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go where the biology takes me.”

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

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GENOTYPING
GENE EXPRESSION



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

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

Devin M. Absher, Ph.D.
Investigator

Jeremy Schmutz
Investigator

Jane Grimwood, Ph.D.
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.

genomic research • educational outreach • economic development



Huntsville, AL • hudsonalpha.org

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.

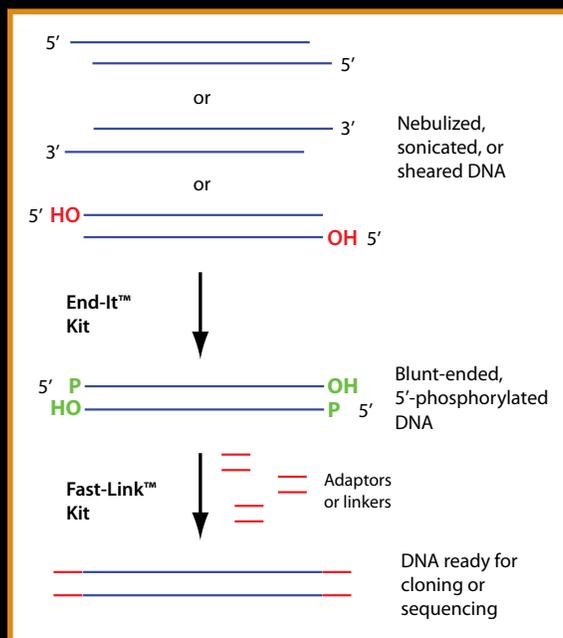
- Repaired DNA is blunt-ended and 5' phosphorylated for immediate blunt-end ligation.
- End-repair up to 5 µg of genomic DNA per reaction.

Then,

Perform Blunt-End Ligations in as Little as 15 Minutes

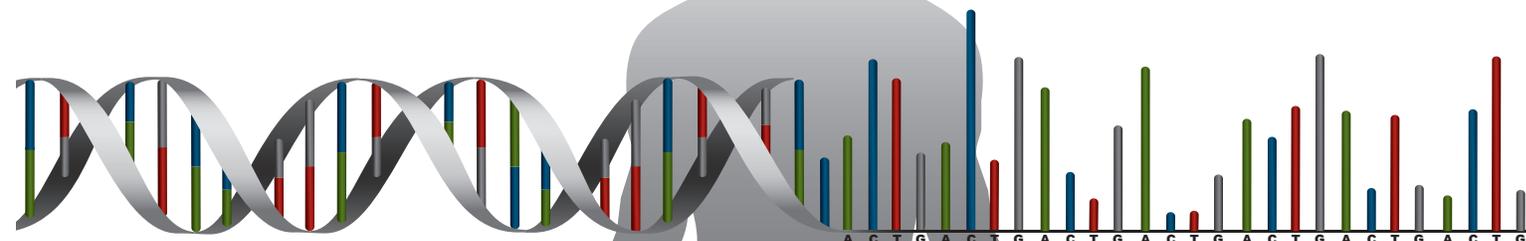
The Fast-Link™ DNA Ligation Kit uses a high-quality, specially formulated ligase to provide extremely rapid, high-efficiency DNA ligations.

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Seize the Exome

NimbleGen Sequence Capture 2.1M Human Exome Arrays

Now Available for 454 Sequencing Systems

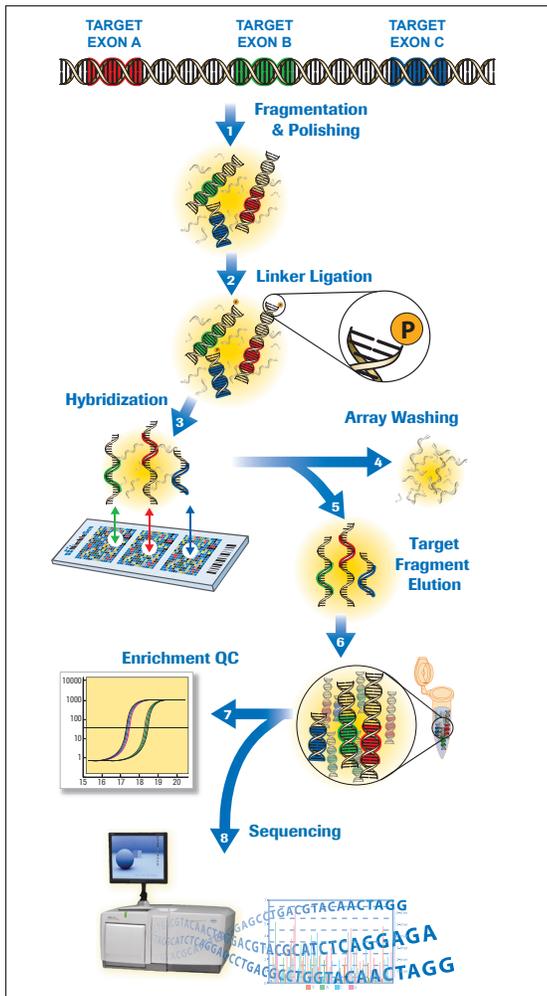


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preparation for targeted
next-generation resequencing*

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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 Million 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.



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



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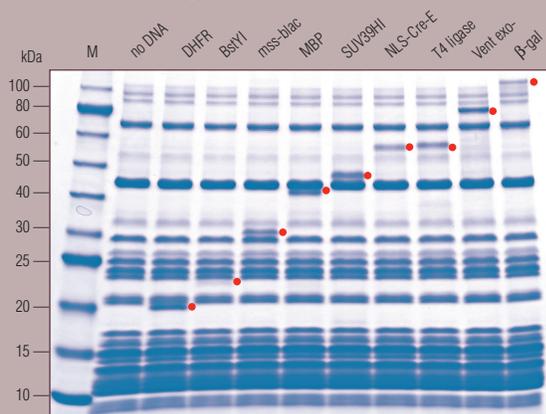


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Protein expression using the PURExpress™ *In Vitro* Protein Synthesis Kit from NEB



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

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



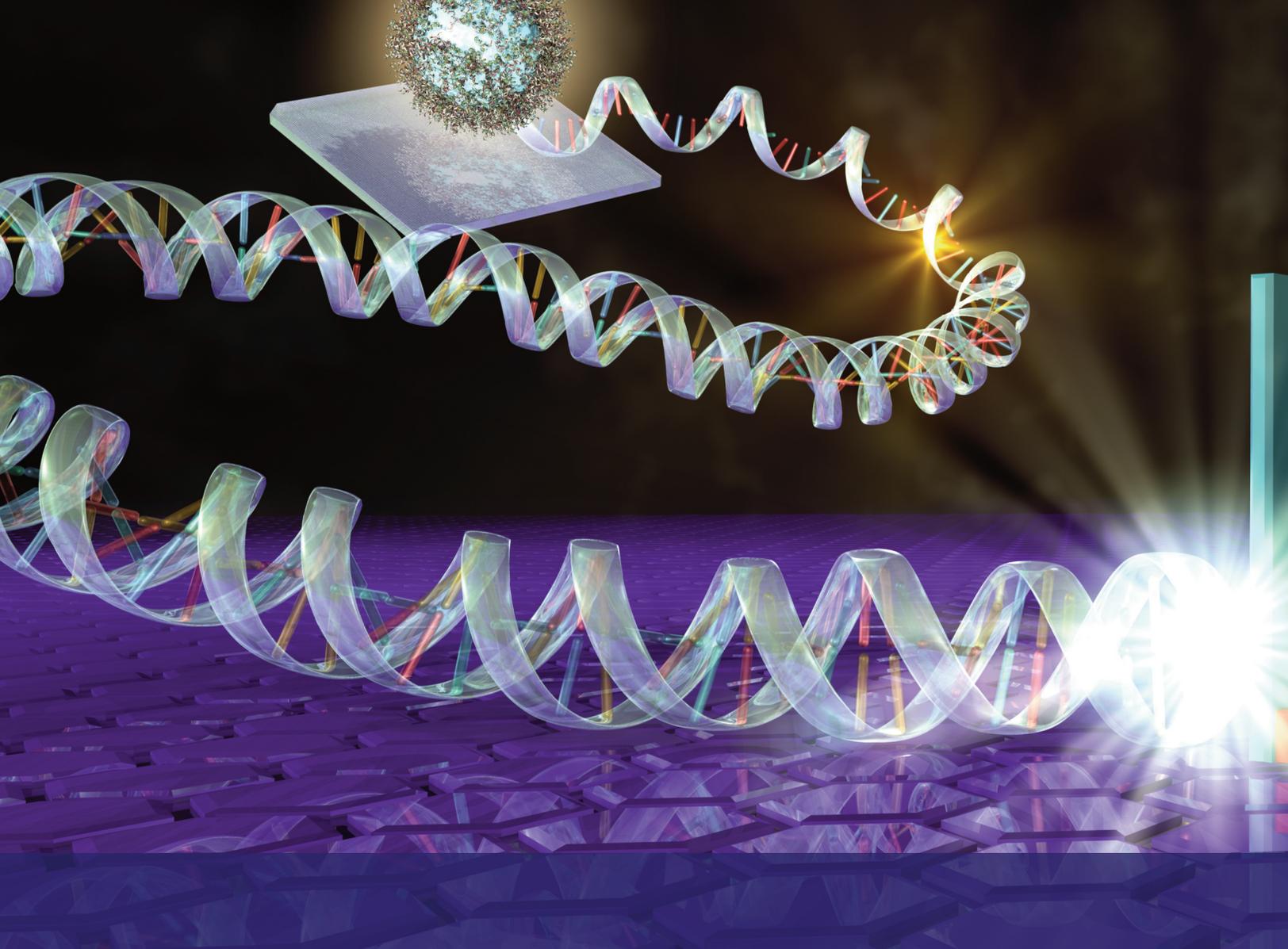
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DNA AMPLIFICATION
& PCR

RNA ANALYSIS

PROTEIN EXPRESSION &
ANALYSIS

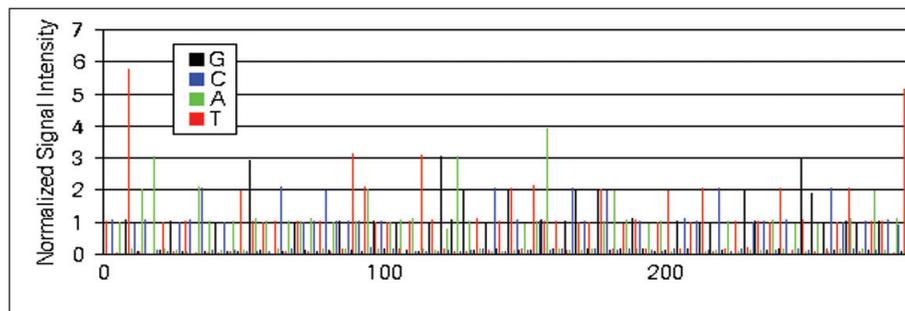
GENE EXPRESSION
& CELLULAR ANALYSIS



Genome Sequencer FLX System

454
SEQUENCING

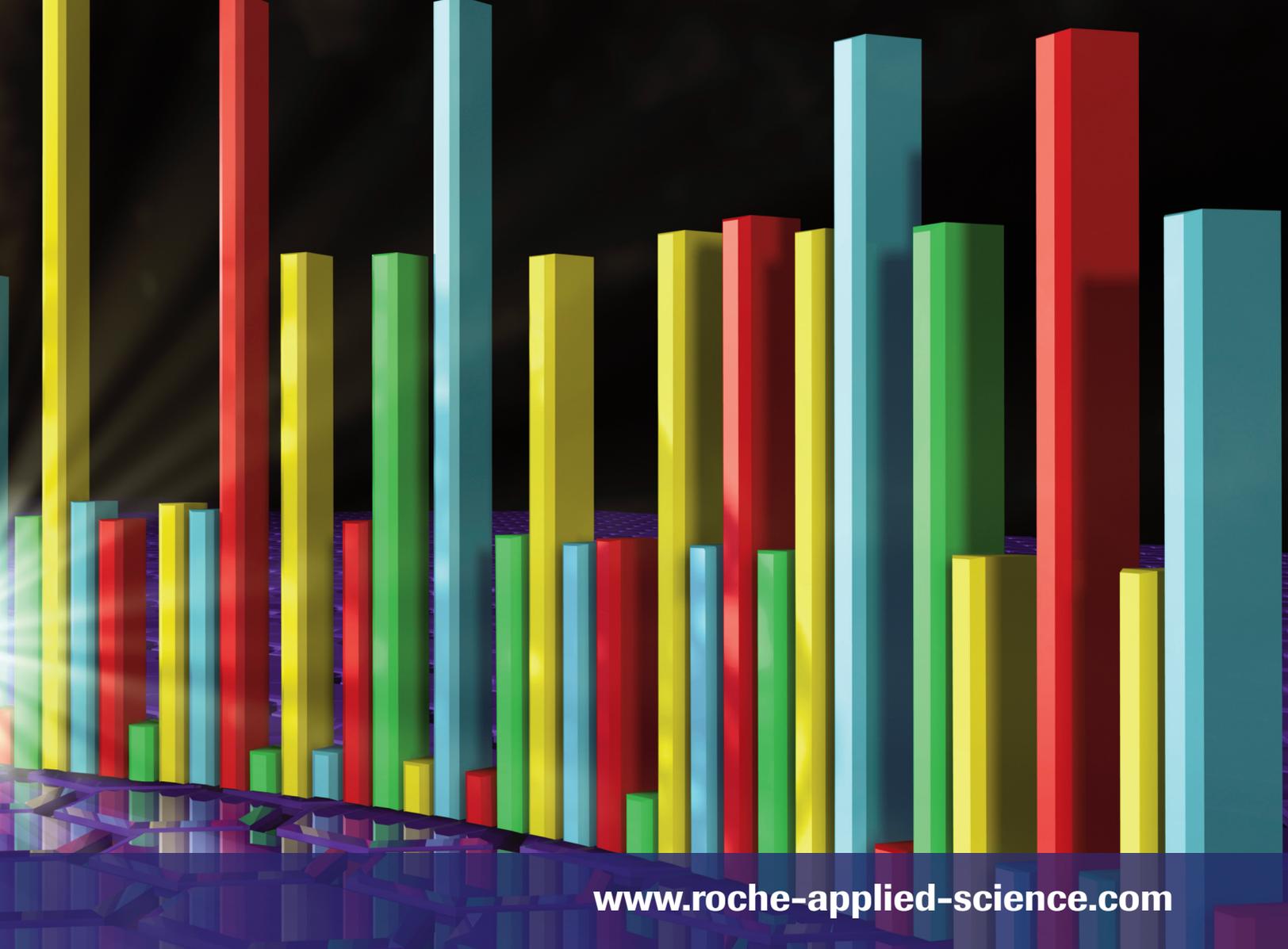
Really Length Matters



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.

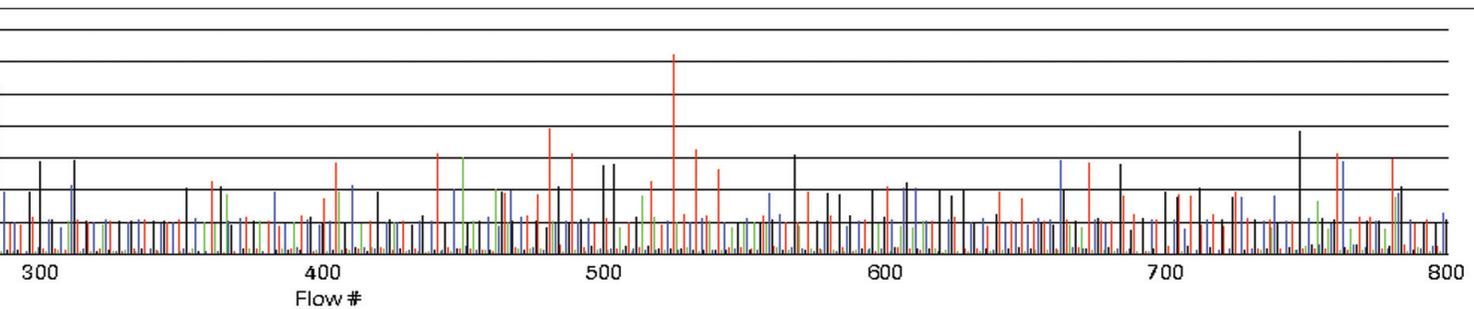
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when:

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:

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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.

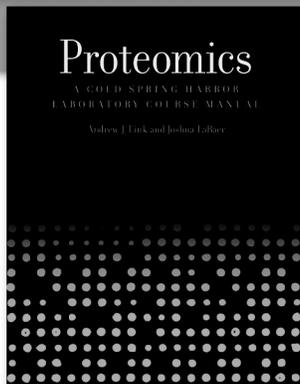
topics / techniques:

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(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!



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.

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