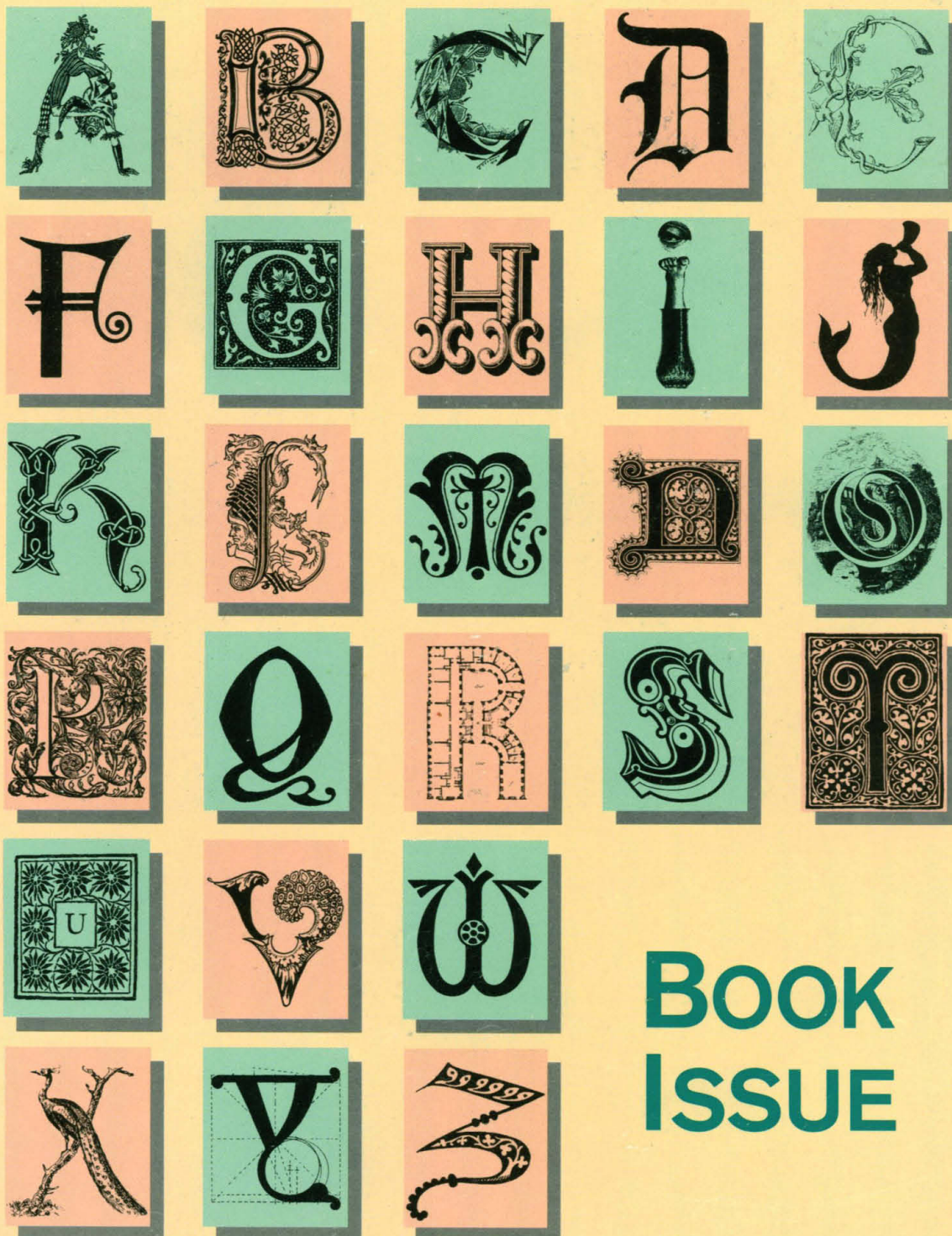


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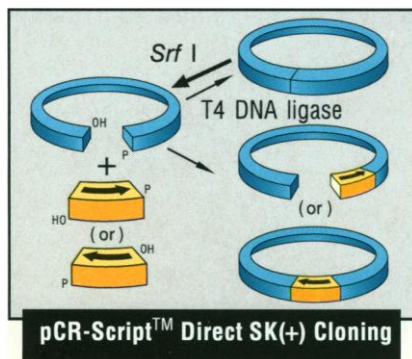
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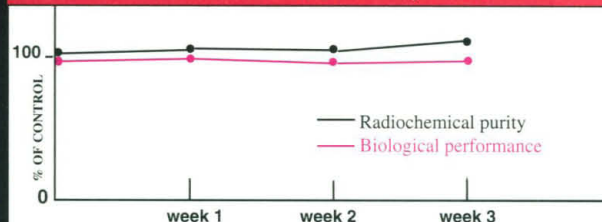
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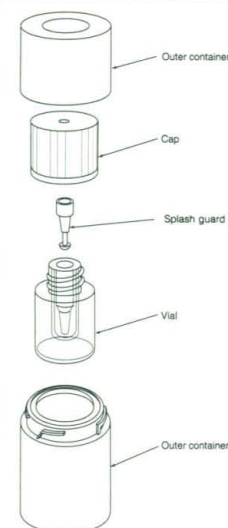
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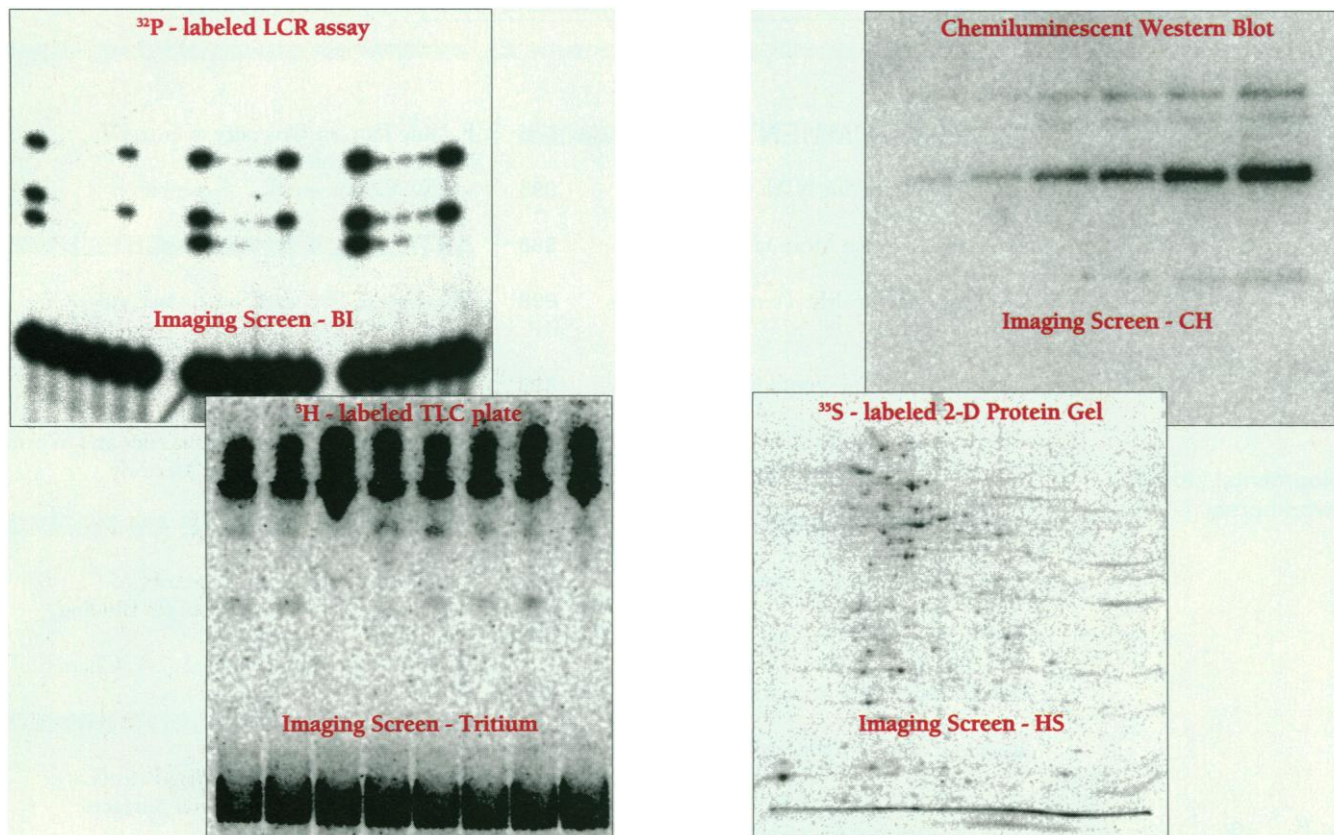
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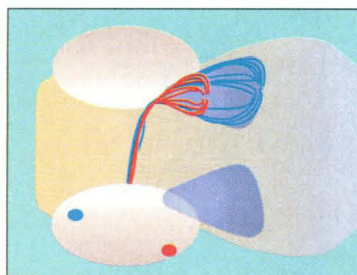
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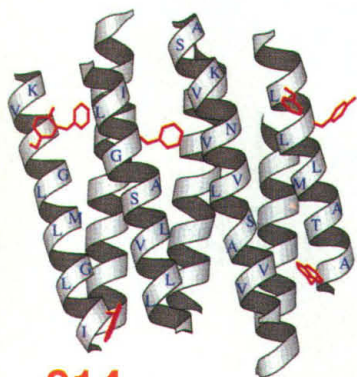
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904

Developmental biology's
new workhorse



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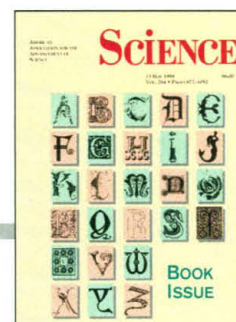
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COVER

From Antarctica and black holes to yeast genetics and zippers, a broad array of subjects are represented by the books covered in this special issue of *Science*. And in the opening group of essay reviews, some current and sometimes unsettling trends in thinking about

science and its place in the world at large are examined. A full listing of the books reviewed appears on page 981. [Cover design: C. Faber Smith. Letters A, C, E, G, and U from Mercury Archives/The Image Bank]



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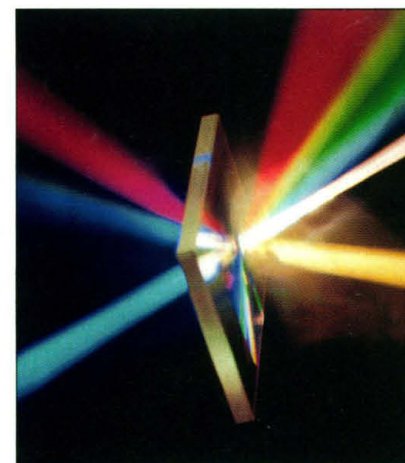
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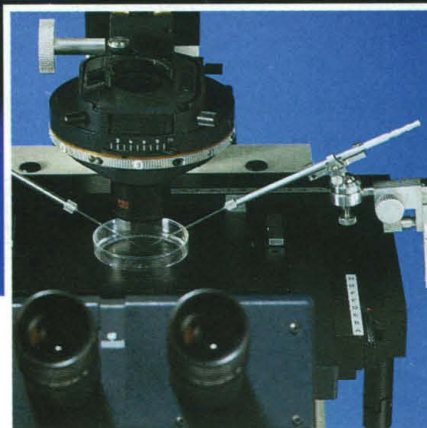
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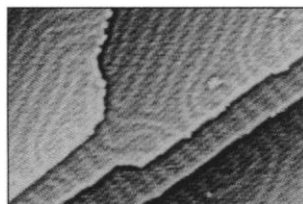
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A little on edge

When confined to small spaces, electrons reveal their quantum nature by exhibiting wave-like interference effects. Avouris and Lyo (p. 942) report the observation of quantum-size phenomena on epitaxially grown surface step edges and surface



islands. When the structures are made sufficiently small, quantum effects are apparent even at room temperature.

Fire and ice

Results from drill cores in and around Greenland are providing records of Holocene volcanism and the timing of the growth of the Greenland ice sheet. One means used to date the recent Greenland ice cores accurately is to correlate major dust and sulfate layers with known times of key volcanic eruptions. In turn, Zielinski *et al.* (p. 948; see Perspective by Simkin, p. 913) now use the detailed sulfate record from the GISP 2 core, which reflects primarily input of volcanic aerosols, to provide a record of volcanism back to 7000 B.C. A large number of eruptions evidently occurred between 7000 and 5000 B.C., only a few of which were known. When extensive glaciation began in Greenland has been uncertain. Larsen *et al.* (p. 952) describe ocean cores off the coast of Greenland that contain glacially derived debris dating back to the late Miocene, about 7 million years ago. Greenland glaciers likely reached the sea intermittently since this time.

Mediating transcriptional activation

The initiation by RNA polymerase II of both basal and regulated transcription requires the TFIID transcription factor, which consists of TBP (TATA binding protein) and multiple TAFs (TATA associated factors). Verrijzer *et al.* (p. 933) cloned and characterized a TAF from *Drosophila*, dTAFII150. Although no yeast homologs for TAFs have been identified, they find that this dTAFII150 contains a homolog in yeast, a gene called TSM-1, that is required for viability. Both dTAFII150 and TSM-1 associate with TBP and another TAF, TAFII250. Surprisingly, TAFII150 is a sequence-specific DNA binding protein that binds to sequences overlapping the transcription start site.

A walk in the park

Was the evolution of bipedality in hominids 5 to 12 million years ago in Africa an adaptive response driven by a changing environment from forest to open grasslands? Kingston *et al.* (p. 955) use carbon isotope data in key soil sequences to track vegetation changes in Kenya during this critical period and address this question. The data show that both forests and grasslands were present throughout and that a succession to predominantly grassland did not occur during this time interval.

Firing practices

Neuronal activity that accompanies learning and memory processes can increase the strength of synaptic connections, but less is known about how activity changes the intrinsic electrical properties of neurons. These electrical properties are determined by the mixture of ion channels in the neuron's cell membrane. Turrigiano *et al.* (p. 974) found that placing lobster stomatogastric neurons in culture and thus isolating them from their normal inputs changed their electrical activity from tonic firing (firing at one frequency) to firing in bursts. Exposed to artificial stimulation that mimicked the in vivo inputs reversed

this effect. Regulation of these intrinsic electrical properties may be an important aspect of neuronal plasticity.

Kept in house

Maturation of small nuclear RNAs (snRNAs) involved in the spliceosome usually occurs only after export to the cytoplasm. These RNAs are trimethylated at their m⁷G caps to m^{2,2,7}G and are then transported back into the nucleus by a process that requires binding to an Sm protein. Terns and Dahlberg (p. 959) found that the precursor to the nucleolar U3 snRNA is not transported to the cytoplasm and that all of its processing occurs in the nucleus.

Host's duties

Cytotoxic T cells can recognize tumor cell antigens but tumors usually grow nonetheless. Current models of antigen presentation would suggest that priming of CD8⁺ cells, which are restricted to major histocompatibility complex class I molecules, would be performed by the tumor cell itself. However, Huang *et al.* (p. 961) show that the tumor antigens are transferred and presented by antigen-presenting cells of the host. This re-

sult suggests that antigen matching may be less of a problem for developing tumor vaccines.

Missing links

The growth factor receptor-bound protein 2 (Grb2) contains a Src homology 2 (SH2) domain flanked by two SH3 domains. Grb2 links proteins that bind to its SH2 domains (tyrosine phosphorylated receptors or other proteins) to Sos, a Ras activator that binds to its SH3 domain. Fath *et al.* (p. 471) discovered an isoform of Grb2, called Grb3-3, that lacks a portion of the SH2 domain. Grb3-3 failed to bind the phosphorylated epidermal growth factor (EGF) receptor but still binds Sos. Grb3-3 appears to function as a dominant negative inhibitor of Grb2. Overexpression of Grb3-3 inhibited EGF-induced activation of Ras, and microinjection of Grb3-3 into cells caused apoptosis. Grb3-3 is particularly abundant in the thymus, where it might function to regulated programmed cell death.

Terminal remodeling

A complex intracellular machinery accounts for the extrusion of an axon from the neuronal cell body and its eventual maturation into a neurotransmitter-releasing specialization, the presynaptic terminal. Synapsins are phosphoproteins that are associated both with the cytoskeleton and synaptic vesicles. Ferreira *et al.* (p. 977) show that inhibition of synapsin II expression in culture resulted in an abnormal distribution of actin filaments and reduction in synaptic vesicle proteins, implicating synapsin II in the early stages of synaptogenesis.

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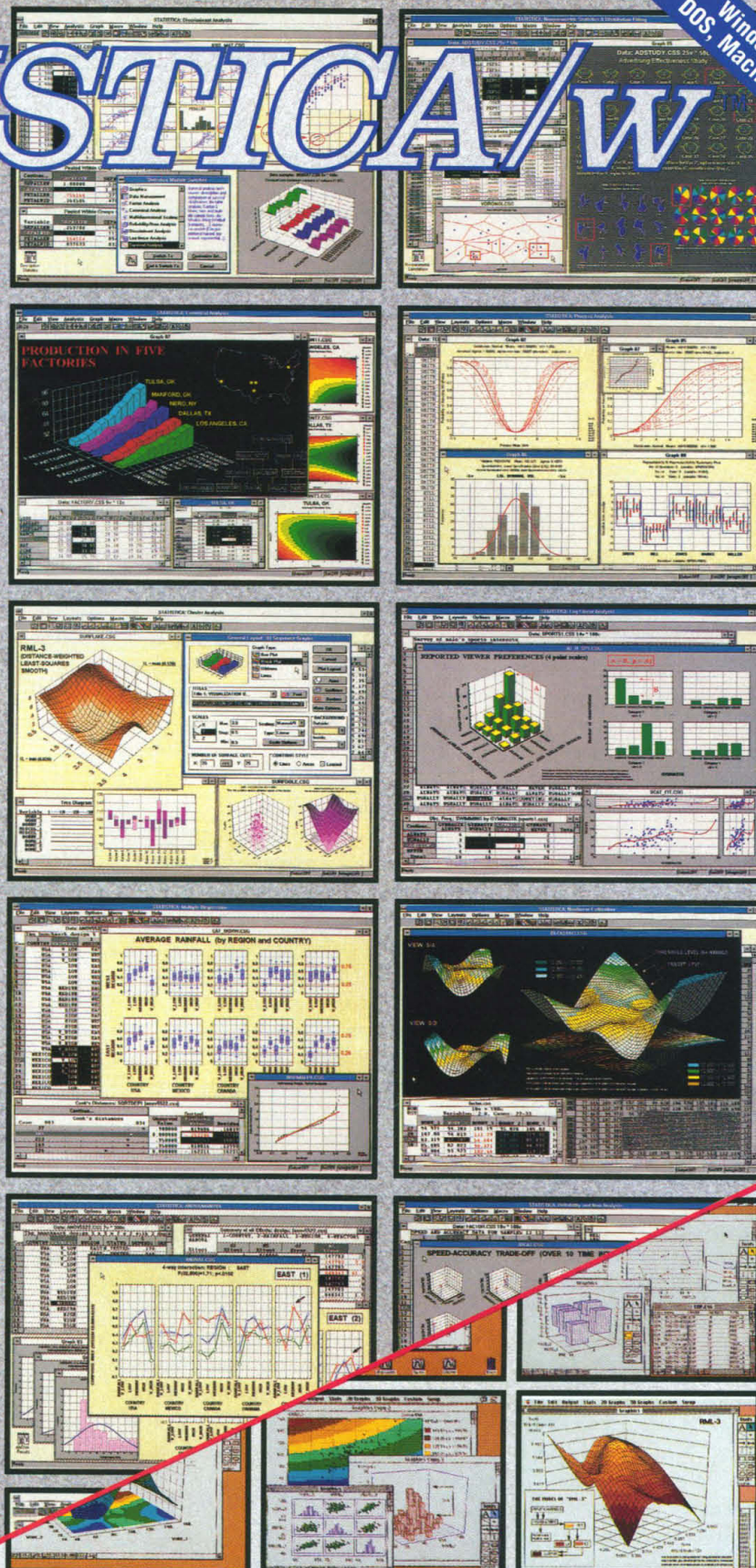


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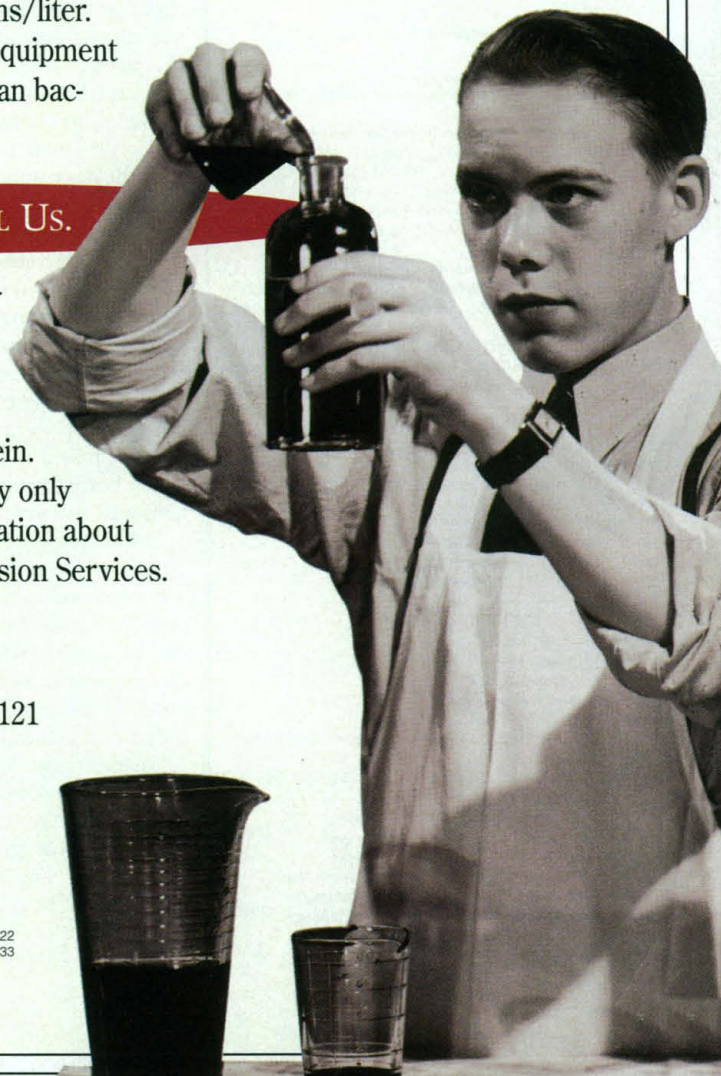


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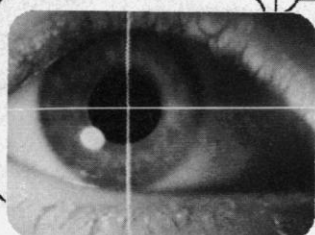


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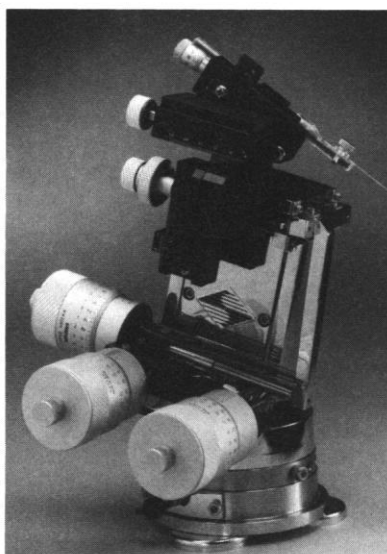
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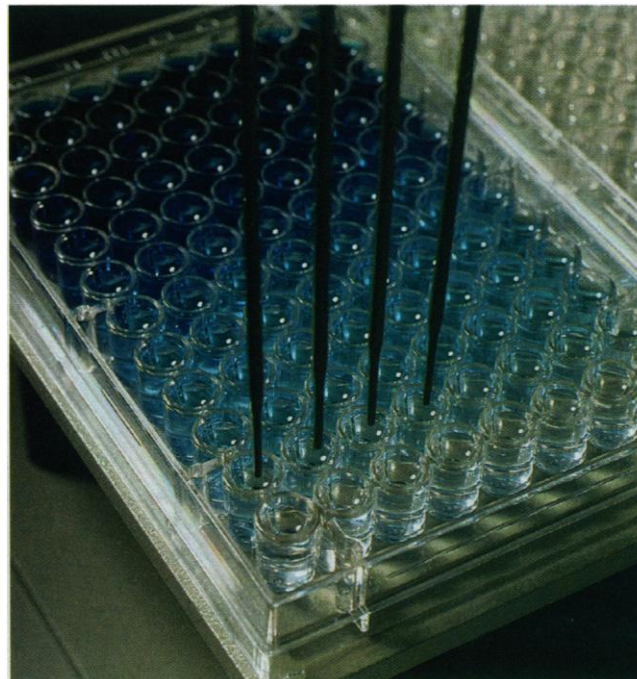
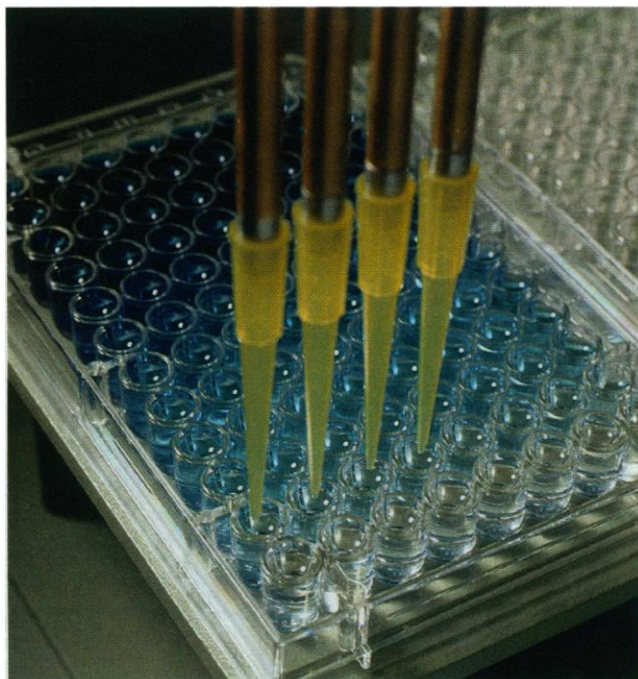
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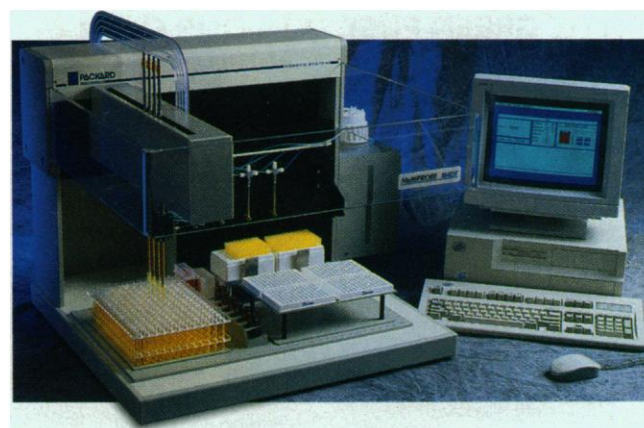
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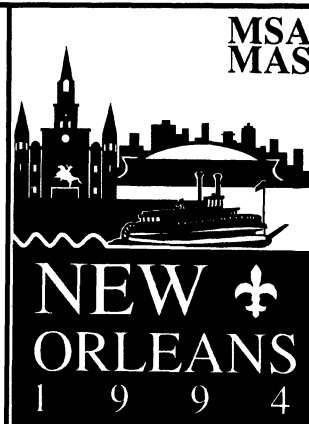
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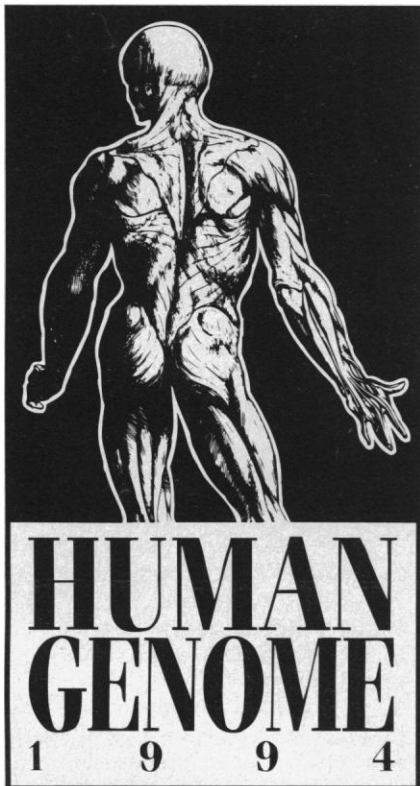
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CONFERENCE AGENDA

SUNDAY, OCTOBER 2

Welcoming Reception

MONDAY, OCTOBER 3

Plenary Session I: Genome Analysis – The New Frontier

“Human Gene Identification by Positional Cloning”

Dr. Francis Collins, National Center for Human Genome Research

“Genetic Basis of Human Colorectal Cancer”

Dr. Bert Vogelstein, Johns Hopkins Oncology Center

“Mapping Genes and Genomes: Genetic Dissection of Complex Traits”

Dr. Eric Lander, Whitehead Institute/MIT

“Human Genome Diversity”

Dr. Mary Claire King, University of California, School of Public Health

“Manipulating Cancer Genes in the Mouth”

Dr. Harold Varmus, National Institutes of Health

“Intellectual Property: DNA and its Offspring”

Dr. Kate Murashige, Morrison & Foerster

“Presymptomatic Diagnosis of Self and Progeny”

Dr. C. Thomas Caskey, HUGO

Concurrent Sessions

M1 *“New Methods of DNA-Based Diagnosis”*

Dr. Stephen P.A. Fodor, Affymetrix, Inc.

M2 *“Human Gene Identification”*

Dr. Kay E. Davies, Institute of Molecular Medicine, University of Oxford

M3 *“Social and Scientific Issues in Genetic Testing”*

Dr. Nancy Wexler, Hereditary Disease Foundation

M4 *“Gene Therapy”*

Dr. Inder M. Verma, The Salk Institute

TUESDAY, OCTOBER 4

Plenary Session II: Development and Signal Transduction

Special Guest: Donna Shalala, U.S. Department of Health and Human Services

“MYOD & Myogenesis”

Dr. Harold Weintraub, Fred Hutchinson Cancer Research Center

“Genome Analysis in the Mouse”

Dr. Shirley M. Tilghman, Princeton University

“Pax: Genes for Mice and Men”

Dr. Peter Gruss, Max Planck Institute of Biophysical Chemistry, Germany

“From an Interferon Clone to the Regulation of Oncogenesis”

Dr. Tadatsugu Taniguchi, Institute for Molecular and Cellular Biology, Osaka University

“C. elegans Genome Project”

Dr. Richard Wilson, Washington University Medical School

“Small GTPases – Switching on Biological Responses”

Dr. Alan Hall, MRC Laboratory for Molecular Cell Biology, U.K.

Concurrent Sessions

T1 *“Gene Targeting”*

Dr. Elizabeth Robertson, Harvard University

T2 *“Sequence to Function”*

Dr. Temple F. Smith, Biomolecular Engineering Research Center, Boston University

T3 *“Education and the Human Genome Project”*

Dr. Paula Gregory, National Center for Human Genome Research, NIH

T4 *“Chromatin Structure and the Regulation of Gene Expression”*

Dr. Gary Felsenfeld, Laboratory of Molecular Biology, NIH

WEDNESDAY, OCTOBER 5

Plenary Session III: Mapping

“Toward the Ultimate Generation of an Integrated Map of the Human Genome”

Dr. Daniel Cohen, C.E.P.H., France

“Application of High Resolution Genetic Maps to Studies of Common Disorders”

Dr. Jeffrey C. Murray, University of Iowa

“Yeast Genome Project”

Dr. André Goffeau, Université Catholique de Louvain, Unité de Biochimie Physiologique

“The Drosophila Genome Project – a Progress Report”

Dr. Gerald M. Rubin, University of California

“Status and Prospects for the Complete Human Genome Sequence”

Dr. Richard A. Gibbs, Baylor College of Medicine

“High Speed DNA Sequencing: Present and Future Technologies”

Dr. Lloyd M. Smith, University of Wisconsin

“Towards a Complete Set of Human Genes”

Dr. J. Craig Venter, The Institute for Genomic Research

Plenary Session IV: Mapping and Applications

“Vertically Integrated Mapping and Sequencing of Human DNA”

Dr. Maynard Olson, University of Washington School of Medicine

“Interpreting Genes and Genomes”

Dr. David J. Lipman, NIH, National Library of Medicine

“Some Applications of a Genome Library”

Dr. Melvin Simon, California Institute of Technology

“Huntington Disease”

Dr. James F. Gusella, Massachusetts General Hospital

“Ancient DNA”

Dr. Svante Pääbo, Zoologisches Institut, Universität München

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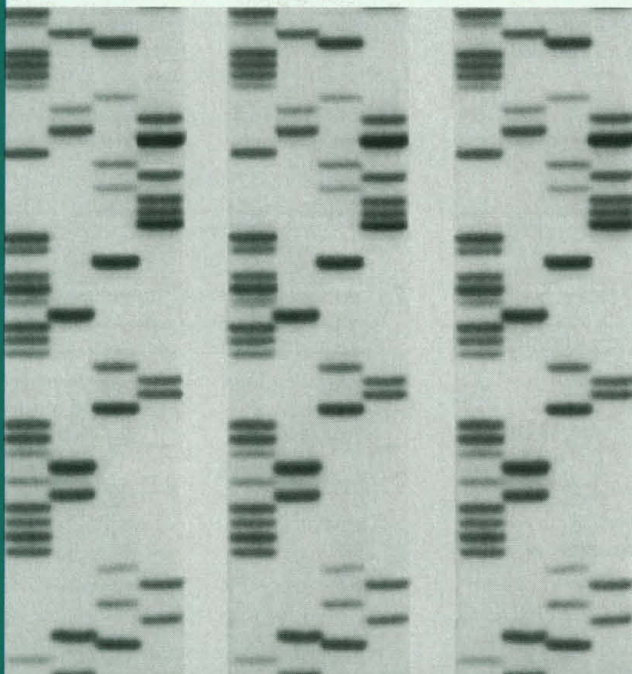
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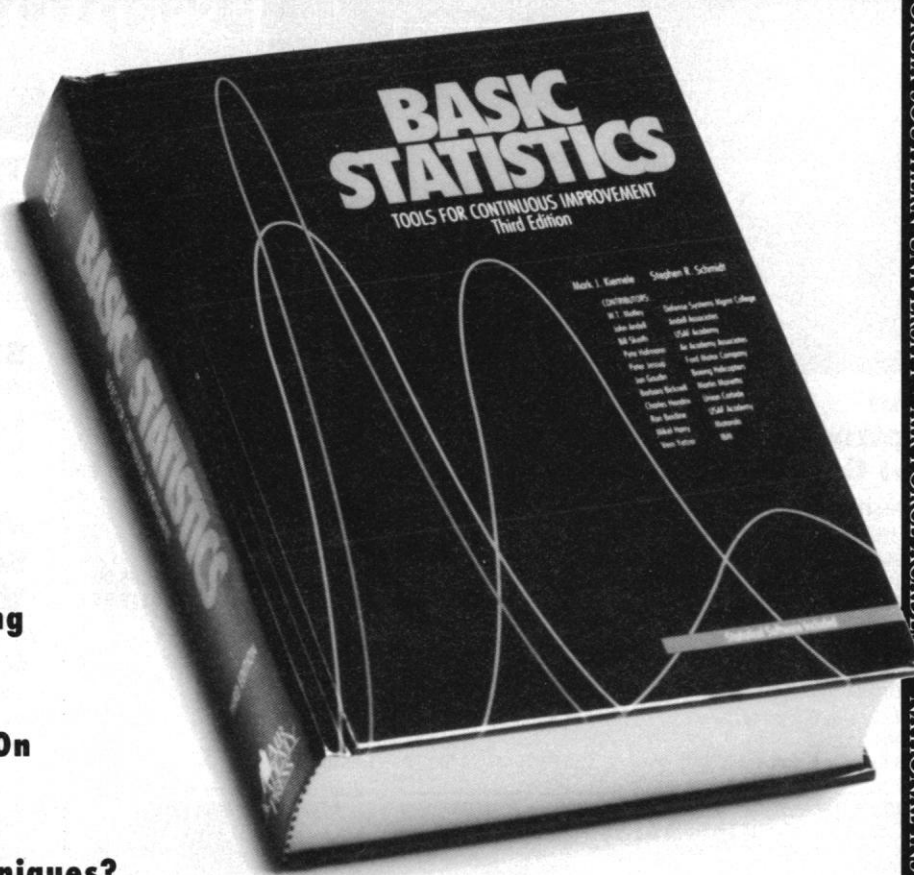
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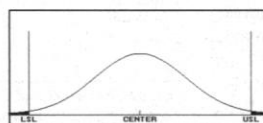
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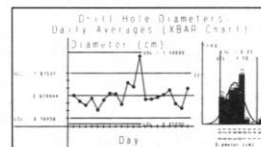
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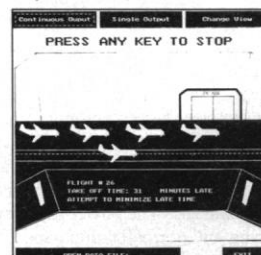
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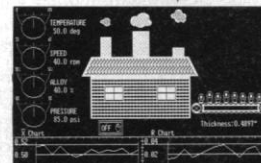
C_p DEMO: Calculates process capability, defects per million and sigma level.



SPC Expert: An artificial-intelligence based expert system that constructs control charts and interprets them.



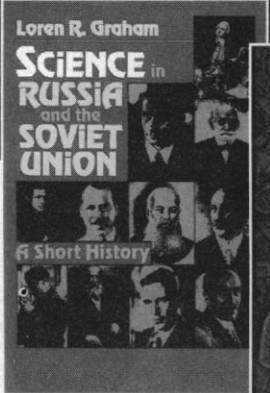
AIRSIM: An animated airline departure simulator for practicing SPC, DOE, and C_p calculation.



FACTSIM: An animated nut factory simulator for practicing SPC, DOE, and C_p calculation.

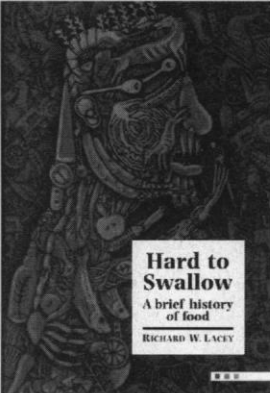
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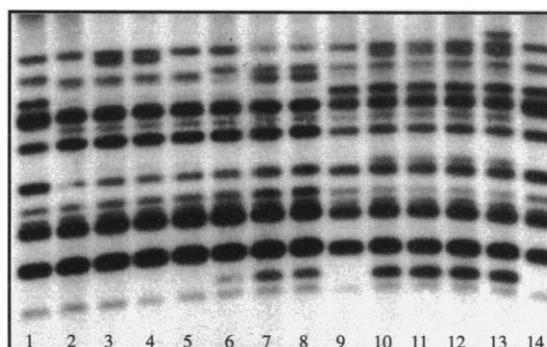
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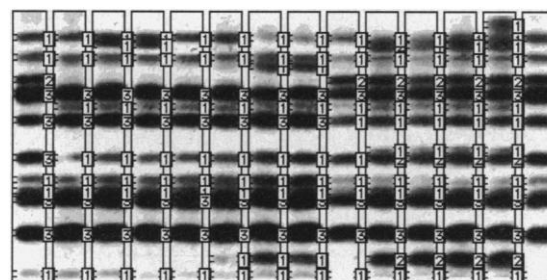
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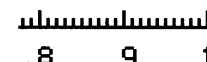
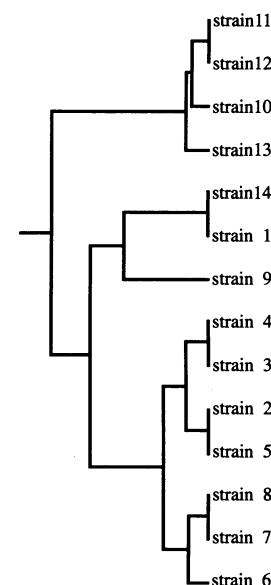
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Original Southern blot of *Candida albicans* strains fingerprinted with the Ca3 probe. Note the linear distortion (curve) along the horizontal axis.

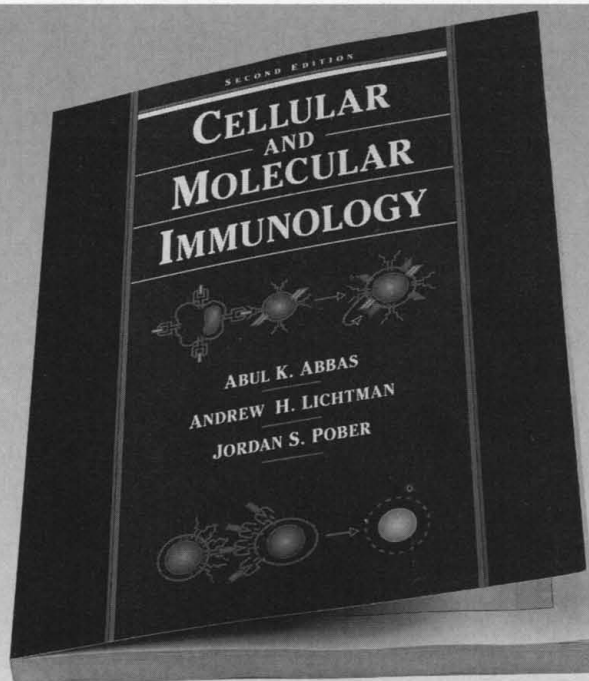


The above *Candida albicans* fingerprinting gel was unwarped and aligned. Bands and intensities were then automatically assigned by DENDRON® based upon the loading factors in the individual lanes.



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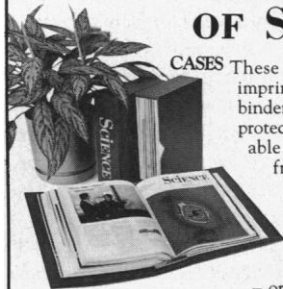
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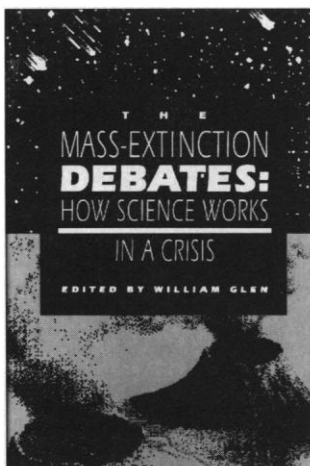
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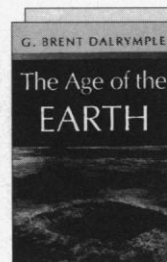
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