"i can go where the biology takes me."

"In research, one discovery leads to another which leads…well, who knows where? The Illumina Genome Analyzer gives me the technology to follow almost any path. Only with this system could we create the most detailed and integrated epigenome map to date for any species."

Dr. Brian Gregory
Postdoctoral Fellow
The Salk Institute for Biological Studies

Study the genome. Epigenome. Transcriptome. All at single base-pair resolution. Do more, and do it better, with the Illumina Genome Analyzer.

~~Next~~-gen Sequencing now

www.illumina.com/sequencingGR

SEQUENCING
GENOTYPING
GENE EXPRESSION

illumina®

HudsonAlpha Institute for Biotechnology

Join us in applying genome-scale technology to humanity's toughest problems

Group Leaders needed for HudsonAlpha Genome Sequencing Center:
Annotation and Assembly Group Leader
Finishing Group Leader
Library Construction Group Leader

Resumes also currently being accepted for:

Senior Research Scientists
Postdocs
Research Associates and Assistants

Current Investigators:

Richard M. Myers, Ph.D.
Director and Investigator

Devin M. Absher, Ph.D.
Investigator

Jane Grimwood, Ph.D.
Investigator

Jian Han, M.D., Ph.D.
Investigator

Jeremy Schmutz
Investigator

Greg Barsh, M.D., Ph.D.
Visiting Investigator

For descriptions of research areas see hudsonalpha.org/pages/sr-researchareas.html

Please send resume and cover letter to:
Dr. Chris Gunter
Director of Research Affairs

resumes@hudsonalpha.org

About HudsonAlpha

From spirit to physical design, the institute's primary facility embodies and nurtures the sharing of ideas and information. Researchers employed by the not-for-profit HudsonAlpha Institute reside in one wing of the 270,000 square-ft. facility, while a separate wing houses 14 for-profit businesses. The wings are physically bridged with walkways spanning a soaring atrium that features inviting common areas. Proximity to the University of Alabama in Huntsville, the University of Alabama at Birmingham, Auburn University and Vanderbilt University adds to a rich intellectual environment for collaboration, discovery and innovation.

HUDSONALPHA
INSTITUTE FOR BIOTECHNOLOGY

Huntsville, AL • hudsonalpha.org

genomic research • educational outreach • economic development

Speed Up Your Genome Research!

Ensure Rapid and Efficient Blunt-End Repair of Genomic DNA

The End-It™ DNA End-Repair Kit rapidly and efficiently converts nebulized, sonicated, or sheared genomic DNA to 5′-phosphorylated, blunt-ended DNA for subsequent genomic cloning or next-gen sequencing.

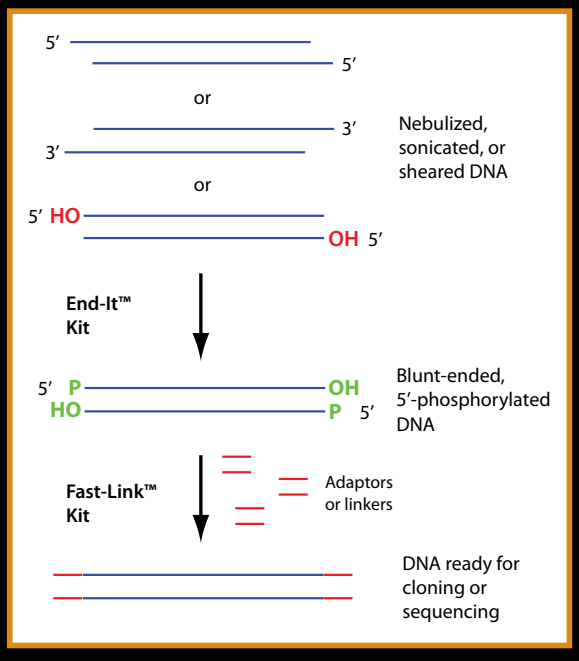
- Repaired DNA is blunt-ended and 5′ phosphorylated for immediate blunt-end ligation.
- End-repair up to 5 µg of genomic DNA per reaction.

Then,

Perform Blunt-End Ligations in as Little as 15 Minutes

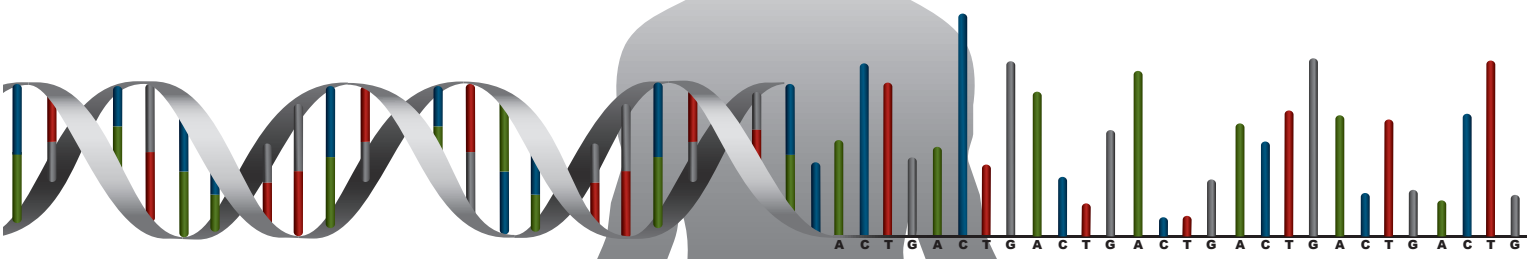
The Fast-Link™ DNA Ligation Kit uses a high-quality, specially formulated ligase to provide extremely rapid, high-efficiency DNA ligations.

- Blunt-end ligations in as little as 15 minutes.
- Cohesive-end ligations in 5 minutes.



EPICENTRE® Biotechnologies

www.EpiBio.com 800-284-8474



Seize the Exome

NimbleGen Sequence Capture 2.1M Human Exome Arrays

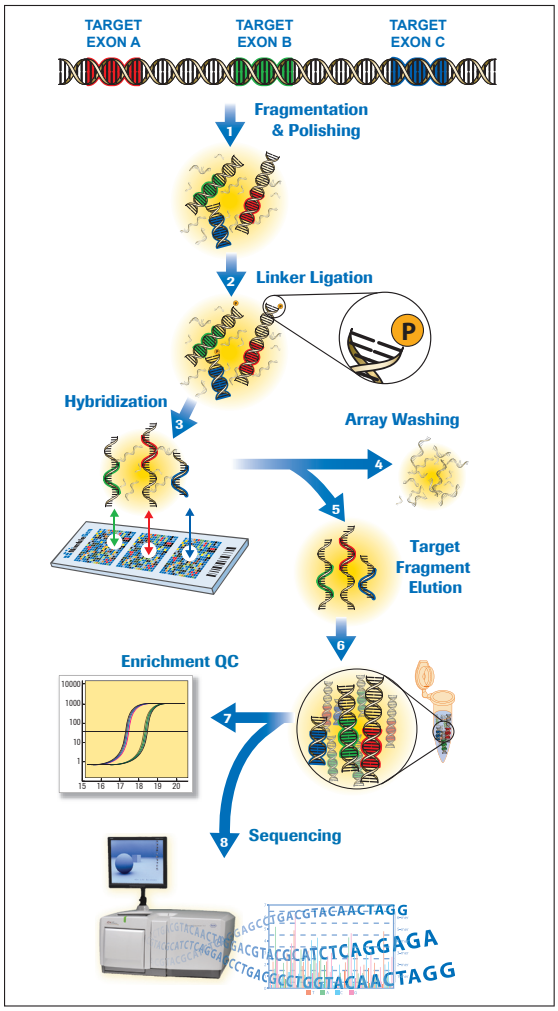
Now Available for 454 Sequencing Systems

NimbleGen

454 SEQUENCING

Revolutionary sample preparation for targeted next-generation resequencing

Design and perform cost-effective targeted resequencing studies that were effectively impossible with PCR-based methods



▲ **The NimbleGen Sequence Capture Protocol.** 1. Genomic DNA sample is fragmented and polished. 2. Linkers are ligated to the fragments. 3. Sample is hybridized to a NimbleGen Sequence Capture 2.1M Human Exome array. 4. Unbound fragments are washed away. 5. Target fragments are eluted. 6. The target-enriched pool is amplified. 7. The enriched, amplified pool is verified by qPCR. 8. Sample is ready for high-throughput sequencing, such as with the Genome Sequencer FLX Instrument from 454 Life Sciences.

2.1 Millon Probes:
Targeted Resequencing Taken to the Next Level

- **Capture the Human Exome:** Use only one 2.1M array to capture ~180,000 exons and ~550 miRNA in your own lab (Table 1).
- **Target Specific Regions of Interest:** Capture up to 30Mb contiguous or non-contiguous human genomic regions with high coverage and specificity, using a 2.1M Custom Delivery array.
- **Reduce Cost:** Save time and cost compared to PCR-based methods.
- **Rely on Design Expertise:** Ensure a high level of specificity and sensitivity for human exome and custom designs with an empirically tested and proven capture design algorithm.

Exome Resequencing of Human Disease Case	
Total size of target region	34Mb
Percentage of 454 unique sequencing reads mapping to exon targets	80%
Percentage of bases with 1x coverage	91%
Median fold coverage	8

▲ **Performance Data.** NimbleGen Sequence Capture 2.1M Human Exome arrays were used to capture approximately 180,000 coding exons and 550 miRNA exons from a research study using a human disease case sample. Two PicoTiterPlate devices were used to generate ~1Gb of raw sequence on the captured sample using GS FLX Titanium kits (400bp reads; 1,000,000 reads per run) and the Genome Sequencer FLX Instrument. Note the high specificity (80%) and percentage of bases with at least one sequencing read (91%) at a median fold coverage of 8-fold.

NimbleGen

To learn more visit **www.nimblegen.com/seqcap**
or call **(877) NimbleGen / (608) 218-7600**

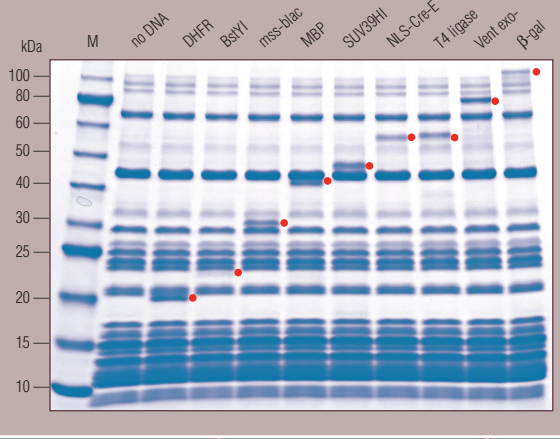
454 SEQUENCING

PURE AND SIMPLE

PURExpress™ *In Vitro* Protein Synthesis Kit

A rapid method for gene expression analysis, PURExpress™ is a novel cell-free transcription/translation system reconstituted from purified components necessary for *E. coli* translation. Express a wide range of proteins free of modification or degradation by simply mixing two tubes followed by the addition of template DNA. With results available in only a few hours, PURExpress saves valuable laboratory time and is ideal for high throughput technologies.

Protein expression using the PURExpress™ *In Vitro* Protein Synthesis Kit from NEB



Reactions were carried out according to manual recommendations. Red dot indicates protein of interest. Marker M is the Protein Ladder (NEB #P7703).

Advantages:

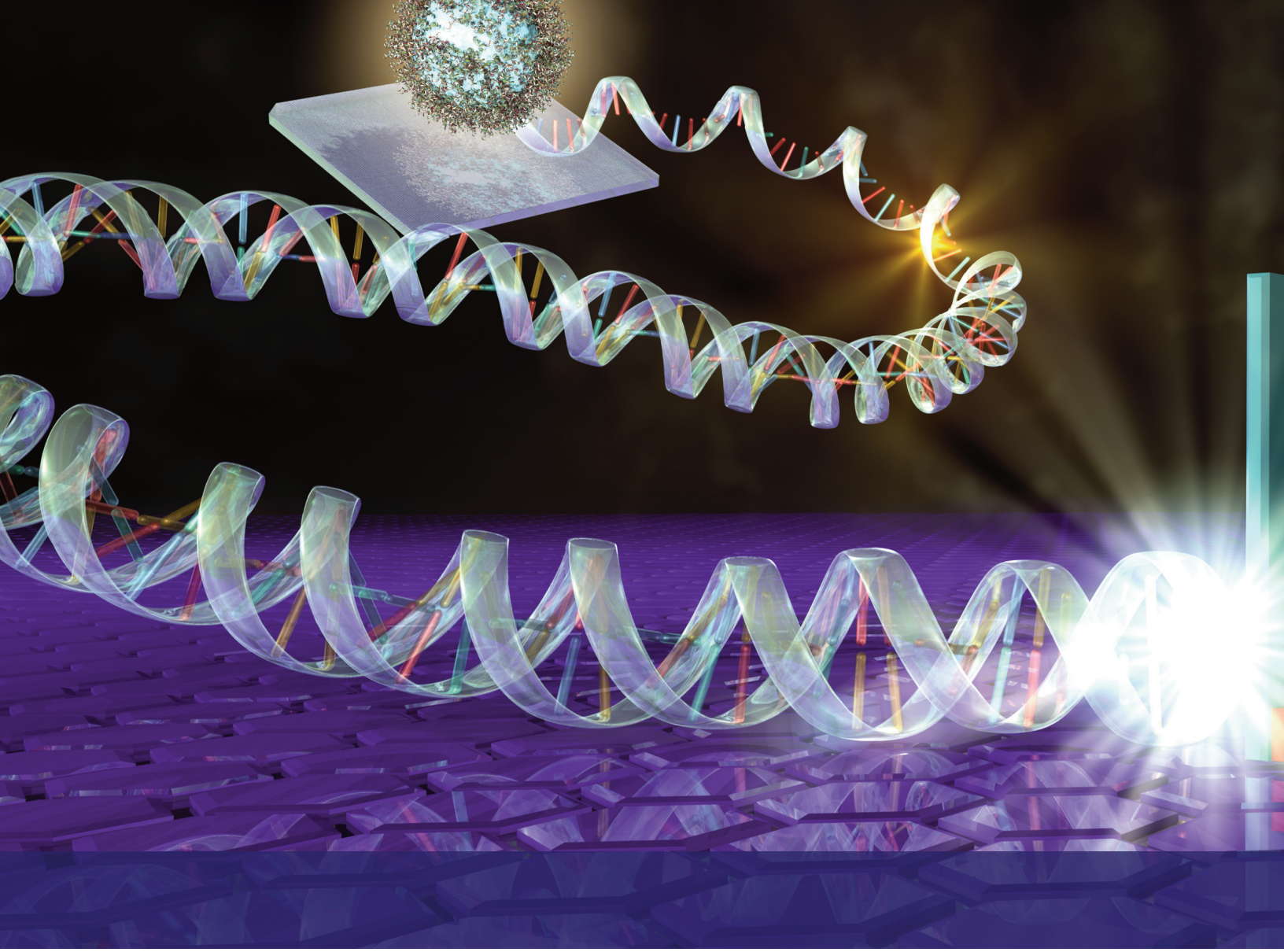
Cleaner system - lack of endogenous proteases or nucleases eliminates sample degradation

Simple analysis - synthesized protein can often be visualized on a Coomassie stained gel

Easy-to-use - requires the mixing of two tubes followed by the addition of template DNA

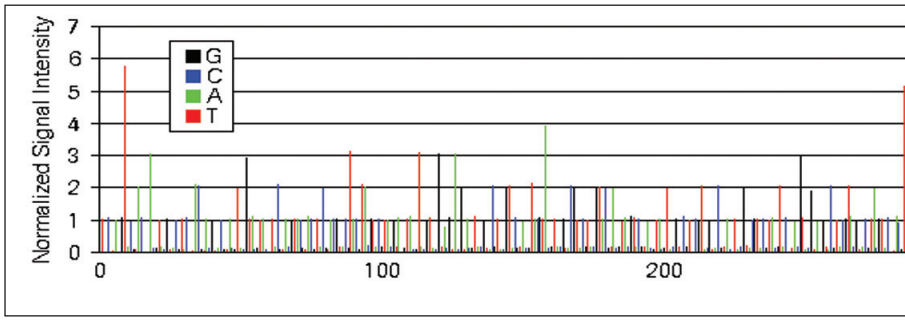
PURExpress *In Vitro* Protein Synthesis Kit E6800S

NEW ENGLAND BioLabs® Inc.
enabling technologies in the life sciences



Genome Sequencer FLX System

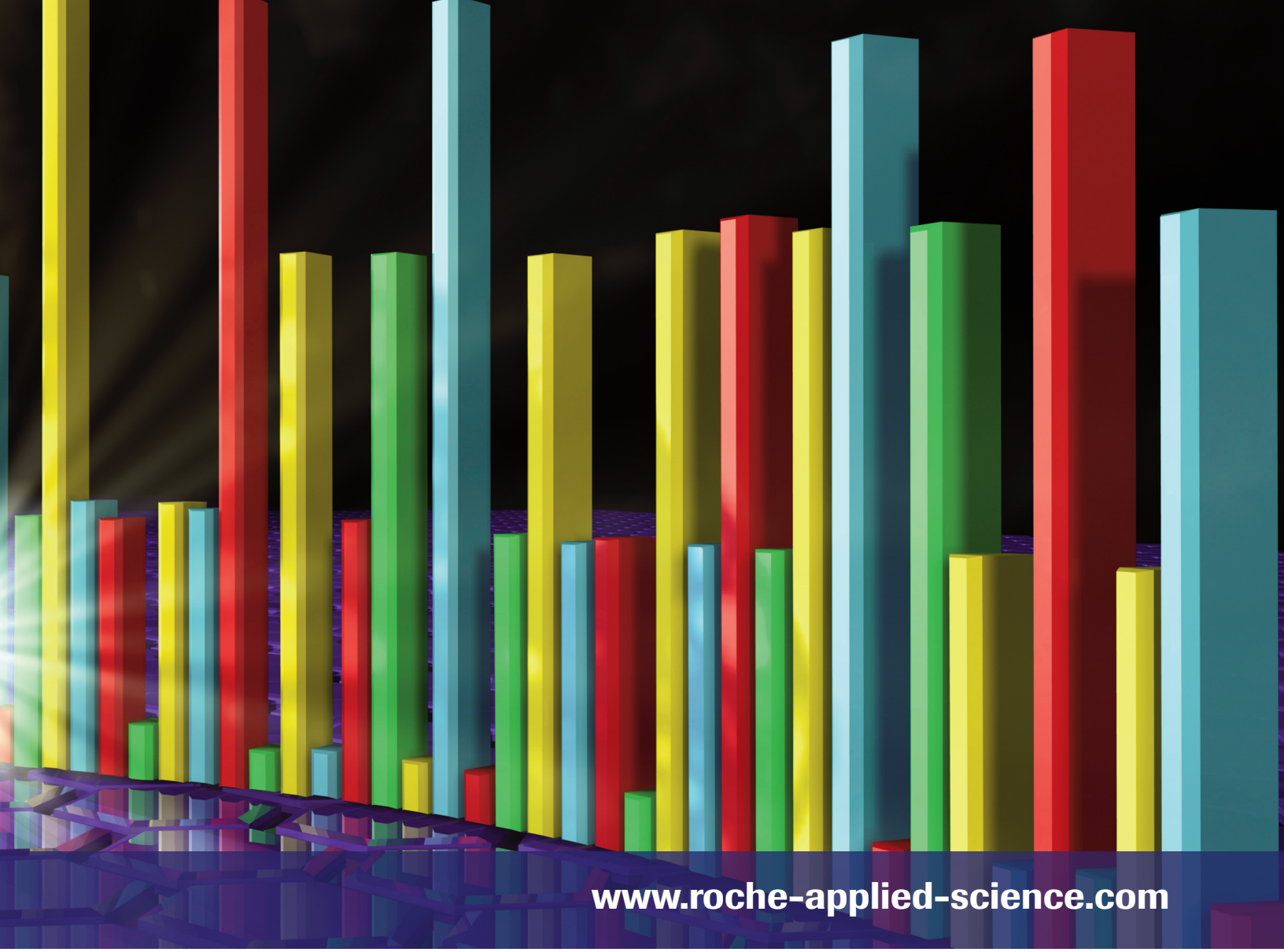
Really Length Matters



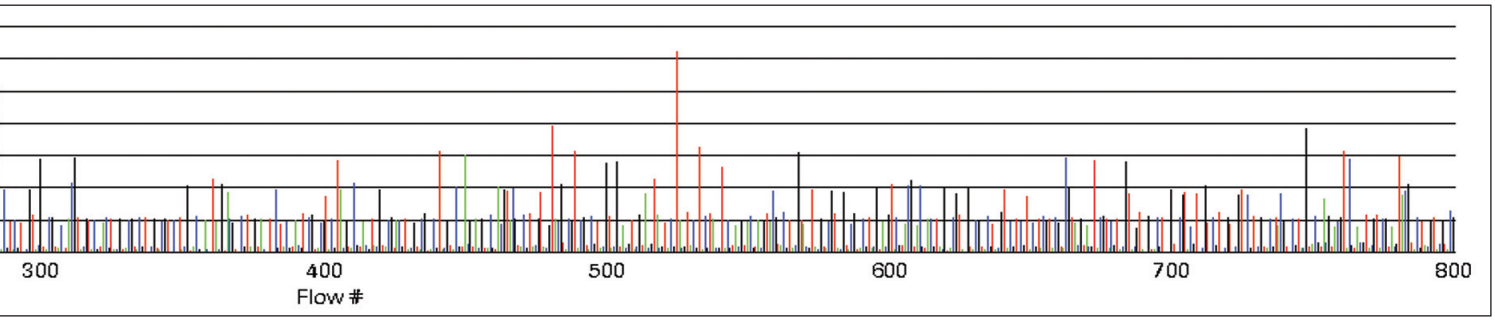
DNA Sequencing Flowgram: Each bar within the flowgram represents a discrete nucleotide (A, T, C, or G) and the height of the bar corresponds to the number of nucleotides detected. Although the majority of sequencing reads are 400 to 500 bases, the above flowgram represents a sequencing read of 543 bases.

454 SEQUENCING

For life science research only. Not for use in diagnostic procedures.



Introducing the GS FLX Titanium Reagents



- **Obtain sequencing read lengths of 400 to 500 bases.**
- **Generate more than 1 million sequencing reads per 10-hour instrument run.**

Learn more at ***www.454.com***

Roche Diagnostics
Roche Applied Science
Indianapolis, Indiana

Roche

BioSupplyNet

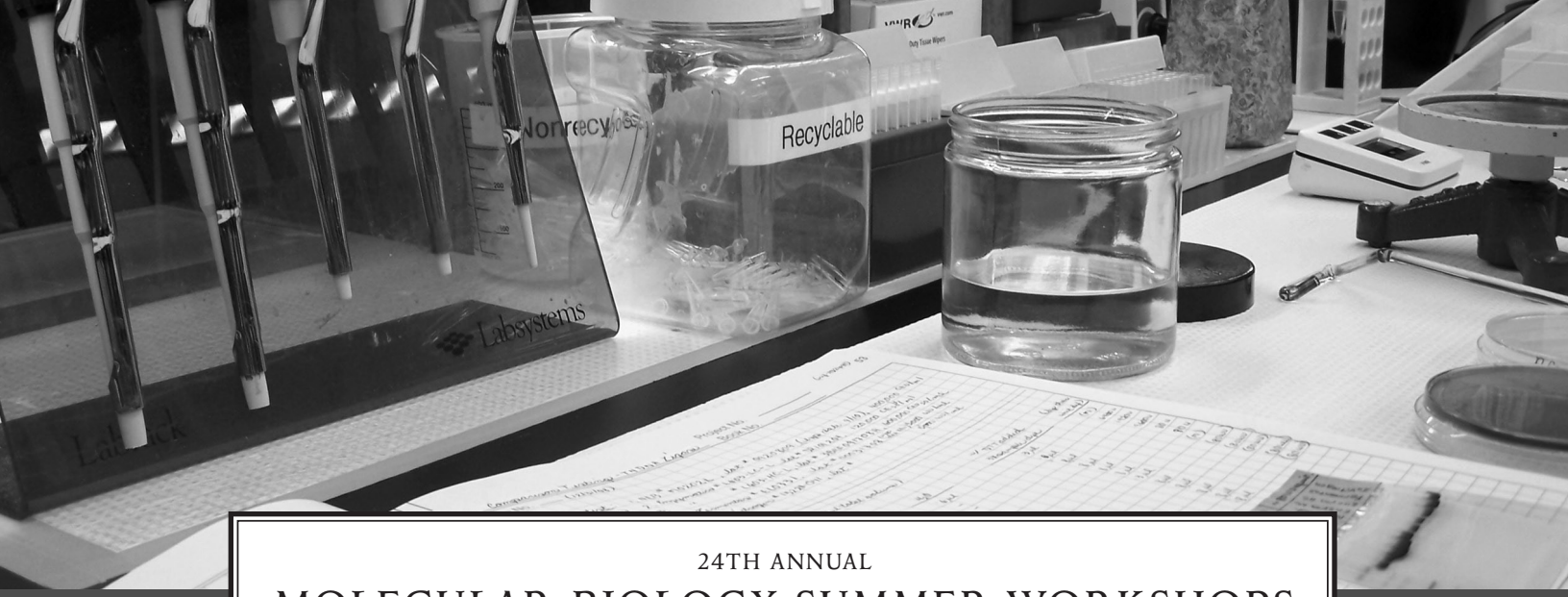
BioSupplyNet.com is your one-stop directory source for life science laboratory supplies and services. Concise and user-friendly, **BioSupplyNet.com** provides direct access to over 6500 companies and 20,000 products.

FEATURES:

- **Download FREE protocols from Cold Spring Harbor Protocols—*www.cshprotocols.org***
- **Search for the latest kits and catalogs**
- **See the latest products and special promotions**
- **Sign up for a free monthly newsletter detailing new protocols and products**
- **Visit our updated career center**

www.BioSupplyNet.com

CSH PRESS



24TH ANNUAL

MOLECULAR BIOLOGY SUMMER WORKSHOPS

Learn Molecular Biology in 1 or 2 Weeks!

We are pleased to announce the twenty-fourth annual Molecular Biology Summer Workshops, sponsored by New England Biolabs in conjunction with Smith College. Workshops are held at the Clark Science Center, Smith College, Northampton, MA, USA. Well over 3,000 people have graduated from this intensive training program in the past twenty-three years. These intensive courses emphasize hands-on molecular biology laboratory work and cover a wide variety of topics and techniques. No prior experience in molecular biology is required.

when:

two-week sessions:
Session 1: June 7 - June 20, 2009
Session 3: July 12 - July 25, 2009

one week sessions:
Session 2: June 25 - July 1, 2009
Session 4: August 2 - August 7, 2009
(lecture course only)

where:

Clark Science Center
Smith College
Northampton, MA USA 01063

Dr. Steven A. Williams

to apply:

website:
http://www.science.smith.edu/neb

email:
biolabs@email.smith.edu

phone:
(413) 247-3004

Both ONE week and TWO week Molecular Biology Sessions available!
Session 2 is a one week short course that covers DNA cloning, PCR, DNA sequencing, genomics and bioinformatics. Sessions 1 and 3 cover twice as much material and are our most popular courses. These sessions add techniques used in gene expression analysis including microarray analysis, RNAi and quantitative RT-PCR, more bioinformatics and genomics and protein expression. All of the above topics are covered in the two-week sessions. Session 4 will cover all of the topics in the two week laboratory course, but will be a lecture-only course for those not requiring hands-on laboratory experience.

application information: No previous experience in molecular biology is required or expected. Forty participants per session will be selected from a variety of disciplines and academic backgrounds, including principal investigators, directors of programs, medical doctors, postdoctoral fellows, graduate students, research assistants, sales associates, equipment engineers, etc.

fee: $3995 per participant (2 week sessions), $2295 pp (Session 2) and $1495 pp (Session 4). This fee includes lab manual, use of all equipment and supplies, and room and board (all rooms are singles).

application deadline: May 1, 2009. First come, first served (apply now!). Late applications will be accepted on a space available basis.

payment deadline: Three weeks following receipt of your email acceptance letter.

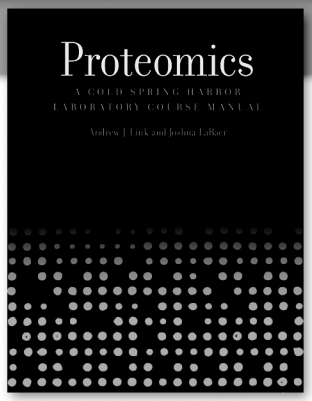
topics / techniques:

- gene cloning (and library construction)
- gene expression analysis
- PCR and quantitative RT-PCR
- genomics and bioinformatics
- DNA sequencing & DNA fingerprinting
- RNAi, siRNA and microarrays
- and much more — visit our website for a complete list!

NEW ENGLAND BioLabs® Inc.

www.neb.com

Proteomics



A Cold Spring Harbor Laboratory Course Manual

By Andrew J. Link, *Vanderbilt University School of Medicine, Nashville, Tennessee* and Joshua LaBaer, *Harvard University School of Medicine*

Based on a popular course at Cold Spring Harbor Laboratory, this new manual assembles cutting–edge protocols, helpful hints, and lecture notes to teach researchers from a wide variety of disciplines the essential methods of proteomics using state–of–the–art instrumentation. Detailed protocols involving protein microarrays, liquid chromatography, high–throughput cloning of expression constructs, IMAC, mass spectrometry, MALDI–TOF, and MudPIT are provided, along with well–illustrated descriptions of experimental procedures and lists of recommended Web sites and reading material. *Proteomics: A Cold Spring Harbor Laboratory Course Manual* can be used both as the basis for a course and as a detailed bench manual for those performing indispensable proteomic experiments. It is authored by Andrew J. Link and Joshua LaBaer, both leaders in their fields, who bring complementary expertise to the manual.

Published in December 2008, 232 pp., illus., appendices, index
Hardcover $150 **ISBN 978-087969793-8**
Paperback $94 **ISBN 978-087969787-7**

CONTENTS

www.cshlpress.com