THE DAWN OF A NEW ERA IN TRANSFORMATION EFFICIENCIES

THE HIGHEST-EFFICIENCY CHEMICALLY COMPETENT CELLS AVAILABLE

3-5 x 10^9 colonies/µg

Stratagene has broken the 1 x 10^9 barrier for competent E.coli! We did it by genetically modifying our Epicurian Coli® XL1-Blue and XL1-Blue MRF' cells. The result is our new XL2-Blue and XL2-Blue MRF' ultracompetent cells,* which achieve transformation efficiencies as high as 5 x 10^9 transformants/µg of plasmid control DNA. To maintain these ultrahigh efficiencies, we package the cells in convenient single-use aliquots that eliminate freeze/thaw cycles.

The 3- to 5-fold increase in efficiency means more colonies per transformation reaction. The XL2-Blue ultracompetent cells are ideal for plasmid library construction. The highest possible efficiency also may be critical when starting DNA concentration is very low and when performing difficult ligations, as in multifragment, blunt-ended and PCR** cloning. These same advantages apply to our new SURE® 2 supercompetent cells,* which offer efficiency of >1 x 10^9 transformants/µg of plasmid DNA.

* Patent pending
** The Polymerase Chain Reaction (PCR) process is covered by patents owned by Hoffmann-La Roche. Use of the PCR process requires a license.

### Transformation Efficiencies

<table>
<thead>
<tr>
<th>genealogy/µg</th>
<th>average of three lots</th>
</tr>
</thead>
<tbody>
<tr>
<td>1-10^9</td>
<td>XL2-Blue</td>
</tr>
<tr>
<td>2-10^9</td>
<td>XL2-Blue MRF'</td>
</tr>
<tr>
<td>3-10^9</td>
<td>DH5α</td>
</tr>
</tbody>
</table>

100 pg of pUC18 DNA 10 pg of pUC18 DNA

USA:
Corporate Headquarters
Telephone: (800) 424-5444
Telefax: (619) 535-0034

Germany:
Stratagene GmbH
Telephone: (06221) 400634
Telefax: (06221) 400639

United Kingdom:
Stratagene Ltd.
Telephone: (0223) 420955
Telefax: (0223) 420234

Switzerland:
Stratagene GmbH
Telephone: (01) 3641106
Telefax: (01) 3657707

An Era of Choice

The XL2-Blue and SURE 2 cells join Stratagene's full range of competent cells for many applications. Our popular XL1-Blue cells are now available as economical competent and subcloning-grade cells, for uses that do not require the highest efficiency. Our standard competent cells include those for stabilizing DNA and cloning toxic genes. Plus we offer electroporation-competent cells with efficiencies as high as 10^10 transformants/µg. The choice is yours.

New Custom Service

Stratagene has initiated a Custom Competent Cell Service that will prepare competent cells of any E. coli K-12 strain that is not commercially available. The service will provide a minimum of 50 x 200-µl aliquots of your strain of choice. Contact Stratagene's Technical Services Department for complete details.

- Epicurian Coli® XL2-Blue Ultracompetent Cells
  Catalog # 200150
- Epicurian Coli® XL2-Blue MRF' Ultracompetent Cells
  Catalog # 200151
- Epicurian Coli® SURE® 2 Supercompetent Cells
  Catalog # 200152
- Epicurian Coli® XL1-Blue Subcloning-Grade Competent Cells
  Catalog # 200130

INTERNET MAIL
tech_services@stratagene.com
The new standard in matched antibody pairs.

Endogen introduces the MiniKit™ For mouse cytokine quantitation.

What are MiniKits?
MiniKits™ are matched antibody pairs supplied with a cytokine standard. These matched components have proven utility for ELISA applications. The capture antibody is provided in coating buffer for application to standard 96-well microtiter plates. The detection antibody is biotinylated for ease of use with streptavidin-enzyme conjugates. The standard is lyophilized for stability.

<table>
<thead>
<tr>
<th>MiniKits™ Available</th>
</tr>
</thead>
<tbody>
<tr>
<td>• IL-2</td>
</tr>
<tr>
<td>• IL-3</td>
</tr>
<tr>
<td>• IL-4</td>
</tr>
<tr>
<td>• IL-5</td>
</tr>
<tr>
<td>• IL-6</td>
</tr>
<tr>
<td>• GM-CSF</td>
</tr>
<tr>
<td>• IFNγ</td>
</tr>
<tr>
<td>• TNFα</td>
</tr>
</tbody>
</table>

These three components and a detailed cytokine-specific instruction manual ensure that the Endogen MiniKit™ will provide you with efficient, sensitive ELISAs to quantitate mouse cytokines.

Economical.
Each MiniKit™ contains sufficient quantities of coating antibody, biotinylated detecting antibody and standard for up to forty 96-well microtiter plates, or 3840 determinations, including standard curves.

Technical Support.
Each MiniKit™ is supplied with a detailed, easy to follow, cytokine specific instruction manual containing recommended buffer recipes, suggested antibody concentrations, typical standard curves and other necessary information to ensure successful in-house optimization of each cytokine assay. Additionally, technical specialists knowledgeable in the development and optimization of mouse cytokine ELISAs are available to assist you. Call us today at 800-487-4885.

MiniKits™ from the people who know and make quality mouse cytokine ELISAs.
THIOFUSION™
THE FIRST SYSTEM FOR
Soluble Protein Expression

IN E. coli.

The ThioFusion™ Expression System from Invitrogen. Finally there is a way to express soluble recombinant protein in E. coli. Now solubilization and refolding of proteins that form inclusion bodies are a thing of the past. Recombinant proteins expressed in the ThioFusion™ Expression System are soluble, even at high levels.

THE IDEAL FUSION PARTNER.

The ThioFusion™ Expression System takes advantage of the unique properties of the E. coli protein thioredoxin. Thioredoxin expresses at levels as high as 40% of the total cell protein, localizes at sites in the E. coli cell called adhesion zones, and is stable at high temperature. These properties make thioredoxin the ideal fusion partner. The plasmid vector, pTrxFus, the key to the ThioFusion™ System, carries the entire thioredoxin gene along with the strong P1 promoter to drive expression. In addition, an enterokinase cleavage site, engineered between thioredoxin and the protein of interest, allows removal of the fusion to restore the native protein.

FAST, SIMPLE PURIFICATION.

The ThioFusion™ System gives you two simple ways to purify your fusion protein. Osmotic shock releases proteins accumulated at adhesion zones into the medium. Heat treatment denatures most native proteins leaving some thioredoxin fusion proteins intact. Both methods are fast and effective.

The ThioFusion™ Expression System (cat. no. K350-01) is the first and only system designed for the expression of soluble recombinant proteins in E. coli. To learn more about the next step in E. coli protein expression, contact Invitrogen today!

1-800-955-6288

European Headquarters:
Invitrogen BV
De Schelp 28, 9251 NV Lelie
The Netherlands
Tel. (0) 5945-15175
Fax: (0) 5860-15312

Toll free Telephone Numbers
The Netherlands 06-0228848
Belgium 076-111173
Germany 030 8102 43
Switzerland 105-1906
Austria 0900-8117

UK Tel: +44 (0)333 330174  FAX: +44 (0)333 333420
France 05 80 72 49
Sweden 050 720149
Norway 800 11003
Denmark 80 01 85 92

Invitrogen is a trademark of Invitrogen Corporation.

This product is sold under patent license from Genetics Institute, Inc. for research use only. Licenses for commercial manufacture or use may be obtained directly from Genetics Institute, Inc., 87 Cambridge Park Drive, Cambridge, MA 02140.
Hominid hand bones from Swartkrans Cave, South Africa. Comparative anatomy of the thumb, from *Paranthropus robustus* (about 1.8 million years ago), shows that this hominid could use tools. Other hominids found along with tools in deposits younger than 2.5 million years ago also evidently could use tools, but hominids that predate the appearance of tools lack the anatomical hallmarks of tool use. See page 1570 and the Perspective on page 1540. [Photo: Randall L. Susman]

Lattice Location of Trace Elements 1555
Within Minerals and at Their Surfaces with X-ray Standing Waves
Y. Qian, N. C. Sturchio, R. P. Chiarello, P. F. Lyman, T.-L. Lee, M. J. Bedzyk

Reduction of Permeability in Granite at Elevated Temperatures
D. E. Moore, D. A. Lockner, J. D. Byerlee

Grain Size–Dependent Alteration and the Magnetization of Oceanic Basalts
D. V. Kent and J. Gee

Rapid Emplacement of Young Oceanic Lithosphere: Argon Geochronology of the Oman Ophiolite
B. R. Hacker

Milankovitch Forcing of the Last Interglacial Sea Level
T. J. Crowley and K.-Y. Kim

Carbon Dioxide Supersaturation in the Surface Waters of Lakes

Fossil Evidence for Early Hominid Tool Use
R. L. Susman

Requirement of Transcription Factor PU.1 in the Development of Multiple Hematopoietic Lineages
E. W. Scott, M. C. Simon, J. Anastasi, H. Singh

Direct Observation of Enzyme Activity with the Atomic Force Microscope
M. Radmacher, M. Fritz, H. G. Hansma, P. K. Hansma

Detection of Endogenous Malondialdehyde-Deoxyguanosine Adducts in Human Liver

Control of Angiogenesis in Fibroblasts by p53 Regulation of Thrombospondin-1
K. M. Dameron, O. V. Volpert, M. A. Tainsky, N. Bouck

Mutations in *aquaporin-1* in Phenotypically Normal Humans Without Functional CHIP Water Channels
G. M. Preston, B. L. Smith, M. L. Zeidel, J. J. Moulds, P. Agre

Reduced Rate of Disease Development After HIV-2 Infection as Compared to HIV-1

Analysis of Sequence Transfers Resembling Gene Conversion in a Mouse Antibody Transgene
B. Xu and E. Selsing

Involvement of Nitric Oxide in the Elimination of a Transient Retinotectal Projection in Development
H. H. Wu, C. V. Williams, S. C. McLoon

Activation of the Sphingomyelin Cycle Through the Low-Affinity Neurotrophin Receptor
R. T. Dobrowsky, M. H. Werner, A. M. Castellino, M. V. Chao, Y. A. Hannun

**TECHNICAL COMMENTS**

Entropic Elasticity of λ-Phase DNA
C. Bustamante, J. F. Marko, E. D. Siggia, S. Smith

Explicit and Implicit Learning and Maps of Cortical Motor Output
M. A. Stadler; A. Pascual-Leone, J. Grafman, M. Hallett

Indicates accompanying feature

<table>
<thead>
<tr>
<th>AAAS Board of Directors</th>
</tr>
</thead>
<tbody>
<tr>
<td>Eloise E. Clark</td>
</tr>
<tr>
<td>Retiring President, Chairman</td>
</tr>
<tr>
<td>Francisco J. Ayala</td>
</tr>
<tr>
<td>President</td>
</tr>
<tr>
<td>Rita R. Colwell</td>
</tr>
<tr>
<td>President-elect</td>
</tr>
<tr>
<td>William A. Lester Jr.</td>
</tr>
<tr>
<td>Simon A. Levin</td>
</tr>
<tr>
<td>Anna C. Roosevelt</td>
</tr>
</tbody>
</table>

SCIENCE (ISSN 0036-8075) is published weekly on Friday, except the last week in December, by the American Association for the Advancement of Science, 1333 H Street, NW, Washington, DC 20005. Second-class postage (publication No. 4844665) paid at Washington, DC, and additional mailing offices. Copyright © 1994 by the American Association for the Advancement of Science. The title SCIENCE is a registered trademark of the AAAS. Domestic individual membership and subscription (51 issues): $92 ($50 allocated to subscription). Domestic institutional subscription (51 issues): $125. Foreign postage extra: Mexico, Caribbean (surface mail) $50; other countries (air assist delivery) $95. First class, airmail, student and emeritus rates on request. Canadian rates with GST available upon request; GST #1254 88122. Printed in the U.S.A.

Change of address: allow 6 weeks, giving old and new addresses and 11-digit account number. Postmaster: Send change of address to Science, P.O. Box 2033, Marion, OH 43305-2033. Single copy sales: $6.00 per issue prepaid includes surface postage. Guide to Biotechnology Products and Instruments, $20. Bulk rates on request. Authorization to photocopy material for internal or personal use under circumstances not falling within the fair use provisions of the Copyright Act is granted by AAAS to libraries and other users registered with the Copyright Clearance Center (CCC) Transactional Reporting Service, provided that the base fee of $1 per copy plus $.10 per page is paid directly to CCC, 27 Congress Street, Salem, MA 01970. The identification code for Science is 0036-8075/94 $1 + .10. Science is indexed in the Reader's Guide to Periodical Literature and in several specialized indexes.

1547
Causes of coral decline

1552
Pinced down
Why do an assay in several places when you can do it all right here.

Incubate, filter, precipitate, immobilize, harvest and detect directly in the MultiScreen assay plate. Compared to conventional methods, its 96 discrete filter tubes reduce reagent usage by 50–90% and radioactive waste by >95%. Compatibility with direct microplate scintillation counters dramatically improves throughput.

MultiScreen handles every assay step. Its patented underdrain assures reliable, multiple incubations. To remove supernatant, just apply vacuum to wash or quantitatively collect filtrate. Easily transfer filters directly into vials for radiodetection.

Whether you’re doing receptor binding, second messenger studies, cell culture and proliferation or immunoassays, MultiScreen has been proven faster, simpler, and more efficient.

Let Millipore's Technical Service help you choose the optimum membrane or filter for your assay—glass fiber, cellulosic or charged membranes, Immobilon™ series, low-binding Durapore® and more.

Call or fax for a complete technical package or to arrange a demo. U.S. and Canada: 1-800-645-5476 • Japan: (03) 3474-9111 • European headquarters in Paris, fax: 33.1.30.12.71.83

Internet Lab Catalogue: access URL menu, type: http://www.millipore.com

Circle No. 23 on Readers' Service Card
This is a powerful, expandable and comprehensive molecular biology package for the Mac, with the best protein analysis and restriction mapping software available. I recommend DNASTAR to any lab requiring this level of power and expandability. DNASTAR is currently unique in its support for networking as well.
Risk Assessments of Low-Level Exposures

In cancer-risk assessments employed by the U.S. Environmental Protection Agency assumptions are made that exaggerate risks by large factors. Among these is an important but unproven hypothesis that results obtained by administering huge doses of substances are predictive of effects of minuscule doses.

To calculate effects of small doses, a linear extrapolation from large doses to zero is employed. The routine use of this procedure implies that pathways of metabolism of large doses and small doses are identical. It implies that mammals have no defense against effects that injure DNA. It implies that no dose, however small, is safe. Examples of instances in which these assumptions are invalid are becoming numerous.

Linear extrapolation of effects from high to lower doses is often not valid. In a third or more of instances in which a toxicologically relevant dose elicited extra tumors in rodents, one-half that dose did not. Bruce Ames and others have pointed out that huge doses of non-genotoxic substances are accompanied by toxicity, cell death, and cell replacements. This creates conditions favorable for growth of tumors. At doses in which cellular death does not occur, tumors would not be produced by non-genotoxic substances. The majority of chemicals are not genotoxic, nor does metabolism of them give rise to genotoxic intermediates. Thus the linear extrapolation is not applicable to the majority of chemicals.

Recently, short-term experiments have measured extent of damage to linear DNA caused by different levels of doses of test substances. In one example, 11 chemicals known to cause cancer at high doses were administered at low levels. With 8 of 11 substances, the minimum amounts of damaged DNA were found not in controls but in the animals that received an amount intermediate between zero and a high dose. Instead of damaging the DNA of the rodents' livers, the low doses were apparently beneficial to them. In another study, female rats administered 0.001 μg/kg per day of dioxin had fewer breast, uterine, pituitary, and liver tumors and fewer tumors overall than did controls. When doses of 0.01 μg/kg per day were administered, the incidence of liver tumors exceeded that of controls, but breast, uterine, pituitary, and total tumors were markedly fewer than in controls. In the above instances, safe (diminished cancer) levels of exposure exist for substances known to cause cancer at higher doses.

The use of linear extrapolation from huge doses to zero implies that “one molecule can cause cancer.” That assertion disregards the fact of natural large-scale repair of damaged DNA. Natural chemical and physical lesions of DNA are caused by thermal and oxidative insults. Metabolic processes employ reactive oxygen species including peroxides and OH. Natural kinds of injury to DNA include depurination, deamination, oxidation, single-strand breaks, double-strand breaks, base modification, and protein-DNA crosslinks. Mammalian cells on average undergo about 10,000 measurable DNA modification events per cell per hour. Adult humans are internally exposed to about 500 g per day of oxygen—a relentless known destroyer of DNA. In contrast, hypothetical insults from anthropogenic sources are usually from substances present in microgram quantities.

Creatures ranging from micro-organisms to mammals could not survive if they did not have mechanisms to respond to challenges from their environments. During exposure to a somewhat elevated temperature, living forms synthesize a host of different proteins that enable them to endure even higher temperatures. This phenomenon has been noted in experiments with cadmium, mercury, copper, zinc, polychlorinated biphenyls, and insecticides. Studies using X-rays show that a large total instantaneous dose is fatal while the same total dose spread over time is not. Repair of DNA occurs. Studies have shown that DNA-damaging agents induce a substantial number of responses, including production of proteases, DNA repair agents, oncogenes, and chromatin changes.*

The current mode of extrapolating high-dose to low-dose effects is erroneous for both chemicals and radiation. Safe levels of exposure exist. The public has been needlessly frightened and deceived, and hundreds of billions of dollars wasted. A hard-headed, rapid examination of phenomena occurring at low exposures should have been a high priority.

Philip H. Abelson

* BELL Newsletters, University of Massachusetts; telephone 413-545-1239.
SCIENCE IS UNDER ATTACK

- John Maddox said so in Nature (vol. 368)
- Gerald Holton said so in Science and Anti-Science
- Richard S. Nicholson said so in Science (vol. 261)
- Paul R. Gross and Norman Levitt said so in Higher Superstition

Formerly the attacks came from outside the academic and scientific disciplines. Increasingly, now, they come from within.

These attacks are dangerous:
- They undermine public confidence
- They alter directions of research
- They affect funding
- They subvert the standards of reason and proof

...alternative sciences or parasciences by themselves may be harmless enough except as one of the opiates of the masses, but...when they are incorporated into political movements they become a time bomb waiting to explode. We have recently been watching just such a possibility in the United States.

— Gerald Holton

The National Association of Scholars is an organization of academics and independent scholars formed to combat the irrationality and politicization now thriving in university life.

Our conference on “Objectivity and Truth in the Natural Sciences, the Social Sciences and the Humanities” will take place November 11–13 at the Boston Marriott, Cambridge. Among our speakers are:

- Steven Weinberg, Nobel Laureate in Physics, University of Texas
- Gerald Holton, Mallinkrodt Professor of Physics, Harvard University
- Paul R. Gross, Professor of Life Sciences and Director of the Center for Advanced Studies, University of Virginia
- Gerald Weissmann, Head, Rheumatology Department, New York University Medical School
- Michael McElroy, Head, Department of Earth and Planetary Sciences, Harvard University

For information about the conference, NAS membership, or our journal, Academic Questions, write to:

National Association of Scholars
575 Ewing Street
Princeton, New Jersey 08540–2741
609-683-7878
(fax) 609-683-0316
(E-mail) nas@nas.org

“for reasoned scholarship in a free society”
**Genetic Testing**

The excellent News & Comment article by Rachel Nowak “Genetic testing set for takeoff” (22 July, p. 464) clearly documents the problems of the use of genetic tests as general screening tools to identify those predisposed to inherited disease in adult life: the current costs are too high, there are too many genes to test with too many mutations in each gene, and there are not enough genetic counselors to interpret the results of the tests to those who have them. Furthermore, the predictive value of these tests is unknown when used in a general screening. In an earlier letter to the editor (1 April, p. 3), David Danks of the Royal Children's Hospital in Melbourne, Australia, examined the mathematics of a case finding by general screening and pointed out that confining such studies to members of families at risk had a far greater yield (and a better predictive value for the interpretation of the test result). He was considering testing as a public health measure; not, as Nowak’s article implies, as a response to market demand.

Nowak contemplates legislative controls on discriminatory uses of genetic testing and refers to the ever-quoted 41 cases described by Paul Billings some years ago. She points out that “all the time people are turned down for life and health insurance” on the basis of test results for the Huntington mutation. As an ex-geneticist, now working in the insurance business, I would like to put the case for our industry into perspective in this discussion.

The predictive value of any laboratory test is a function of sensitivity, specificity, and prevalence of the disease in the test group. Most genetic mutations are rare in the general population and provide low predictive value. The genes MSH2 and MLH1 are thought to be mutated in 18% of 5% of the population (thus predisposing them to hereditary nonpolyposis colon cancer), or less than 1 out of 1000 individuals. At this time, no one is quite sure what the mortality risk for these mutations will be. In contrast, serum cholesterol, for which a test is performed on most insurance applicants, is elevated in 40% of them, and the insurer, the applicant, and his family doctor all believe they have some understanding of the risk the elevation represents.

The discriminatory function of genetic tests will be prone to error unless the tests are done in the extended families of identified probands. Insurance testing is not structured on a random access basis, but uses only general screening tools. The cost, for example, of separating those who should have MSH2 or MLH1 tests from those that should have a test for the APC gene (so as to detect proneness to familial adenomatous polyposis, another cause of colon cancer) would be prohibitive in this industry. That situation is unlikely to change.

Insurers today do not do any genetic testing. They clearly recognize the problems as being excellent reasons to avoid DNA screening tests. On the other hand, insurers do want to know the results of tests that have been done by others, for cause, on those who are applying for insurance. Insurance is sold to provide financial protection against unanticipated loss. If people who know they will die at an early age are allowed by law to purchase insurance, then they are at an advantage not only over the insurer but over all the other policyholders covered by that company. As a basic principle, insurance is priced so that those at equal assumed risk pay equally for their protection. If that is not the case, the price of all insurance must change. It is true that people are denied insurance on the basis of family history alone (because, for example, their parent died with Huntington's disease), but they are also turned down if they had cancer surgery 6 months ago—even though they may appear otherwise healthy. They are turned down because their risk of early death is expected to be extremely high and appropriate premiums cannot be calculated. In those instances both the applicant and the insurer know the nature of the risk.

If, however, the applicant is privileged to know his or her risk and may legally conceal it from the insurer, then insurance will become too expensive for all but those who know they will succumb at an early age. When “everyone” has been tested and all their lifetime genetic risks identified, only those like Billings’ unfortunate 41 will be buying insurance while the rest of us, who by definition will have perfect genes, need not bother. In reality, the complete genome test, with interpretation, is a long way in the future. Competitive market forces continue to drive the insurance industry to sell as much insurance as possible and to determine individual risks on the basis of information that is already known to the applicant. If legislation is enacted today to limit the use of test results done by others, it will only provide a new
logical monitoring could include surveillance for pests and their impacts on agriculture, nutrition, and health.

Paul R. Epstein
Harvard Medical School,
Cambridge Hospital, 1493 Cambridge Street,
Cambridge, MA 02139, USA

Godfrey P. Chikwenera
Department of Research and
Specialist Services,
Plant Protection Research Institute,
Ministry of Agriculture,
Post Office Box 550, Causeway, Zimbabwe

References
2. R. Levins et al., Am. Sci. 82, 52 (1994).

In our sometimes desperate struggle to minimize the ongoing massive extinction event, scientists and conservationists have resorted to arguments about the value of biodiversity. Arguments with direct or indirect economic components are often front and center, and moderate support for them is abundant (1). However, such arguments run the risk of becoming the primary reason for the conservation of biodiversity, a result likely to doom many species (2). Evidence for the economic necessity of high species richness is hard to produce, as evidenced in the article by Baskin in which she reports the difficulty in demonstrating clearly the practical value of many species in maintaining ecosystem function.

The “wildlife must pay its way” approach to conservation must be only a part of an overall strategy that also relies on noneconomic values. Increasingly, the public worldwide is aware of and sympathetic to the conservation of biodiversity in its own right, independent of direct or indirect economic benefits (3). This is only hinted at in the single disclaimer in Baskin’s article (p. 203) that “[c]onversely, participants emphasized even a species that seems to be a fifth wheel in the working of an ecosystem might be worth saving for economic, moral, or aesthetic reasons.” We as a species are in the process of deciding that all species are worth saving and that our devastating assault on the world’s biodiversity can no longer be justified on any grounds.

Truman P. Young
Department of Biology, Fordham University,
Bronx, NY 10458, USA, and
Mpala Research Centre,
Post Office Box 555, Nanyuki, Kenya

References
2. B. W. Ehrenfeld, in Biodiversity, E. O. Wilson and F.


Protein Configurations
The Research Article “Protein design by binary patterning of polar and nonpolar amino acids” by Satwik Kamtekar et al. (10 Dec. 1993, p. 1680) describes a strategy to test and validate the idea that only the sequence location, not the identity of the polar and nonpolar amino acid residues, must be specified explicitly in order for a stably folded protein structure to form. We previously published a related approach, based on a symmetrical characteristic of genetic information (1), which we believe should have been cited. Specifically, our work was based on the fact that the first two bases of a codon specify a particular amino acid, whereas the second base of the triplet encodes the amino acid’s hydrophobic character; therefore in-frame amino acid assignment to messenger RNA in the nonconventional 3’ to 5’ direction changes the primary sequence, but maintains the polar and nonpolar (binary) pattern for any peptide or protein (1, 2). My colleagues and I exploited the symmetrical characteristic to ascertain whether the linear array of hydrophathy (or binary code) patterned by a specific nucleotide sequence could determine structure (1, 3) and function (3). By preparing peptides decoded from a 3’ to 5’ reading of the mRNA for both ACTH and GHRH, we showed antigenic cross-reactivity, receptor binding, signal transduction, and hormonal activity (1, 3). The elegant studies of Kamtekar et al. strongly confirm our previous findings on the role of the linear pattern of hydrophathy (or binary code) in protein structure and clearly establish its degenerate nature.

J. Edwin Blalock
Department of Physiology and Biophysics,
University of Alabama, 1918 University Boulevard,
Birmingham, AL 35294–0005, USA

References

Corrections and Clarifications
The 1994 meeting of the American Institute of Biological Sciences, held concurrently with the meeting of the Ecological Society of America covered in the Meeting Briefs of 26 August (Research News, p. 1178), took place in Knoxville, Tennessee, not Nashville, as the title indicated.

SAVE YOUR COPIES OF SCIENCE

CASES These custom-made, imprinted cases and binders are ideal for protecting your valuable Science copies from damage. Each binder or case holds one volume of Science, or 13 weekly issues—order four binders or cases to hold a complete year of issues. Constructed from reinforced board and covered with durable, leatherlike red material and stamped in gold, the cases are V-notched for easy access; binders have a special spring mechanism to hold individual rods which slide easily into place.

NAMES: Jesse Jones Industries, Dept. SCE
499 East Erie Ave., Philadelphia, PA 19134
Enclosed is $ for Cases:
Binders Add $1 per case/binder for postage & handling. Outside USA $2.50 per case/binder (US funds only). PA residents add 7% sales tax.
Print Name
Address
City
State/Zip

CALL TOLL FREE 7 days, 24 hours 1-800-825-6690

Satisfaction Guaranteed
Sensitive touch

The disc-like adhesive pads on the hands and toes of the tree frog enable this nimble creature to perform the most sensitive acrobatic maneuvers. From often perilous heights, the tree frog clings to the most delicate twigs as it leaps from branch to branch in pursuit of insect prey.

The Boehringer Mannheim Genius System makes sensitive scientific procedures equally as swift and safe. In hours—not days—probes prepared with the Genius System can detect single copy genes in as little as 1 μg of DNA in a genomic Southern blot, and are guaranteed to detect 0.03 pg of DNA in a direct dot blot.

But unlike other nonradioactive methods, the Genius System uses a unique antibody-based protocol that minimizes background interference, maximizes the signal-to-noise ratio, and produces your results faster.

Safety and sensitivity combined

Every time you make a Southern blot or dot/slot blot, screen a library or conduct an in situ hybridization with radioactive methods, you expose yourself and those around you to the risks of radiation. Every time you use the Genius System to perform these same procedures, you receive the assured safety that only nonradioactive products provide, along with guaranteed sensitivity and specificity.

Sensitivity to your needs

Boehringer Mannheim's user-training programs and technical support personnel can help make your conversion to nonradioactive DNA labeling and detection procedures smooth and trouble-free. Contact your Boehringer Mannheim representative or call 1-800-262-4911 (514-686-7141 in Canada).
The last thing you want automation to do is restrict your choices. So when we designed ALF® our automated DNA sequencer, we made sure that it gave you maximum choice - in chemistry, in methodology, in data presentation. One important example of the choice it offers is the ability to use labeled or unlabeled primers, an economical way of dealing with the need for a variety of chemistries and the ability to present raw as well as processed data. ALF ensures that you get the results you want for the data you want. Which means that when it comes to choosing a DNA sequencer, go for the one that gives you choice.

What's the least you can expect from automated DNA sequencing?

Pharmacia Biotech

Pharmacia Biotech

Pharmacia Biotech

Put time on your side.
What distinguishes a chemical company: First and foremost - service; which is Sigma’s approach to supporting the future of research. Should technical questions arise, a Sigma specialist is available to assist you with the use or application of our 33,000-plus products. In addition - quality; every one of Sigma’s products is thoroughly assayed in state-of-the-art analytical laboratories using the most demanding analytical criteria.

Another distinguishing factor is expertise; as in Sigma’s family of experts in life science research. Sigma’s chemists are constantly at work on a wide spectrum of specialty chemicals for targeted areas of research, adding over 2,000 new products each year. And they’re continually refining and improving the products that established Sigma’s reputation over 50 years ago.

Service, quality and expertise distinguish Sigma as the leading choice of laboratories worldwide. Weigh all the advantages. Consider Sigma as your single source for research biochemicals.
According to a report in the May 1994 edition of *Welch Library Issues*, SCIENCE tops the list of the most frequently used journals in one of the largest biomedical collections in the world: The William H. Welch Medical Library, Johns Hopkins University School of Medicine. Four times a year for a two-week period the Welch Library staff tracks the usage of scientific and medical journals in the library. According to the data collected from 1990 to March of 1994, SCIENCE received 1,953 uses. That's over 100 more uses than the second most used journal listed.

Each week 160,000 subscribers around the globe turn to SCIENCE for the most important leading-edge research and the latest scientific news stories. No wonder copies of SCIENCE in libraries look a bit dog-eared and rumpled. SCIENCE is the journal scientists turn to first.
Both Chromatography Systems Are About The Same Low Price. But That's Where The Similarity Ends.

Why bog down your work with a traditional chromatography system? You can achieve even better resolution, in a fraction of the time, outside the cold room, with a ConSep LC100™ system from Biosearch.

Whether you are purifying proteins or nucleic acids, the ConSep system delivers high biological activity and purity in just 15 in. of bench space.

And it's so simple to use. The patented Auto-Blend™ four-buffer blending feature lets you alter both the pH and the ionic strength of your buffers with just a few keystrokes, so you can run pH and salt gradients simultaneously.

The ConSep system is compatible with all conventional low-pressure bead-based columns. And for ion exchange chromatography, the "flow through pores" of our MemSep® cartridges speed the transport of biomolecules, for sharper peaks and faster results.

The ConSep LC100 system.

Using anything else just doesn't add up. For information and a free video or demonstration in your lab, call the Biosearch Group in the US and Canada at 1-800-872-0071 (Option 1), in Germany at (49) 040-853267-36, in Japan at (03) 3471-8191, in France at (33) 1 30127002, and in the UK and the rest of Europe at (44) 0923 211107.

Circle No. 12 on Readers' Service Card
Every clinical trial calls for personal attention. No matter how many people, and places, are involved.

That’s why we’ve developed systems for working with tens of thousands of patients. Why we’ve put together an extensive network of high-quality investigator sites.

And why we’ve assembled a team of over four hundred professionals to oversee it all.

The big picture?

Over the years, we’ve successfully completed projects for a wide range of biotech and pharmaceutical companies, both large and small, on spec, on time and on budget.

We can do the same for you. While making sure that you don’t get lost in the crowd.
Don’t let small sample dialysis get out of hand.

Take control with the new Pierce Slide-A-Lyzer™ Dialysis Cassettes!

Load a sample for dialysis easier and faster than ever with this revolutionary new system. The new Pierce Slide-A-Lyzer™ Dialysis Cassette replaces the mess and hassles of conventional tubing with a more convenient, more effective approach.

No more boiling, soaking, tying, or clamping— all you need is a syringe to load and remove your sample from these ready-to-use, disposable cassettes. The exclusive cassette design gives you total sample control, good surface-to-volume ratio and consistently reliable sample recovery. For even greater convenience, use the accessory Buoys to float your sample during dialysis, and as a bench-top cassette stand during loading and recovery.

Pierce Slide-A-Lyzer™ Cassettes have a 0.5 - 3.0 ml sample capacity, 10,000 molecular weight cut-off, and are ideal for routine dialysis of protein, nucleic acid and carbohydrate samples.

<table>
<thead>
<tr>
<th>Product #</th>
<th>Description</th>
<th>U.S. Price</th>
</tr>
</thead>
<tbody>
<tr>
<td>66425</td>
<td>Slide-A-Lyzer™ 10K Dialysis Cassettes, 10 pack</td>
<td>$49</td>
</tr>
<tr>
<td></td>
<td>Contains: 10 cassettes (10,000 Molecular Weight Cut-off, 0.5 - 3.0 ml sample capacity)</td>
<td></td>
</tr>
<tr>
<td>66430</td>
<td>Slide-A-Lyzer™ Buoys, 10 pack</td>
<td>$12</td>
</tr>
<tr>
<td>66490</td>
<td>Slide-A-Lyzer™ Syringe and 18G Needle Accessories, 10 pack</td>
<td>$9</td>
</tr>
<tr>
<td></td>
<td>Contains: 10 each of 5 cc single-use, sterile, polypropylene syringes with Luer-Lok™ tips and single-use, sterile, 18-gauge, 1&quot; needles compatible for use with the Slide-A-Lyzer™ Dialysis Cassette. Ideal for nucleic acid applications.</td>
<td></td>
</tr>
</tbody>
</table>

Call for your FREE copy of Pierce’s Life Science & Analytical Research Products or Molecular Biology Catalog!
Eighteenth Annual Symposium

Presentations of the Ciba Drew Award in Biomedical Research will be made to:

**Thomas R. Cech, PhD**
University of Colorado
Boulder, CO
"Catalytic RNA: Mechanism and Structure"

**Albert Eschenmoser, PhD**
ETH–Zurich
Switzerland
"Toward a Chemical Etiology of the Natural Nucleic Acids"

**Manfred Eigen, PhD**
Max Planck Institute
Göttingen, Germany
"Molecular Diagnostics and Evolutionary Biotechnology"

The proceedings will be introduced and moderated by:

**George deStevens, PhD**
Research Professor of Chemistry
Drew University

Baldwin Gymnasium
William and Carol Simon Forum
and Athletic Center
Madison, NJ 07940
Tuesday, 11 October 1994
1:30 pm–5:30 pm

Address inquiries to:
**George deStevens, PhD**, Frontiers in Biomedical Research
Drew University, Madison, New Jersey 07940

---

Yes! I want to show my support for *SCIENCE*. Please send me the *SCIENCE* T-shirts I've checked off below. I have enclosed a check for the amount of the shirts (plus shipping charges for non-US orders). I understand my order is refundable if I am not completely satisfied.

**Shipping Address (please print)**

Name

Address

City, State/Province, Country, Postal Code

Telephone and Fax

Please allow 4 weeks for delivery inside the US. Outside the US please allow 6 weeks for delivery. Prices and shipping charges subject to change without notice. Shirts returned must be in salable condition. Wash, D.C. residents please add sales tax.

**Payment Information**

☐ US dollar check  ☐ Visa  ☐ MasterCard

Important: All payments must be made in US dollars. $25 minimum order for all credit card orders. Make check payable to AAAS Science Publications, Inc.

Credit card number

Expiration date

Signature

AAAS Membership No

**QTY SIZE STYLE NO. DESCRIPTION PRICE**

Discount: less than 10% for two or more T-shirts.

Subtotal

Outside the US: Add $3.50 per shirt/or delivery

Total Enclosed
For over 1,000 years the art of reading ancient Egyptian hieroglyphics was lost to the world. Then, in 1799 the Rosetta Stone was discovered. It was the key to unlocking the language of hieroglyphics. The Wisconsin Sequence Analysis Package provides you with the key to discovering information in a language even older than hieroglyphics: DNA, the language of life.

How long can your research afford to wait?

When trying to decipher a complex language, certain tools are necessary for quick, successful interpretation. The Wisconsin Sequence Analysis Package developed by Genetics Computer Group (GCG) is a complete sequence analysis package, handling database searching, sequence comparison, secondary structure prediction, sequence assembly and much more. And Digital’s Alpha AXP computers give the Wisconsin Package the power you need to work in a field where new sequences are added to the databases at a rate of over 250,000 residues per day.

Look to the Wisconsin Package for:
- a comprehensive range of sequence analysis programs
- access to all major sequence data resources
- multi-user computing environments
- comprehensive database updating services
- professional support and education
- low cost

Digital Alpha AXP systems provide:
- a wide range of high performance computers
- leadership in industry standards
- Open OSF/1 UNIX and OpenVMS operating systems
- the fastest system available today
- the best price/performance

For more information about the Wisconsin Package, call (608) 231-5200, FAX (608) 231-5202 or E-Mail to Rosetta@GCG.Com.

For information on the Digital Equipment Corporation Alpha AXP: Telnet: telnet.educonnect.digital.com, call (800) DIGITAL or your local Digital representative.

For information on Digital Equipment Corp., Circle No. 25
For information on GCG, Circle No. 26
**THE WELCOMING PLenary**

**OCTOBER 2-5, 1994**

“The Human Genome Diversity”
Dr. Mary Claire King, University of California, School of Public Health

“Manipulating Cancer Genes in the Mouse”
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

---

**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. Andre 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 Paabo, Zoologisches Institut, Universitat Munchen
INSTRUCTIONS
1. Complete all portions of this form. Return it to: HUMAN GENOME 1994, c/o GLOBAL TRADE PRODUCTIONS, INC., Two Skyline Place, 5203 Leesburg Pike, Suite 1313, Falls Church, Virginia 22041, Ph. (703) 671-1400.
2. A check payable to Global Trade Productions, Inc. must accompany this form. Correct fees must be received to be registered.
3. Your name and organization will appear exactly as you indicate on the form below.
4. PRINT OR TYPE ALL INFORMATION REQUESTED.

REGISTRATION INFORMATION
Is this your first Human Genome Conference?
☐ Yes ☐ No
If not, how many have you attended?
☐ 1 ☐ 2-5 ☐ more than 5
Name__________________________
Title __________________________
Organization ____________________
Address _______________________
City ____________________________ State ______ Zip ______
Phone _______________________
☐ Please check here if you have a disability that requires auxiliary aids during the Conference. Describe your special needs: __________________________

CONCURRENT SESSIONS
To aid us in planning, please check the sessions you are most likely to attend. You are not committed to these specific sessions. (See Preliminary Agenda for presentation titles.)

Monday, October 3 Tuesday, October 4
☐ M1 ☐ T1
☐ M2 ☐ T2
☐ M3 ☐ T3
☐ M4 ☐ T4

Please check if you will attend the Welcoming Reception, Sunday, October 2.
☐ Yes ☐ No
Please check if you plan to submit an abstract.
☐ Yes ☐ No

REGISTRATION OPTIONS
Mark your selection(s) below by circling the appropriate fee.

Advance Through June 30, 1994
☐ Regular $250 ☐ Non-Member $325
☐ Postdoctoral $175 ☐ Student $225
☐ Student $80 ☐ $115

Regular July 1—September 30, 1994
☐ Regular $285 ☐ Student $350
☐ Postdoctoral $200 ☐ $275
☐ Student $90 ☐ $125

On-Site
☐ Regular $300 ☐ Student $375
☐ Postdoctoral $225 ☐ $275
☐ Student $95 ☐ $130

Daily Rates $150 $150
☐ Monday ☐ Tuesday ☐ Wednesday

PAYMENT
Meeting registration fee: __________________________
(Make check payable to Global Trade Productions, Inc.)

AAAS MEMBERSHIP
* Non-members can take advantage of the conference member rate by joining AAAS when submitting this application. Join AAAS today and enjoy 51 weeks of Science magazine. (Make separate check for membership payable to AAAS and return with your conference registration form.)
☐ Regular $92 ☐ Postdoctoral $67 ☐ Student $50
☐ International: AAAS will invoice you directly.
(Prices are valid until 12/31/94. International and Canadian rates are higher and are available upon request $50.00 allocated to Science. Allow 6-8 weeks for delivery.)

For Management Use Only: Check# ______ Date Recvd ________
Amount $__________


27. There is no evidence that the nationwide algal bloom in Jamaica was caused by increased nutrients, because it occurred throughout the Caribbean immediately following the Didemna die-off (16, 20), usually far from sources of pollution. Some groundwater input does occur into the shallow margins of the back-reef at Discovery Bay, which enhances nitrates and reduces salinity close to the shore ([C. F. D’Elia, K. L. Webb, J. W. Porter, Bull. Mar. Sci. 31, 903 (1981)]. These conditions produce localized areas around submarine springs, typically 2 to 3 m in diameter, which contain characteristic brackish-water algal assemblages (dominated by Chaetomorpha, Enteromorpha, and Ulva) that are quite unlike those occurring on the reef further offshore. None of the sites in Figs. 3 to 6 are located close to urban areas or point sources of pollution, with the exception of the Port Royal cays on the south coast near Kingston.


29. Densities of Echinometra viridis, Eucladeras tribuloides, Lytocrinus williamsii, and Trypaeosoma ventricosum in 1973 were reported for two Jamaican patch reefs by W. P. Sarmstrong [J. Exp. Mar. Biol. Ecol. 61, 31 (1982)]. The combined total was 27.5 and 54.0 per square meter, respectively. By 1986, the combined total had fallen two- to threefold (10). In 1993, mean densities [number per square meter ± SE] on these same reefs were 14.0 ± 1.5 and 14.4 ± 1.2.


32. Coral and algal abundance (percent cover) shown here were measured from annual photographs of 10 to 20 permanent 1-m² plots at each depth (7, 10, and 15 to 20 m at Rio Bueno; 35 m at Pinnacle 1). All corals (approximately 38,000 records over 17 years) were traced and digitized to obtain relative abundances, while algal cover was estimated by superimposing a grid of dots on each image (100 per square meter) and counting those covering algae. The small-scale trends reported here for permanent plots mirror almost exactly the results from a larger scale program that was based on replicate 10-m line-intersect transects. For example, in 1993 mean coral cover (±SE) estimated from 20 random transects at each of the 7-, 10-, 15- to 20-, and 35-m stations in Fig. 3A was 5.0 ± 0.8, 5.4 ± 1.2, 5.6 ± 0.9, and 12.8 ± 2.4, respectively. Reef degradation at an even larger scale is shown in Fig. 5.

33. Data for 1976 are from (19), based on a random collection of 97 Diadema antillarum from the East Back Reef at Discovery Bay, Jamaica. Data for 1993 are based on 207 individuals from the same site.

34. Coral and macroalgae cover in Figs. 5 and 6 is based on 5 to 10 10-m line-intersect transects run at 10 m from 1976 to 1980 (mosty in 1977 and 1978) on fore-reefs at Negri, Chaolet Caribe, Rio Bueno, Discovery Bay (two locations), Pear Tree Bottom, Port Maria, Port Antonio (on the north coast), and Port Royal (on the south coast). These measurements were repeated in 1990 to 1993 with 20 transects, with the addition of five more north coast sites.

35. I thank J. H. Connell, F. Jeal, and J. B. C. Jackson for providing encouragement over 20 years; J. D. Woodley and the staff of Discovery Bay Marine Laboratory for excellent logistic support; M. J. Boyle, G. Bruno, M. Carr, L. Dinsdale, F. Jeal, M. Gleason, S. Penning, D. Reed, L. Sides, L. Smith, J. Tanner, C. Tyler, and many others for field and lab assistance; and D. Bellwood, H. Chao, T. Done, B. Willis, and the Coral Group at James Cook University (JCU), whose comments improved an early draft of the manuscript. Supported by the National Science Foundation, the National Geographic Society, the Whitehall Foundation, the Australian Research Council, and JCU. This contribution is no. 133 of the Coral Group at JCU.

**AAAS–Newcomb Cleveland Prize**

To Be Awarded for a Report, Research Article, or an Article Published in *Science*

The AAAS–Newcomb Cleveland Prize is awarded to the author of an outstanding paper published in *Science*. The value of the prize is $5000; the winner also receives a bronze medal. The current competition period began with the 3 June 1994 issue and ends with the issue of 26 May 1995.

Reports, Research Articles, and Articles that include original research data, theories, or syntheses and are fundamental contributions to basic knowledge or technical achievements of far-reaching consequence are eligible for consideration for the prize. The paper must be a first-time publication of the author’s own work. Reference to pertinent earlier work by the author may be included to give perspective.

Throughout the competition period, readers are invited to nominate papers appearing in the Reports, Research Articles, or Articles sections. Nominations must be typed, and the following information provided: the title of the paper, issue in which it was published, author’s name, and a brief statement of justification for nomination. Nominations should be submitted to the AAAS–Newcomb Cleveland Prize, AAAS, Room 924, 1333 H Street, NW, Washington, DC 20005, and must be received on or before 30 June 1995. Final selection will rest with a panel of distinguished scientists appointed by the editor-in-chief of *Science*.

The award will be presented at the 1996 AAAS annual meeting. In cases of multiple authorship, the prize will be divided equally between or among the authors.
discussions of the historiographic approaches taken by the 19th-century historians of mathematics Moritz Cantor and H. G. Zeuthen (J. Lützen and W. Purkert), of the 1770–1940 "prehistoric" or linear programming (I. Grattan-Guinness), and of David Hilbert’s activities in support of his "axiomatic programme" (V. Peckhaus). In three following papers, devoted more specifically to mathematical ideas, are examined Rudolf Lipschitz’s 1869–73 work on differential geometry and mechanics (R. Tazzioli), Karl Weierstrass’s 1841 proof of the Laurent expansion for functions on an annulus (P. Ullrich), and the discovery by Weierstrass and rediscovery by Bernhard Riemann of the "removable singularity theorem" (Ullrich). The contributors then turn to the social aspects of the history of mathematics, with accounts of the development of a "strong, active, deeply-rooted community" of American mathematicians at the turn of the last century and of the participation of women in that community (D. D. Fenster and K. H. Parshall) and an overview of interactions between mathematicians of the United States and China in the period 1850–1890 (D. Zhang and J. Dauben). Each paper is preceded by an abstract, and the tables of contents of the two earlier volumes are included, but there are no indexes.

—Katherine Livingston


This book is devoted to "the genesis of a theory that has been on the cutting edge of physics ever since P. A. M. Dirac’s quantization of the radiation field in 1927" but whose history has had less attention than developments that preceded it. To make the subject accessible to those with limited resources to explore it, Miller here presents a "frame-setting essay" and reprints of 11 classic papers emphasizing "conceptual transformations... which carried physicists to the threshold of renormalization theory." Miller’s essay (116 pages including notes and references) traces the subject in some mathematical detail from Bohr’s atomic theory as enunciated in 1913 through the researches of Sin-Itoro Tomonaga, Julian Schwinger, Richard Feynman, and Freeman Dyson up to about 1950. The "selected papers," all but one of them appearing in new English translations, begin with Werner Heisenberg’s "The self-energy of the electron" (1930) and "Remarks on radiation theory" (1931) and two 1934 papers by Dirac and end with H. A. Kramers’s "The interaction between charged particles and the radiation field" of 1937–38. Authors of the intervening papers are (alone or in combination) Viktor Weiskopf, Heisenberg twice again, Wolfgang Pauli, and Marcus Fierz. An index to Miller’s essay concludes the volume.