



BLOW UP YOUR GENOMICS WORKFLOW.

Automate nucleic acid QC and get on with your life sciences.

If sample QC takes you more than two minutes, it's too manual. Fragment Analyzer™ takes the job off your hands—streamlining lab operations and wiping out errors. Just pipette once and it delivers truly reliable results via automated capillary electrophoresis.

No chips. No tapes. No compromises.

- Setup in seconds
- Get resolution down to 2 base pairs
- Detection starts at 5 pg/µL

DITCH YOUR TIRED OLD WORKFLOW AT FRAGMENTANALYZER.COM.



Oligo Modifications?

Your wish is our command.



SKILLED AND ACCOMPLISHED CAPABILITIES

All Modifications and Oligo Types Synthesized

- Long oligos up to 250 mer
- Fluorescent Molecular Probes
- Ultra-Modified, DNA, RNA, Chimeric, Fluorescent, and Antisense Oligos
- Specializing in the design and synthesis of challenging combinations of modifications

An actual gel photo of each oligo is affixed on the oligo report.

An absolute testimony of quality.



Oligo Synthesis

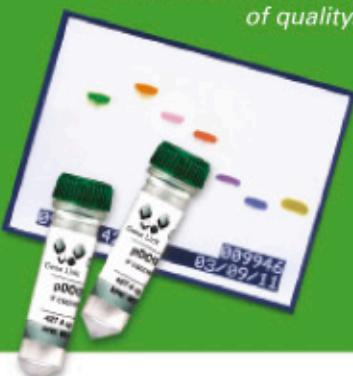
Providing oligos for demanding applications and consistent results for more than a decade

Gene Link. Results you can rely on.

toll free: **1-800-GENE LINK** | www.genelink.com

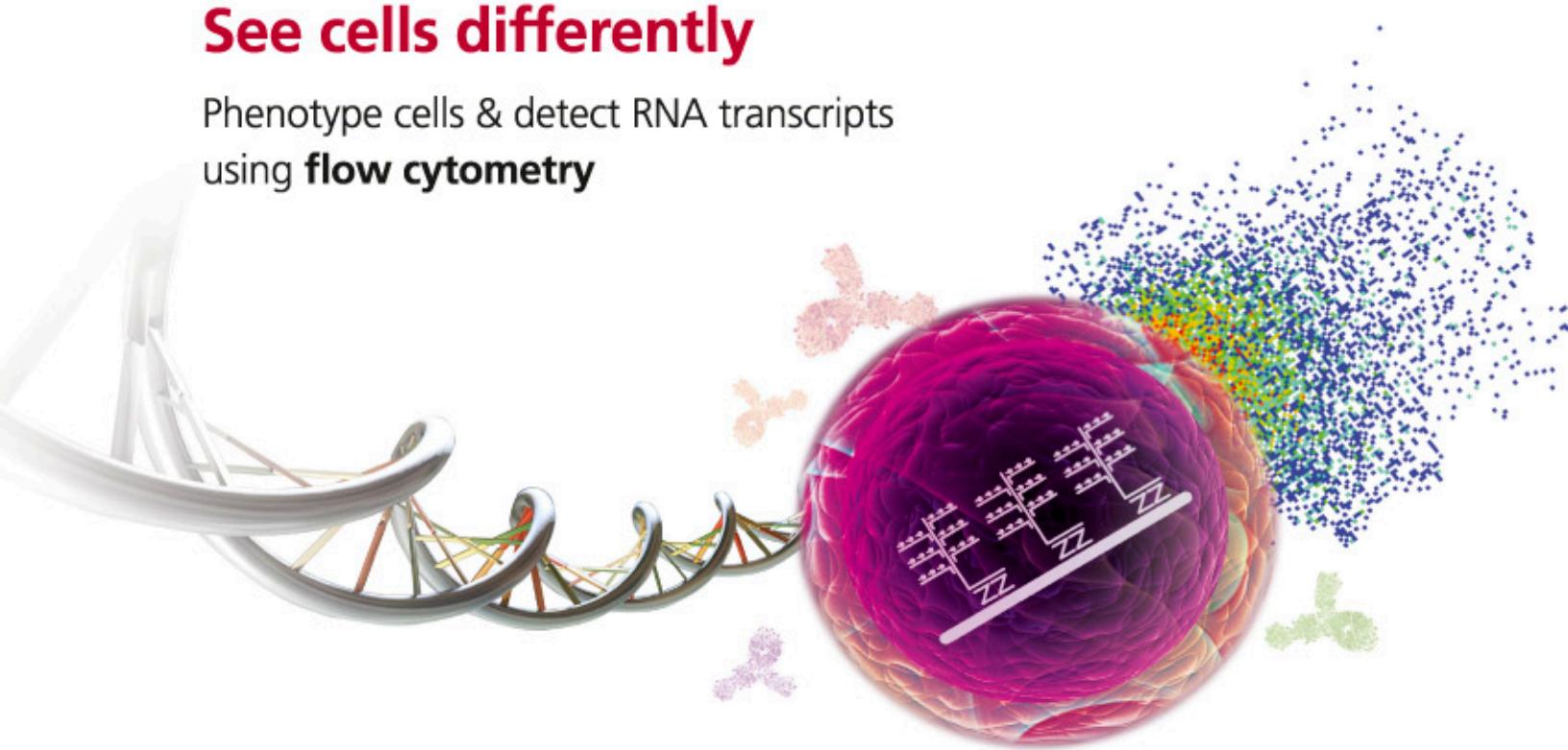


190 Saw Mill River Road
Hawthorne, NY 10532
tel: 914-769-1192
email: support@gene-link.com



See cells differently

Phenotype cells & detect RNA transcripts
using **flow cytometry**



Need to take a closer look at your cell's signature? Want to understand transcription regulation and patterns? Is RNA expressed intermittently or consistently?

Gain insight into single cell analysis with the QuantiGene® FlowRNA Assay,
a novel multiplex RNA hybridization protocol using a standard flow cytometer. Choose
from a catalog of more than 4,000 probes or request a custom set at no additional charge.

Show
Me
Data

Download scientific poster at ebioscience.com/FlowRNA-Genes

eBioscience, an Affymetrix company, provides innovative solutions to researchers and clinicians worldwide looking to answer questions driving today's life science community.

Biology for a better world.

NORTH AMERICA: 888.999.1371 ■ EUROPE: +43 1 796 40 40-304 ■ JAPAN: +81 (0)3 6430 4020 ■ INQUIRIES: info@ebioscience.com

©Affymetrix, Inc. All rights reserved. For Research Use Only. Not for use in diagnostic or therapeutic procedures.

eBioscience

GeneChip

Panomics

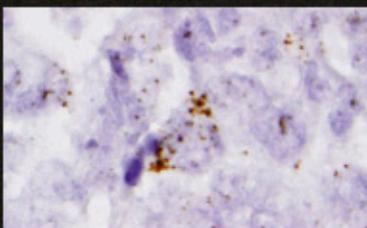
USB

BIGFOOT OR BACKPACKER?

Don't let ambiguous images lead you to the wrong conclusions. Get definitive results with RNAscope® technology.



IHC fails to detect Napsin A expression in lung adenocarcinoma



RNAscope ISH detects Napsin A RNA molecules in the same specimen

Take the RNAscope challenge:

Are IHC antibodies giving you ambiguous results? RNAscope is an RNA biomarker detection technology that delivers single molecule sensitivity with single cell resolution. Try RNAscope ISH and we'll credit your antibody expenses towards your purchase. We guarantee that RNAscope assay will work with your samples.*

Learn more at acdbio.com/RNAscopechallenge



Advanced Cell Diagnostics

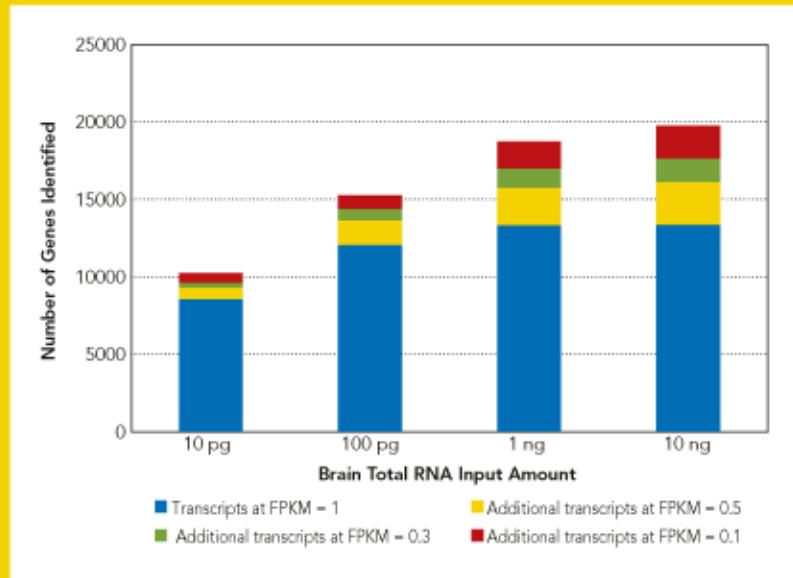
*Share your poor antibody results and expenses with us. We will provide you a credit of up to \$500 USD towards your purchase of RNAscope products, and guarantee that RNAscope will work with any samples where RNA is present. Limit one promotional credit per antibody.

For Molecular Biology Applications (MBA), not intended for diagnosis. Refer to appropriate regulations. RNAscope® is a registered trademark of Advanced Cell Diagnostics, Inc. Doc# 321084/031314/revA

Simply Lower Input.

Ovation® Single Cell RNA-Seq System

Generate strand-specific libraries with novel technology that enriches for coding and regulatory transcripts using as little as 10 picograms total RNA.



One tube. One day. It's that simple.



www.nugen.com

©2014 NuGEN Technologies, Inc. All rights reserved. The Encore®, Ovation® and Applause® families of products and methods of their use are covered by several issued U.S. and International patents and pending applications (www.nugen.com). NuGEN, Ovation, SPIA, Ribo-SPIA, Applause, Encore, Prelude, Mondrian and Imagine More From Less are trademarks or registered trademarks of NuGEN Technologies, Inc. Other marks appearing in these materials are marks of their respective owners.

For Research Use Only.

RNA-Seq libraries from degraded samples?



cDNA Synthesis Kits

cDNA SYNTHESIS FOR NEXT GEN SEQUENCING

Get it with SMARTer® confidence!

Generate Illumina® ready libraries with strand information in under 4 hours!



Extreme sensitivity. Robust performance. Reproducible data.

SMART™ technology has been adopted as the industry standard for experiments that require exceptional sensitivity and complete transcriptome coverage. The new SMARTer Stranded method uses the same core technology used in our acclaimed SMARTer Ultra™ Low kits but with random hexamer primers for transcriptome analysis of polyA, non-polyA or degraded samples (like FFPE) to provide both coding and non-coding information.

The kit is highly sensitive and works with input ranges of 100 pg to 100 ng to generate quality RNA-seq data. The kit has also been developed to be compatible with both upstream commercial ribosomal RNA removal methods or polyA isolated material.

See more data at
www.clontech.com/SMARTer-stranded
or call 1.800.662.2566



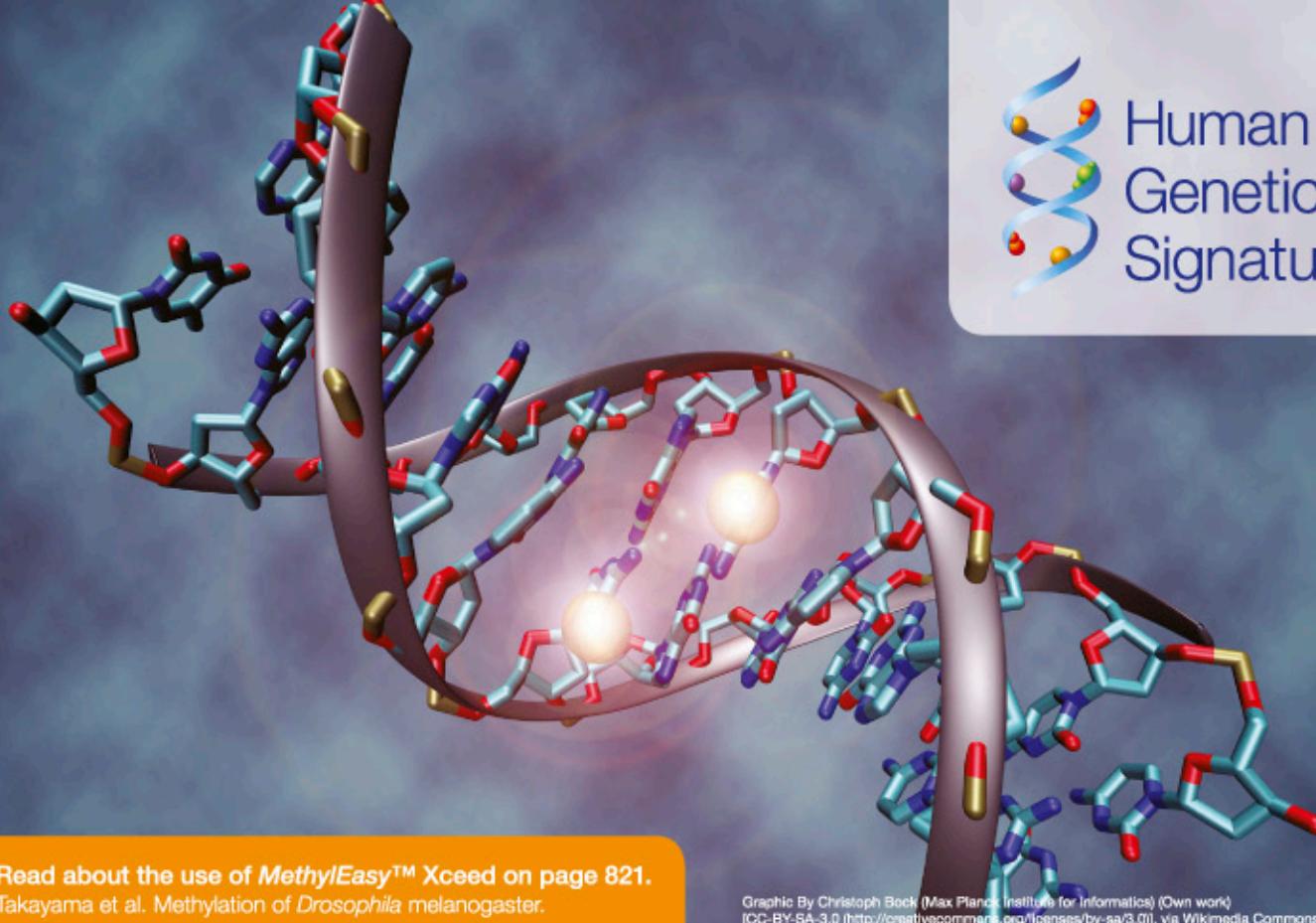
Scan to find out more.



Clontech Laboratories, Inc. • A Takara Bio Company

United States/Canada: +1.800.662.2566 • Asia Pacific: +1.800.910.7300 • Europe: +33.011.3804.6880 • Japan: +81.0377.543.7247
For Research Use Only. Not for use in diagnostic or therapeutic procedures. Not for resale. Illumina is a trademark of Illumina, Inc. Clontech®, the Clontech logo, SMART, SMARTer, Ultra, and that's GOOD science! are trademarks of Clontech Laboratories, Inc. Takara and the Takara logo are trademarks of TAKARA HOLDINGS, Kyoto, Japan. All other marks are the property of their respective owners. Certain trademarks may not be registered in all jurisdictions. © 2014 Clontech Laboratories, Inc.

www.clontech.com 04.14 US 633648



* Read about the use of *MethylEasy™ Xceed* on page 821.
Takayama et al. Methylation of *Drosophila melanogaster*.

Graphic By Christoph Bock (Max Planck Institute for Informatics) (Own work) [CC-BY-SA-3.0 (<http://creativecommons.org/licenses/by-sa/3.0>)], via Wikimedia Commons

MethylEasy™ Xceed Enabling Leading DNA Methylation Research*

Methylation has been shown to be important in cancer development, embryogenesis and stem cell function. *MethylEasy™ Xceed* was developed by the pioneers of the original bisulfite sequencing method¹ to deliver world-class DNA conversion efficiencies. The power of *MethylEasy™ Xceed* has been demonstrated in landmark papers providing single base resolution of methylated cytosines, such as in the human genome².

MethylEasy™ Xceed provides you with a simple, sensitive and, rapid conversion method that eliminates the need for pre-treatment, improves sensitivity, increases amplification efficiency, generates longer fragments and increases stability of the template DNA.

What our Customers are saying

It's easy! I routinely use *MethylEasy™* for my DNA methylation work. It's consistent, reliable and now much easier with *MethylEasy™ Xceed* cutting down conversion times to just a few hours. Simply brilliant!

Dr. Nicholas Wong
Ludwig Cancer Research

- ✓ **Easy to Use** – No DNA pre-treatment necessary and easy column purification
- ✓ **Sensitive** – Start from as little as 50 picograms of DNA (approx. 8 mammalian cell equivalents)
- ✓ **Fast Reactions** – Processing time is 90 mins total from wild type to fully modified DNA
- ✓ **Excellent DNA Preservation** – Reduce DNA degradation by more than 90% to obtain truly representative analysis of methylated cytosines
- ✓ **Better Conversion** – No evidence of DNA non-conversion found in sequencing analysis
- ✓ **Internal controls** – Included for absolute reaction confidence and product support
- ✓ **Great value per reaction**

1. Frommer M, McDonald C, Millar DS et al (1992). A genomic sequencing protocol that yields a positive display of 5-methylcytosine residues in individual DNA strands. *Proc Natl Acad Sci, USA* 89: 1827-1831.

2. Lister R, Pelizzola M, Dowen RH, et al (2009). Human DNA methylomes at base resolution show widespread epigenomic differences. *Nature*, 462(7271): 315-22.

Historical Breakthroughs



Breathtaking Progress

Radical Reinvention



Introducing **NextSeq™**
A Whole Human Genome on Your Desktop

RNA-Seq Starting at \$450!

Total RNA-Seq: Save up to \$1800!

(lncRNA + mRNA + small RNA)

For an in-depth approach to analysing RNA regulatory mechanisms at a great price with short turnaround times, come to BGI, where more than 60,000 RNA-Seq samples have been sequenced and analysed.

Promotion Details:

Valid for Americas and Europe customers NOW through June 30

A Total RNA sequencing (including lncRNA, mRNA, miRNA) save up to 1,800 USD per sample

- Available when purchasing the Whole Transcriptome RNA-Seq (long non-coding RNA and mRNA) together with the small RNA-Seq (miRNA) services
- Comprehensive analysis of the entire transcriptome, including the traditional mRNA and miRNA analysis, as well as lncRNA assembly, prediction, quantification and function prediction
- Turnaround time: 8 weeks; minimum order: 5 samples.

B RNA-Seq quantification (mRNA) starting at \$450/sample

- Promotional pricing available for 10M to 40M clean reads
- 50 bp single-end sequencing on HiSeq 2000
- Affordable bioinformatics analysis at only \$125/sample, including data filtering and QC, gene expression quantification, differential gene expression analysis, gene ontology and pathway analysis, and group differential expression analysis
- Turnaround time: 6-8 weeks; minimum order: 20 samples.

BGI also provides RNA-Seq quantification by Ion Proton with 4 weeks turnaround time at the same affordable prices

C RNA-Seq transcriptome (mRNA) starting at \$500/sample

- Promotional pricing available for 10M to 40M clean reads
- 100 bp paired-end sequencing on HiSeq 2000
- Affordable bioinformatics analysis starting at \$200/sample, including data filtering and QC, gene expression quantification, differential gene expression analysis, gene ontology and pathway analysis, identification of alternatively spliced and novel transcripts, SNP calling and annotation, and gene fusion analysis
- Turnaround time: 6-8 weeks; minimum order: 20 samples.

Sequencing power for every scale.



The HiSeq X Ten contains 10 sequencing systems.

NEW
HiSeq X™ Ten

Population power.

\$1000 human genome and extreme throughput for population-scale sequencing.



HiSeq® 2500

Production power.

Power and efficiency for large-scale genomics.



NEW
NextSeq™ 500

Flexible power.

Speed and simplicity for whole-genome, exome, and transcriptome sequencing.



MiSeq®

Focused power.

Speed and simplicity for targeted and small-genome sequencing.



MiSeqDx™

Focused Dx power.

The first and only FDA-cleared *in vitro* diagnostic next-generation sequencing system.

Find the right sequencer to fit your every need. www.illumina.com/power

©2014 Illumina, Inc. All rights reserved.

illumina®



immunogenomics 2014

September 29–October 1, 2014
HudsonAlpha Biotechnology Campus
Huntsville, AL, USA

**Join us at the intersection of genomics and immunology
and change the way you view disease**



Our keynote speakers:

Christophe Benoist

*Professor, Department of Microbiology and Immunobiology,
Harvard Medical School*

Mary Ellen Conley

*Federal Express Chair of Excellence and Professor, Department
of Pediatrics, University of Tennessee, College of Medicine, Memphis*

Mark Davis

*Investigator, Howard Hughes Medical Institute; Professor, Department
of Microbiology and Immunology; Director, Institute for Immunity,
Transplantation, and Infections, Stanford University School of Medicine*



Abstract deadline: July 18, 2014
Early booking deadline: August 1, 2014

Register today at haig.aaas.org

presented by



HUDSONALPHA
INSTITUTE FOR BIOTECHNOLOGY

Science

AAAS

What's Next?

For your NGS Library Prep from New England Biolabs

With NEBNext[®], take advantage of our suite of products specifically designed for an improved NGS library prep experience. You asked and we delivered products to address the most common challenges with library prep.

NEBNext Ultra[™] Kits for DNA and RNA (including Directional)

- ✓ Fast, streamlined workflows
- ✓ Low input amounts (low ng to μ g)
- ✓ High yields
- ✓ Robust, reliable protocols
- ✓ Ultra high fidelity
- ✓ Multiplexing
- ✓ Minimized GC bias

Visit NEBNext.com to view a webinar on how NEBNext Ultra is enabling library prep for multiple applications.



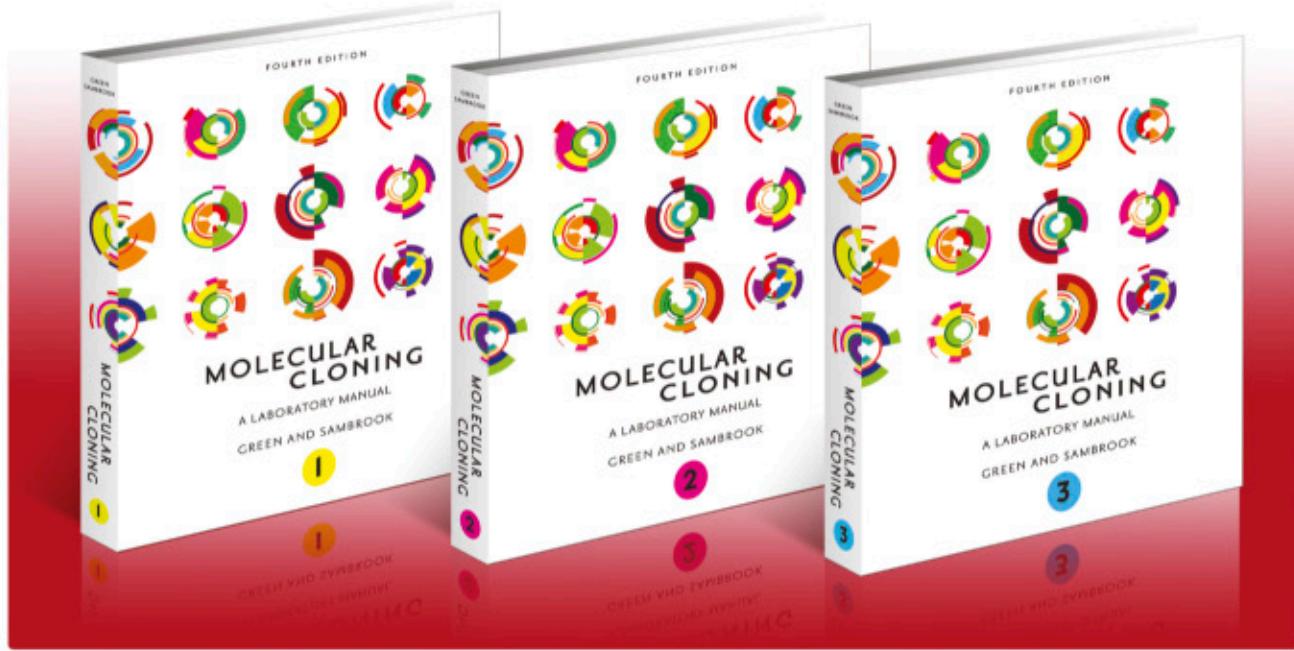
NEBNext.com

NEW ENGLAND BIOLABS[®] and NEBNEXT[®] are registered trademarks of New England Biolabs, Inc.
ULTRA[™] is a trademark of New England Biolabs, Inc.

 NEW ENGLAND
BioLabs[®]_{Inc.}
enabling technologies in the life sciences



MOLECULAR CLONING 4



By Michael R. Green, *Howard Hughes Medical Institute, University of Massachusetts Medical School* and Joseph Sambrook, *Peter MacCallum Cancer Institute, Melbourne, Australia*

Molecular Cloning: A Laboratory Manual has always been the one indispensable molecular biology laboratory manual for protocols and techniques. The fourth edition of this classic manual preserves the detail and clarity of previous editions as well as the theoretical and historical underpinnings of the techniques presented. Ten original core chapters reflect developments and innovation in standard techniques and introduce new cutting-edge protocols. Twelve entirely new chapters are devoted to the most exciting current research strategies, including epigenetic analysis, RNA interference, genome sequencing, and bioinformatics. This manual is essential for both the inexperienced and the advanced user.

2012, 2,028 pp., illus., appendices, index

Cloth (three-volume set)

\$395

Paperback (three-volume set)

\$365

ISBN 978-1-936113-41-5

ISBN 978-1-936113-42-2

Contents

VOLUME 1

Part 1 Essentials

1. Isolation and Quantification of DNA
2. Analysis of DNA
3. Cloning and Transformation with Plasmid Vectors
4. Gateway Recombinational Cloning
5. Working with Bacterial Artificial Chromosomes and Other High-Capacity Vectors
6. Extraction, Purification, and Analysis of RNA from Eukaryotic Cells
7. Polymerase Chain Reaction
8. Bioinformatics

VOLUME 2

Part 2 Analysis and Manipulation of DNA and RNA

9. Quantification of DNA and RNA by Real-Time Polymerase Chain Reaction
10. Nucleic Acid Platform Technologies
11. DNA Sequencing
12. Analysis of DNA Methylation in Mammalian Cells
13. Preparation of Labeled DNA, RNA, and Oligonucleotide Probes
14. Methods for In Vitro Mutagenesis

Part 3 Introducing Genes into Cells

15. Introducing Genes into Cultured Mammalian Cells
16. Introducing Genes into Mammalian Cells: Viral Vectors

VOLUME 3

Part 4 Gene Expression

17. Analysis of Gene Regulation Using Reporter Systems
18. RNA Interference and Small RNA Analysis
19. Expressing Cloned Genes for Protein Production, Purification, and Analysis

Part 5 Interaction Analysis

20. Cross-Linking Technologies for Analysis of Chromatin Structure and Function
21. Mapping of In Vivo RNA-Binding Sites by UV-Cross-Linking Immunoprecipitation (CLIP)
22. Gateway-Compatible Yeast One-Hybrid and Two-Hybrid Assays

Appendices

1. Reagents and Buffers
2. Commonly Used Techniques
3. Detection Systems
4. General Safety and Hazardous Material

Index



WWW.CSHLPRESS.ORG

SGHDNA

From the innovators of the Gibson™ Assembly Method, and the first synthetic cell...

...A proprietary suite of DNA synthesis and assembly technologies at your fingertips.



DNATILES



DNA CLONES



DNALIBRARIES

- Linear dsDNA products up to 3kb in length
- Sequence confirmed
- Compatible with Gibson™ Assembly Method
- Faster delivery and more affordable

- Up to 2 Mbp in length
- Error free sequence confirmed
- plasmid DNA
- Complex synthesis

- Flexible formats
- Digital Library design
- Available as Tiles™ or Clones

Double stranded DNA made easy:

Don't clone your gene. Order it!

Find out more:

SGI-DNA, Inc

www.sgidna.com

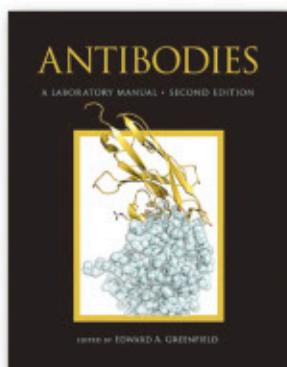
info@sgidna.com

t.(855) 4SGI-DNA



ANTIBODIES

A Laboratory Manual, Second Edition



Edited by Edward A. Greenfield, *Dana-Farber Cancer Institute*

The second edition of the now-classic lab manual *Antibodies*, by Harlow and Lane, has been revised, extended, and updated by Edward Greenfield of the Dana-Farber Cancer Center, with contributions from other leaders in the field. This manual continues to be an essential resource for molecular biology, immunology, and cell culture labs on all matters relating to antibodies. The chapters on hybridomas and monoclonal antibodies have been recast with extensive new information and there are additional chapters on characterizing antibodies, antibody engineering, and flow cytometry. As in the original book, the emphasis in this second edition is on providing clear and authoritative protocols with sufficient background information and troubleshooting advice for the novice as well as the experienced investigator.

2013, 847 pp., illus. (32 4C, 103 B&W), appendices, index

Hardcover \$260

Paperback \$175

ISBN 978-1-936113-80-4

ISBN 978-1-936113-81-1

Contents

Preface

1 Antibody Production by the Immune System
Stefanie Sarantopoulos

2 The Antibody Molecule
Stefanie Sarantopoulos

3 Antibody-Antigen Interactions
Stefanie Sarantopoulos

4 Antibody Responses
Stefanie Sarantopoulos

5 Selecting the Antigen
Edward A. Greenfield, James DeCaprio, and Mohan Brahmandam

6 Immunizing Animals
Edward A. Greenfield

7 Generating Monoclonal Antibodies
Edward A. Greenfield

8 Growing Hybridomas
Edward A. Greenfield

9 Characterizing Antibodies
Frances Weis-Garcia and Robert H. Carnahan

10 Antibody Purification and Storage
Jordan B. Fishman and Eric A. Berg

11 Engineering Antibodies
James Dasch and Amy Dasch

12 Labeling Antibodies
Eric A. Berg and Jordan B. Fishman

13 Immunoblotting
Larisa Litovchick

14 Immunoprecipitation
James DeCaprio and Thomas O. Kohl

15 Immunoassays
Thomas O. Kohl and Carl A. Ascoli

16 Cell Staining
Scott J. Rodig

17 Antibody Screening Using High Throughput Flow Cytometry
Thomas D.L. Duensing and Susan R. Watson

Appendix I: Electrophoresis

Appendix II: Protein Techniques

Appendix III: General Information

Appendix IV: Bacterial Expression

Appendix V: Cautions

Index



www.cshpress.org

www.macrogen.com

Opening of \$1,000 Genome Era by Macrogen

New Genome Analysis Technologies
Can Change Your Future.



Advancing through Genomics

Macrogen Inc.
10F, 254 Beotkkot-ro Geumcheon-gu,
Seoul, Rep. of Korea



Macrogen Clinical Laboratory
11330 Piccard Drive, Suite 205,
Rockville, MD 20850 U.S.A.



**YOUR
EXPERIMENTS** **OUR
EXPERTISE**

RNA SEQUENCING | METHYLATION ANALYSIS | CANDIDATE GENE/PANEL SEQUENCING | WHOLE EXOME SEQUENCING | MICRO RNA SEQUENCING

GENOMIC KNOW-HOW®. IT'S HOW YOUR EXPERIMENTS SUCCEED.

You need answers to complex biological questions. We have deep expertise across a wide range of genomic technologies to help you make the best choices to get it right the first time. Our experienced scientists leverage innovative bioinformatics to provide insightful genomic data. When it comes to your precious samples, EA | Quintiles is the right choice to deliver the genomic information you need to succeed. Tell us about your experiment at genomicknowhow.com.

