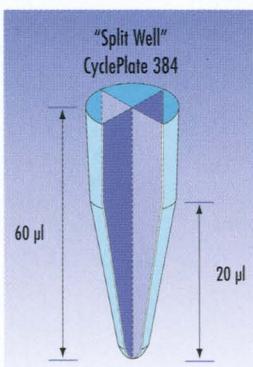


Go Fourth and Multiply.

Quadruple Your PCR Reactions With "Split Well" CyclePlates.™

Take advantage of the simplest, most inexpensive method available to increase the sample processing capacity of your thermal cycler up to 4 times! Designed for high throughput PCR and cycle sequencing applications, new Split Well* thin wall PCR CyclePlates are rigid, polypropylene 96 well plates with one (CyclePlate-192) or two (CyclePlate-384) dividers molded into each of the wells. This creates independent reaction chambers within the confines of a standard dimension, 0.2 ml "V-shaped" tube. Prepare reactions by hand or to really increase throughput, assemble and collect reactions with the Hydra-96 Microdispenser with special plate positioner for precise handling of microliter volumes of reagents within each set of 96 reaction chambers.



Each chamber in the CyclePlate-384 has a 20 μl working volume and a 60 μl total volume.

*Patent Pending

It's Like Cloning Your Thermal Cycler!

With CyclePlate-384 or CyclePlate-192, you can double or even *quadruple* the number of reactions performed in your existing thermal cyclers without buying additional hardware.

Universal Fit

Split Well CyclePlates fit most standard 96 well thermal cyclers including the Perkin-Elmer 9600 and MJ Research PTC 100/200.

Economical

The cost per reaction using CyclePlate-384 and -192 is up to 60% less than the cost of reactions performed in standard plates.

Boost your PCR and sequencing capacity without buying another thermal cycler.

Call 1-800-752-8585 for more information.



The Hydra-96 and special plate positioner is used for quick dispensing of reagents into the reaction chambers of CyclePlate-384 and -192.

Robbins Scientific®

Robbins Scientific Corporation, 814 San Aleso Ave., Sunnyvale, CA 94086-1411 (408) 734-8500 (800) 752-8585 FAX (408) 734-0300

e-mail: custserv@robsci.com

Reader Service No. 268

GENOME RESEARCH

Volume 6 Number 11
November 1996

Editors

Mark Boguski
National Center for Biotechnology
Information, NIH
Aravinda Chakravarti
Case Western Reserve University
Richard Gibbs
Baylor College of Medicine

Eric Green
National Center for Human Genome
Research, NIH
Richard Myers
Stanford University School of Medicine

Editorial Board

Rakesh Anand
Zeneca Pharmaceuticals
Stylianos Antonarakis
University of Geneva
Charles Auffray
CNRS
Philip Avner
Institut Pasteur
Andrea Ballabio
Telethon Institute of Genetics and
Medicine
David Bentley
The Sanger Centre
Bruce Birren
Whitehead Institute/MIT Center for
Genome Research
Michael Boehnke
University of Michigan School of
Public Health
Anne Bowcock
University of Texas Southwestern
Medical Center
David Burke
University of Michigan Medical School
Jeffrey Chamberlain
University of Michigan Medical School
Ellison Chen
Perkin-Elmer Corporation
David R. Cox
Stanford University School of Medicine
Ronald W. Davis
Stanford University School of Medicine
Richard Durbin
Sanger Centre, UK
Joseph Ecker
University of Pennsylvania
Beverly S. Emanuel
Children's Hospital of Philadelphia
Raymond Fenwick
Biodate Laboratories
Chris Fields
National Center for Genome Resources
Simon Foote
Walter and Eliza Hall Institute of
Medical Research

Phil Green
University of Washington
Kenshi Hayashi
Kyushu University
Philip Hieter
The Johns Hopkins University School
of Medicine
Clare Huxley
St. Mary's Hospital Medical School
Howard J. Jacob
Massachusetts General Hospital-East
Alec Jeffreys
University of Leicester
Mark Johnston
Washington University School of
Medicine
Mary-Claire King
University of Washington
Ben Koop
University of Victoria
Pui-Yan Kwok
Washington University School of
Medicine
Ulf Landegren
Uppsala Biomedical Center
Mark Lathrop
The Wellcome Trust Centre
Michael Lovett
University of Texas Southwestern
Medical Center
Jen-i Mao
Genome Therapeutics Corporation
Douglas Marchuk
Duke University Medical Center
Thomas Marr
Cold Spring Harbor Laboratory
W. Richard McCombie
Cold Spring Harbor Laboratory
Susan Naylor
University of Texas Health Science
Center
David Nelson
Baylor College of Medicine

Managing Editor

Judy Cuddihy
Cold Spring Harbor Laboratory
News and Reviews Editor
Alison Stewart
Cambridge, U.K.

Maynard Olson
University of Washington
Svante Pääbo
University of Munich
Leena Peltonen
National Public Health Institute, Helsinki
David Porteous
MRC Human Genetics Unit
Western General Hospital, Edinburgh
Roger Reeves
Johns Hopkins University School of
Medicine
Bruce Roe
University of Oklahoma
Rodney Rothstein
Columbia University College of P&S
Gerald Rubin
University of California, Berkeley
Lloyd Smith
University of Wisconsin-Madison
Randall Smith
Baylor College of Medicine
Marcelo Bento Soares
Columbia University and the New
York State Psychiatric Institute
William Studier
Brookhaven National Laboratory
Grant Sutherland
Women's and Children's Hospital,
Adelaide
Barbara Trask
University of Washington
Gert-Jan B. van Ommen
Leiden University
Robert B. Weiss
University of Utah
Jean Weissenbach
Genethon, CNRS
Richard Wilson
Washington University School of
Medicine
James Womack
Texas A&M University

Editorial Office

Cold Spring Harbor Laboratory Press
1 Bungtown Road
Cold Spring Harbor, New York 11724
Phone (516) 367-8492
Fax (516) 367-8334
<http://www.cshl.org>

Editorial/Production

Nadine Dumser, Technical Editor
Kristin Kraus, Production Editor
Cynthia Grimm, Production Assistant
Doris Lawrence, Editorial Secretary

RESEARCH

Complete Genomic Sequence and Analysis of 117 kb of Human DNA Containing the Gene *BRCA1* Todd M. Smith, Ming K. Lee, Csilla I. Szabo, Nicole Jerome, Mark McEuen, Matthew Taylor, Leroy Hood, and Mary-Claire King 1029

A Nonsense Mutation in the Cathepsin K Gene Observed in a Family with Pycnodynostosis Maureen R. Johnson, Mihael H. Polymeropoulos, Hans L. Vos, Rosa Isela Ortiz de Luna, and Clair A. Francomano 1050

Long-range Map of a 3.5-Mb Region in Xp11.23-22 with a Sequence-ready Map from a 1.1-Mb Gene-rich Interval Dirk Schindelhauer, Heide Hellebrand, Lena Grimm, Ingrid Bader, Thomas Meitinger, Manfred Wehnert, Mark Ross, and Alfons Meindl 1056

Novel Susceptibility Locus for Mouse Hepatomas: Evidence for a Conserved Tumor Suppressor Gene Jean C. Zenklusen, Lewis V. Rodriguez, Margaret LaCava, Zhi Wang, Lawrence S. Goldstein, and Claudio J. Conti 1070

LETTERS

The Exon Structure of the Mouse *Sc1* Gene Is Very Similar to the Mouse *Sparc* Gene Peter J. McKinnon, Manuela Kapsetaki, and Robert F. Margolskee 1077

Alu Fossil Relics—Distribution and Insertion Polymorphism Santosh S. Arcot, Aaron W. Adamson, Jane E. Lamerdin, Brian Kanagy, Prescott L. Deininger, Anthony V. Carrano, and Mark A. Batzer 1084

Mapping the *RP2* Locus for X-linked Retinitis Pigmentosa on Proximal Xp: A Genetically Defined 5-cM Critical Region and Exclusion of Candidate Genes by Physical Mapping Dawn L. Thiselton, R. Mark Hampson, Manimekelei Nayudu, Lionel Van Maldergem, Mitchel L. Wolf, Bratin K. Saha, Shomi S. Bhattacharya, and Alison J. Hardcastle 1093

(continued)

**Isolation and Characterization of the Mouse
Cystatin B Gene**

Len A. Pennacchio and
Richard M. Myers

1103

GENOME METHODS

**Lane Tracking Software for Four-color
Fluorescence-based Electrophoretic Gel Images**

Matthew L. Cooper, David R.
Maffitt, Jeremy D. Parsons,
LaDeana Hillier, and David J. States

**End Sequence Determination from Large Insert
Clones Using Energy Transfer
Fluorescent Primers**

Marco Marra, Lori A. Weinstock,
and Elaine R. Mardis

**A Simple and Efficient Method for Making
Site-directed Mutants, Deletions, and Fusions of
Large DNA Such as P1 and BAC Clones**

Jan Borén, Isabelle Lee, Matthew J.
Callow, Edward M. Rubin, and
Thomas L. Innerarity

Product News

1131

COVER Genomic sequence and analysis of 117 kb of human DNA containing the *BRCA1* gene. (For details, see Smith et al., p. 1029.)