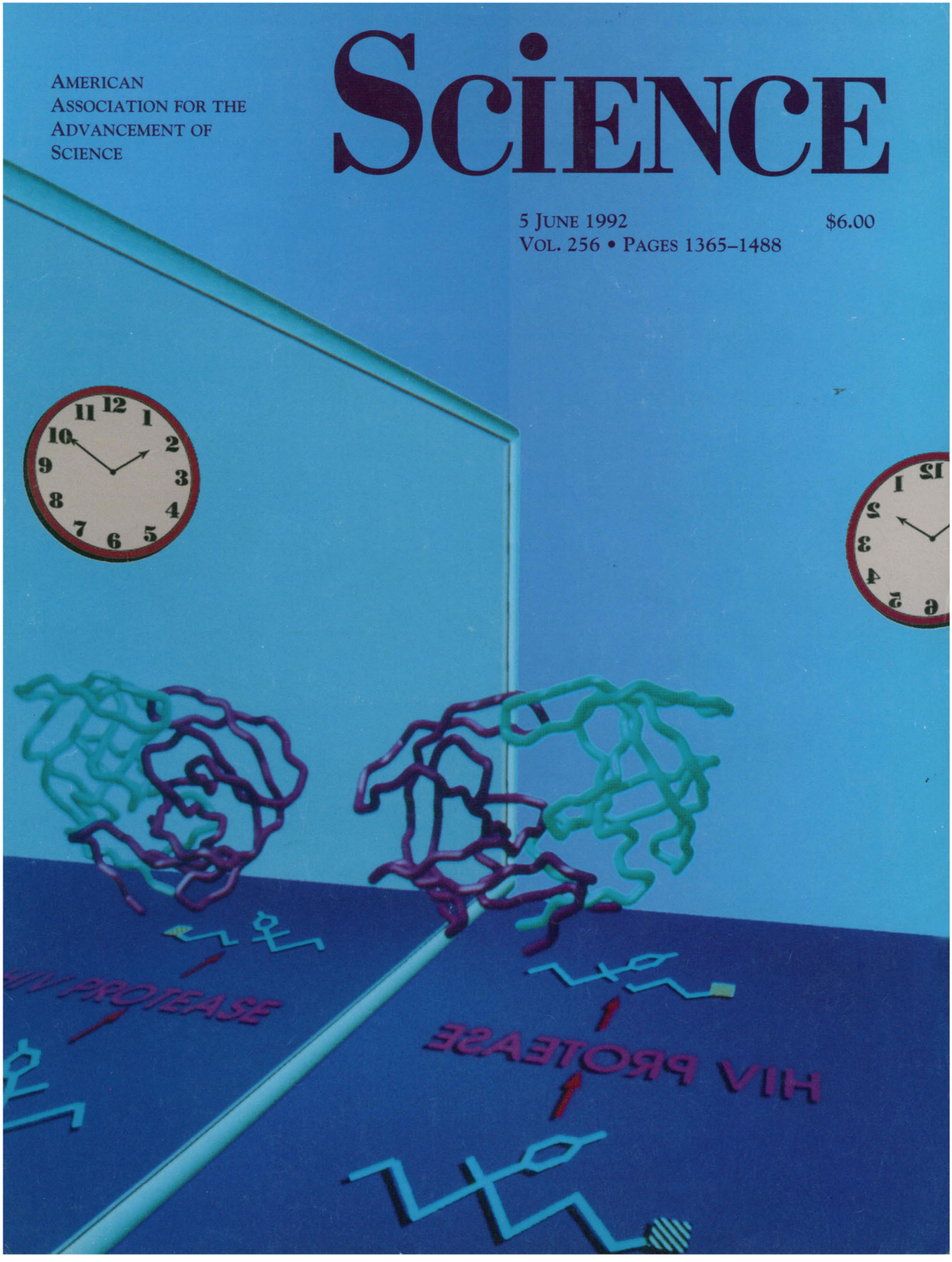

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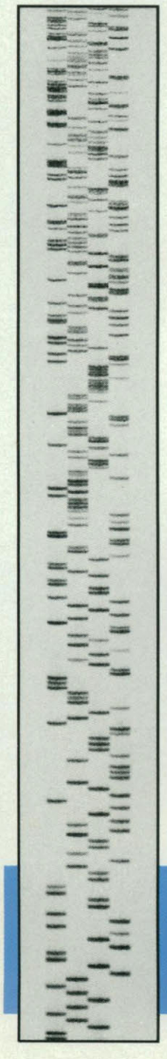

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Figure Legend : Autoradiograph of sequencing gel using the BaseAce Sequencer and the FeatherVolt 2000 power supply. 1.0 µg M13 ssDNA was labeled with S-35 ATP and run for 3 hrs at 65 watts on a 6% acrylamide (7M Urea, 1X TBE) gel.

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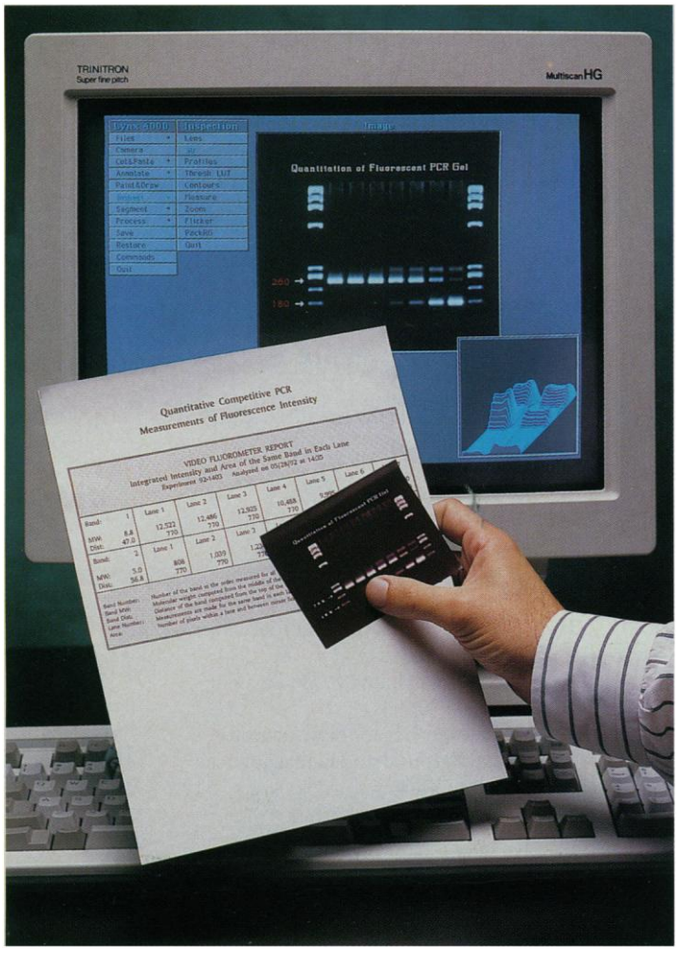

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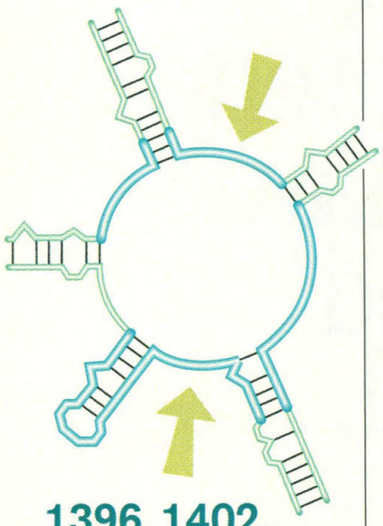


1396, 1402, 1416 & 1420
RNA makes peptide bonds and that's not all

NEWS & COMMENT

RESEARCH NEWS

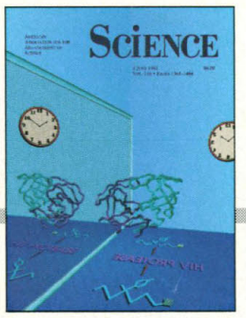
1392 & 1448 Knockout mice find favor with biologists

PERSPECTIVES

ARTICLES

DEPARTMENTS

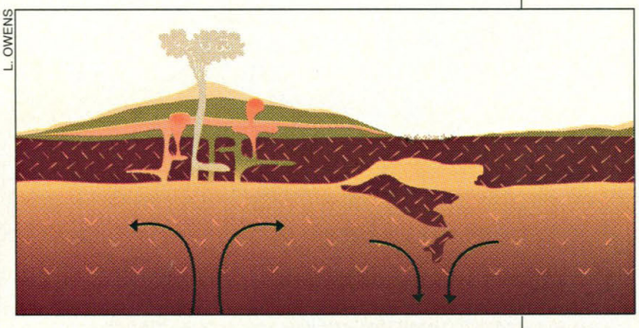
COVER



A "left-handed" enzyme, HIV-1 protease (shown in front of the mirror as a dimer), that contains D-amino acids has been chemically synthesized. It preferentially cleaves peptide chains of D-amino acids (reaction shown below the molecule). The chemically synthesized "right-handed" form (the L-enantiomer, shown in the mirror) has reciprocal chiral specificity and preferentially cleaves commonly occurring L-amino acid peptides. See page 1445 and the Perspective on page 1403. [Computer graphics modeling and photography: Arthur Olsen, Yng Chen, and Garrett Morris. Additional illustration: Diana DeFrancesco]

RESEARCH ARTICLES

REPORTS



L. OWENS

1405

Early formation of continents

◩ Indicates accompanying feature

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THIS WEEK IN SCIENCE

edited by PHIL SZUROMI

Ribosome as catalyst

Amino acids are assembled into proteins by the ribosome, which is made up of RNA molecules and proteins; Noller *et al.* (p. 1416) present evidence that RNA molecules catalyze peptide bond formation (peptidyl transferase activity) in the ribosome. Piccirilli *et al.* (p. 1420) show that RNA enzymes (ribozymes), which are usually thought of as acting on phosphorus-containing groups, can hydrolyze aminoacyl esters. Pace (p. 1402) comments on how these results expand our view of catalytic RNA. Implications of this work for the RNA world (prebiotic chemistry) are discussed in a news story by Waldrop (p. 1396).

Nanocrystal melting

As the size of a crystal decreases, its physical properties change. Small crystals (10 to 100 angstroms) of metals or frozen inert gases melt at temperatures well below the bulk melting point. In contrast to these materials, semiconductors are characterized by highly directional and covalent bonding. However, Goldstein *et al.* (p. 1425) found that crystals of cadmium sulfide similarly show dramatic melting-point depressions with decreasing size. This behavior is of both practical and theoretical interest: new ways to prepare defect-free materials and thin films at lower temperatures may be one result.

Just as important

Although small earthquakes, because they occur frequently, have been of critical importance for the identification of buried structures and characterization of regional strain, they appear to be insignificant in terms of seismogenic energy release and displacement on faults, that is, for earthquake hazards. Hanks (p. 1430), however, uses earthquake scaling relations to show that in terms of redistributing the tectonic forces driving motion on faults, the many small earthquakes are just as important as the few large ones. The relation has several possible implications for earthquake predictions.

Silica scale

The record of Pleistocene climate changes has been based heavily on oxygen isotope variations of foraminiferal calcite preserved in deep sea cores. The problem is that the ratio of ^{18}O to ^{16}O in the calcite reflects the paleotemperature of seawater and its isotopic composition, which depends primarily on the amount of water stored in ice caps on continents. Shemesh *et al.* (p. 1434) show that these two effects can be resolved by also analyzing biogenic silica of diatoms in the cores because the temperature-dependent fractionation of oxygen isotopes is different in silica than calcite. Data from a South Atlantic core show that glacial-age sea surface temperatures there were not significantly different from Holocene values.

Sexual antagonism

Evolution of sex chromosomes may have proceeded through sexually antagonistic (SA) genes, which are favored by selection in one sex but disfavored in the other. Rice (p. 1436) describes artificial selection studies in *Drosophila melanogaster* in which an autosomal marker (a dominant eye-color gene) was made to segregate as if it were a female sex-determining gene. Theory predicts that this gene should attract genes favorable to females but detrimental to males. Substantial buildup of such genetic variation was found after 29 generations. These results support models proposed for the evolution of suppressed recombination between primitive sex chromosomes and also indicate that SA genes may be common in natural genetic pools.

Big matchup

Alignments of protein sequences, which are useful for determining protein homology, for predicting protein structure, for interpreting genomic data, and for resolving phylogenetic issues, can now be based on an analysis that makes use of the entire protein database. Gonnet *et al.* (p. 1443) point out that the theory for such an analysis is not new; the problem has been that using the Needleman-Wunsch algorithm becomes prohibitive in terms of computer time as the number of sequences analyzed is increased. By reorganizing the data (indexing it on what is called a patricia tree), a complete analysis could be performed: an attempted alignment of every subsequence was made with every other subsequence. The analysis produces mutation matrices as well as models for scoring sequence gaps.

LYME DISEASE

Brown and Lane (p. 1439) show that transmission of Lyme disease in California differs from that reported for the eastern United States and involves a nonhuman-biting tick; see news story by Barinaga (p. 1385).

Knocked out T cells

T cells in vertebrates express either an $\alpha\beta$ T cell receptor (TCR) or a $\gamma\delta$ TCR. In order to resolve how these two forms relate to one another in development and to study the influence of $\alpha\beta^+$ T cells on B cell development, Philpott *et al.* (p. 1448) studied mice that were homozygous for a disrupted TCR α gene. Although $\alpha\beta^+$ T cells were eliminated in these mice and the thymic medullae were absent, $\gamma\delta^+$ T cells were still present in normal numbers and the number of B cells in the spleen increased. In a news story, Travis (p. 1392) overviews this and other uses of knockout mice.

Nontransformed T cells

Tumor cells lines are often used as models for gene regulation because they are easily grown and manipulated, but in the case of T cells, some important cellular responses, such as proliferative responses to antigen, are exhibited only by nontransformed cells. Kang *et al.* (p. 1452) were able to overcome some of the difficulties in using a nontransformed T cell clone, such as resistance to DNA transfection and the need for stimulation by antigen-presenting cells. The T cell clone was used to study regulation of the interleukin-2 (IL-2) gene by the p50 and p65 subunits of the DNA binding protein NF-κB. Homodimers of p50 appear to inhibit IL-2 expression; antigen stimulation is needed to synthesize a protein that causes p50 to be in a non–DNA binding form, allowing heterodimeric p50-p65 complexes to stimulate transcription.

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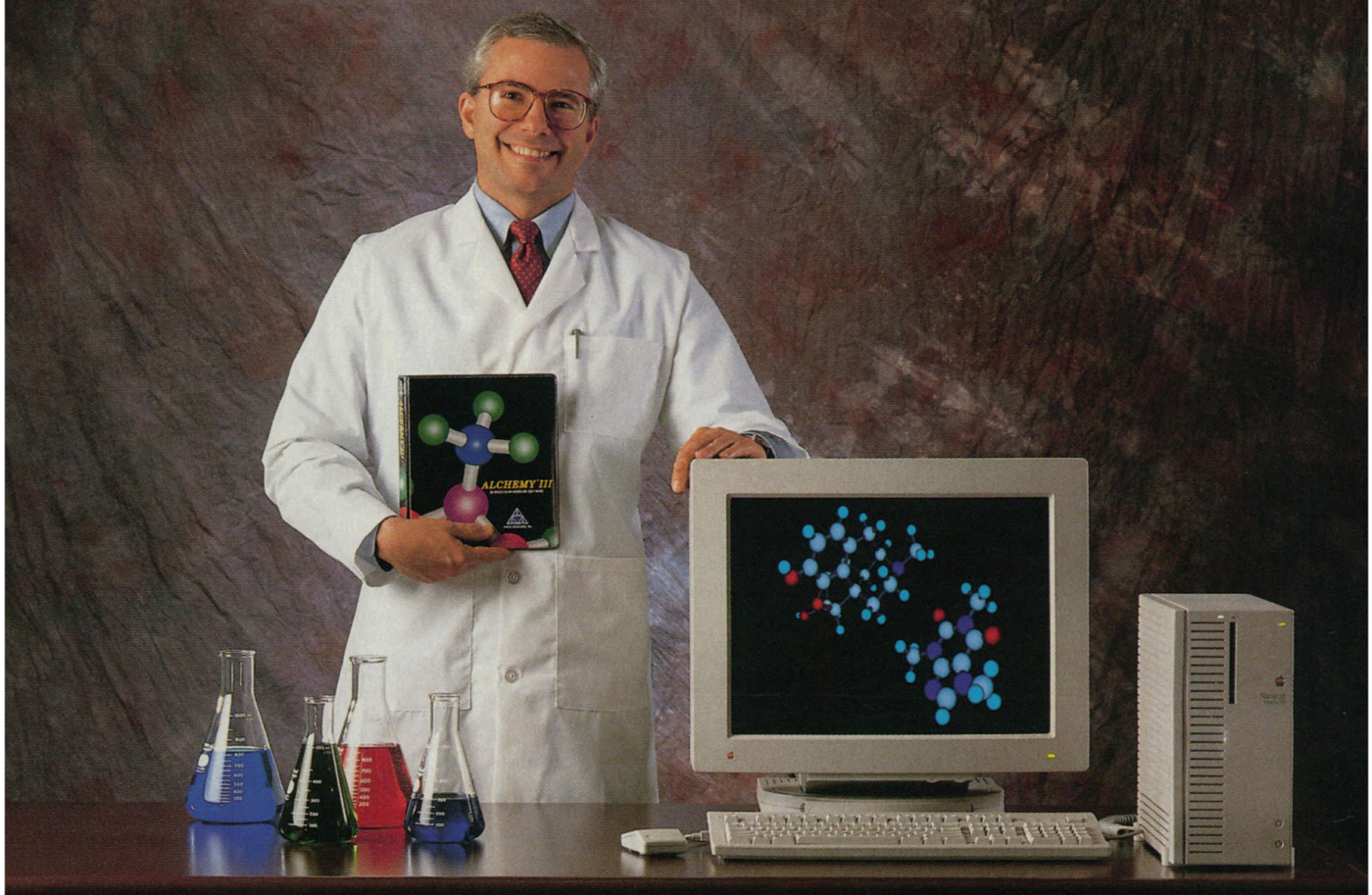

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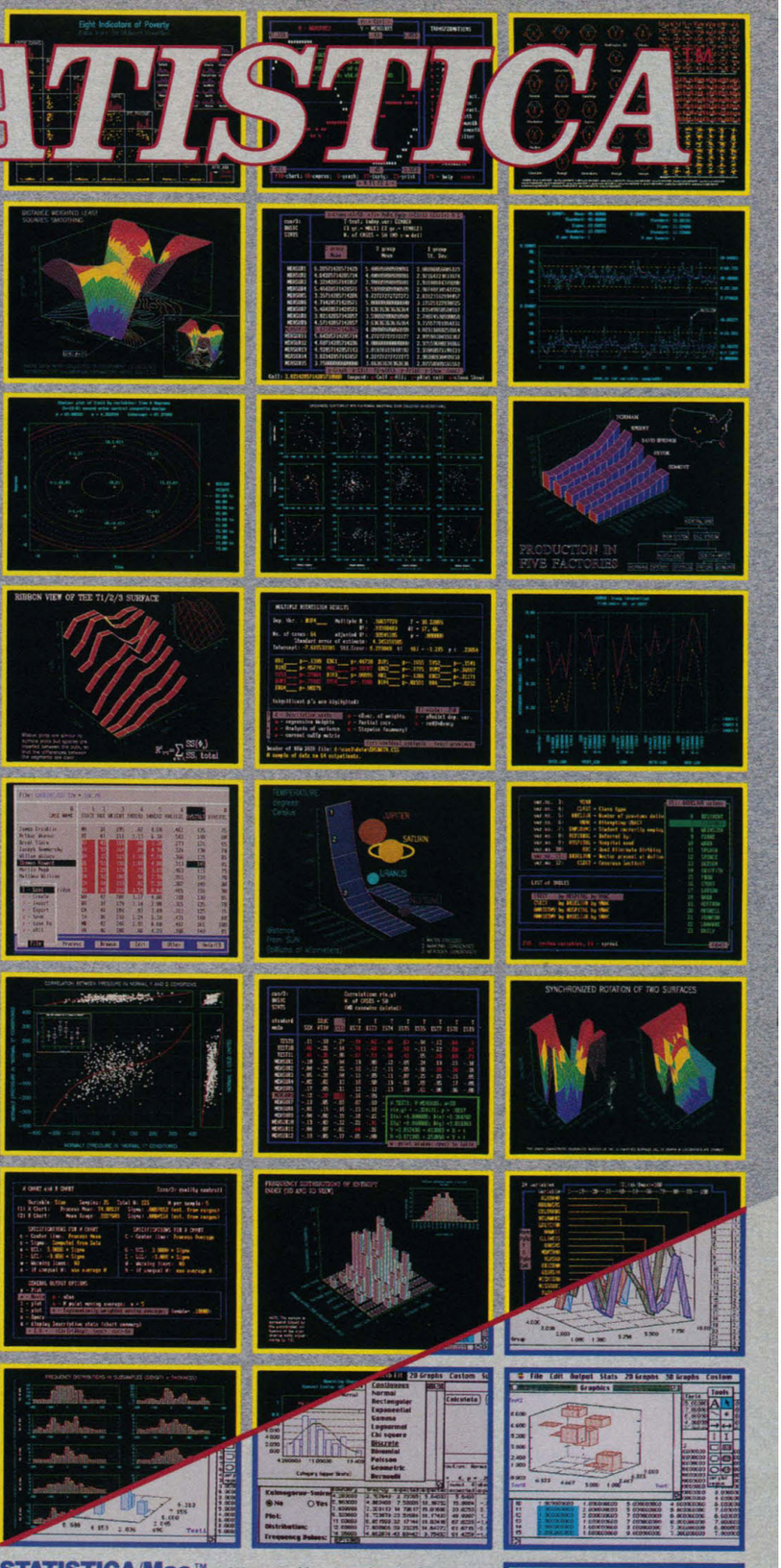

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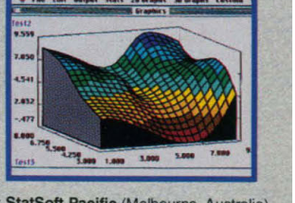

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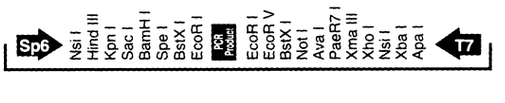

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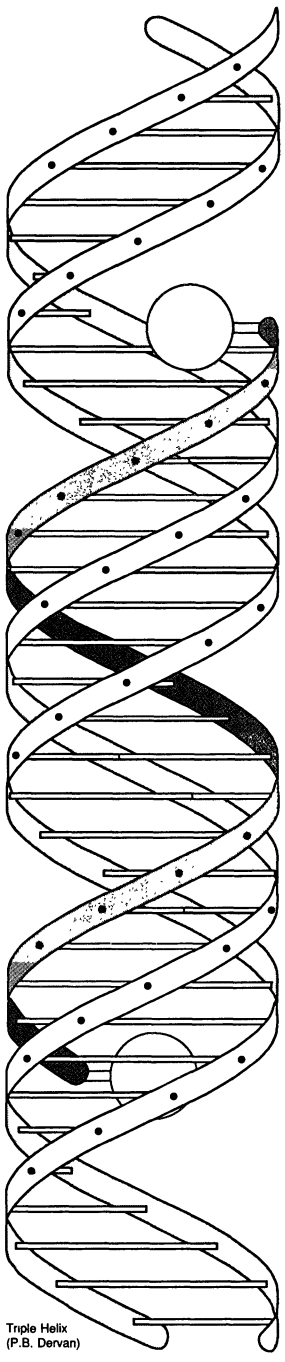

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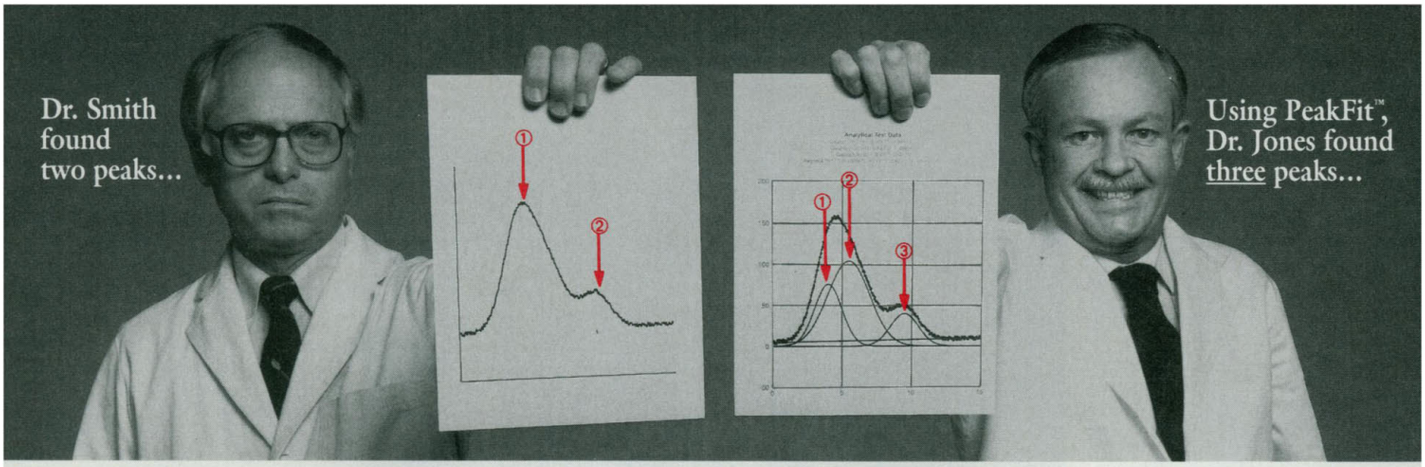

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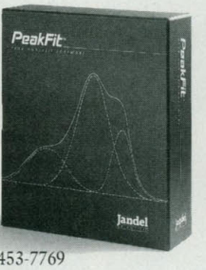

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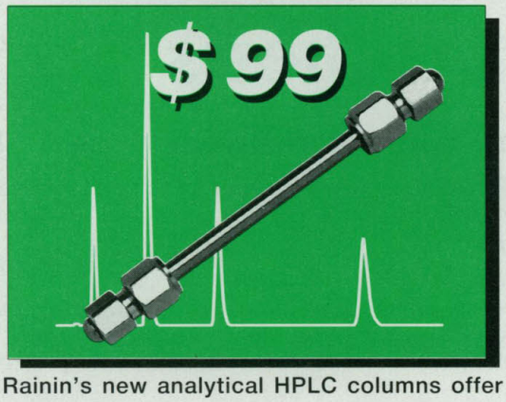

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Program

Mapping

Bertrand R. Jordan (chair), *INSERM-CNRS*

Jean Weissenbach, *CNRS, Inst. Pasteur,* "The second generation of human linkage maps: The Genethon linkage mapping project"

Daniel Cohen, *Ctr. d'Etude du Polymorphisme Humain*

Malcolm Ferguson-Smith, *Cambridge Univ.*, "Gene order by FISH and FACS"

Cassandra L. Smith, *Univ. of California, Berkeley,* "Progress and new approaches in making physical maps of human chromosomes"

Yoshihide Hayashizaki, *Natl. Cardiovascular Research Inst.*, "Restriction landmark genomic scanning method and its application"

Human Genetic Diversity

P. Fasella* (chair), *Comm. of European Communities*

L.L. Cavalli-Sforza, *Stanford Univ.*, "Genetic diversity and history of the human species"

Alberto Piazza, *Univ. of Torino,* "Population genetics of Europe"

Kenneth Kidd, *Yale Univ. School of Medicine*

Svante Paabo, *Univ. of Munich,* "Ancient and modern DNA sequences as a tool to reconstruct human history"

Julia Bodmer, *Imperial Cancer Research Fund,* "HLA allele and haplotype frequencies in world populations"

Model Organisms

Marc van Montagu, *Univ. of Ghent,* "The *Arabidopsis* genome"

Piotr Slonimski, *CNRS,* "The esoteric, elusive, but conspicuous genes of *Saccharomyces cerevisiae*"

Eric Lander, *Whitehead Inst.*

Michael Ashburner, *Cambridge Univ.*, "Genome mapping in *Drosophila*"

A.K. Raap*, *Univ. of Leiden*

Contributed Papers: Oral Presentations

(Speakers for this session will be chosen from among those submitting abstracts for poster sessions.)

Applications of the Human Genome Project

John Hardy*, *St. Mary's Hospital Medical School*

Yusuke Nakamura, *Japanese Fdn. for Cancer Research,* "The Human Genome Project and cancer genetics"

Ulf Landegren, *Univ. of Uppsala,* "Ligase-mediated gene detection"

cDNA Sequences and Intellectual Property

Lennart Philipson (chair), *EMBL*

J. Craig Venter, *Natl. Insts. of Health,* "Changing the pace of human gene discovery and public policy paradigms"

Kenichi Matsubara, *Osaka Univ.*, "Functional analyses of the human genome"

Rebecca Eisenberg, *Univ. of Michigan,* "Patenting the human genome"

Charles Auffray, *Inst. d'Embryologie du CNRS,* "The Genexpress cDNA Program: Towards an inventory of the repertoire of transcribed human sequences"

Andrei Mirzabekov, *Soviet Academy of Sciences,* "cDNA sequencing and sequence comparison by hybridization with oligonucleotide matrix: Advantages and implications"

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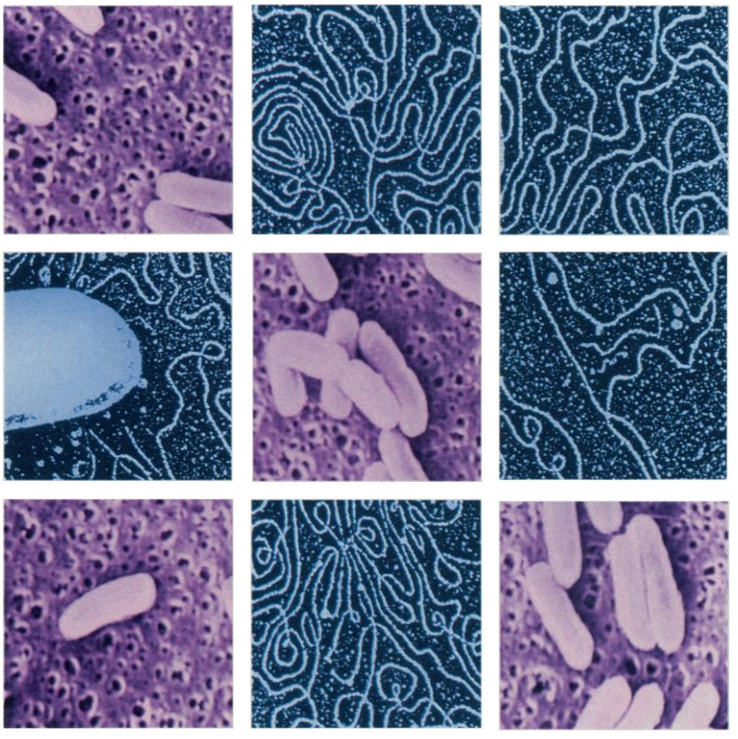

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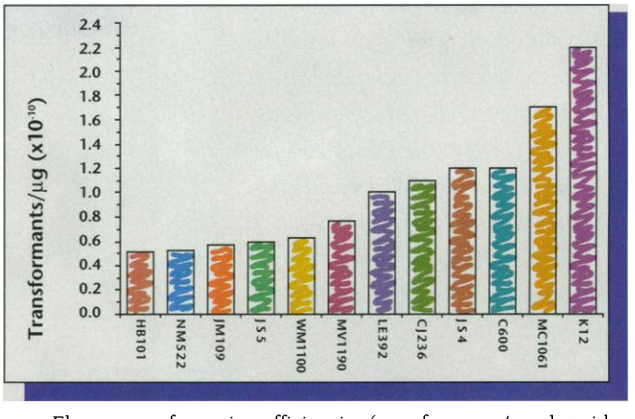

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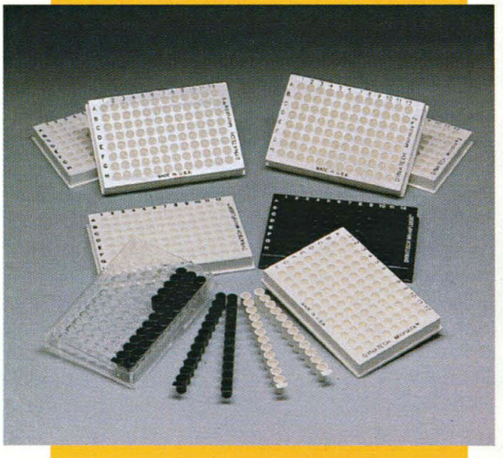

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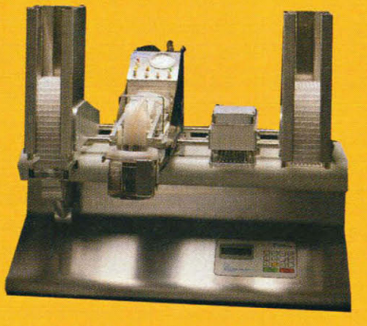

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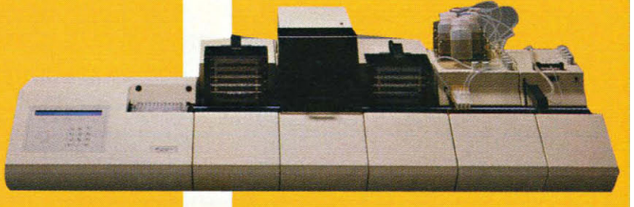

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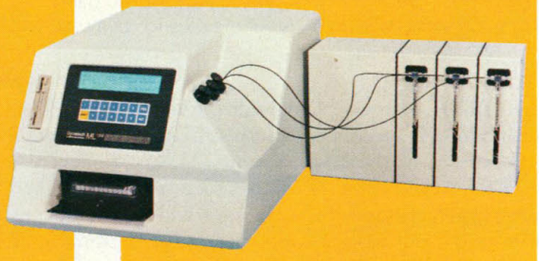

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