

ADOPT RNA SEQ ASAP

TO MOVE YOUR RESEARCH IN THE RIGHT DIRECTION.

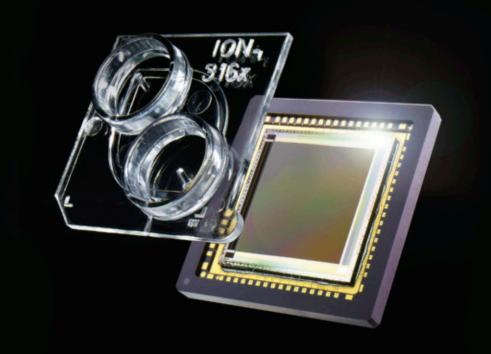
Only Expression Analysis enables you to harness the power of mRNA-Seq with your existing microarray bioinformatics infrastructure. Now you can explore allele-specific expression, alternative splice sites, previously unknown isoforms, cSNPs, and rare and novel transcripts — all in a single experiment.

- 100% array-compatible data
- · Gene and isoform level relative abundance estimates
- 10 years of leadership in gene expression data processing

Learn more at expressionanalysis.com/RNASEQ







fastest next-gen workflow 10X more throughput fastest-selling sequencer all in six months

Everything moves faster when The Chip is the Machine.™

Semiconductor technology has transformed every industry it has touched, from computing to photography to music. And now it's transforming the life sciences. The Ion Personal Genome Machine™ sequencer is powered by an innovative semiconductor chip that makes it faster, easier to use, and more accessible than any light-based solution. Get the speed, simplicity, and scalability of semiconductor sequencing on your side with the Ion PGM™ sequencer.



Watch the video at www.lifetechnologies.com/ionfirstsix/gr Get the free mobile app for your phone at http://gettag.mobi







Reach your scientific destinations faster with the most accurate Hi-Res Melting® systems on the market.

Our LightScanner systems will take your lab to the next level of high-sensitive mutation screening and genotyping. As the pioneers of both rapid real-time PCR and Hi-Res Melting, Idaho Technology is the only company that offers a complete system capable of superior performance at an affordable price.

LightScanner Express>>>

Arrivals

RAPIDLY GENERATE HIGH QUALITY GENE EXPRESSION DATA.

SPECIALIZED FOR T/A HOMOZYGOTE SMALL AMPLICON GENOTYPING.
GENOTYPE SAMPLES WITH GREATER SPECIFICITY THAN
HYDROLYSIS PROBE GENOTYPING AT A FRACTION OF THE COST.

Proven technology and exceptional customer support from the inventors of rapid PCR, the LightCycler®, and Hi-Res Melting.



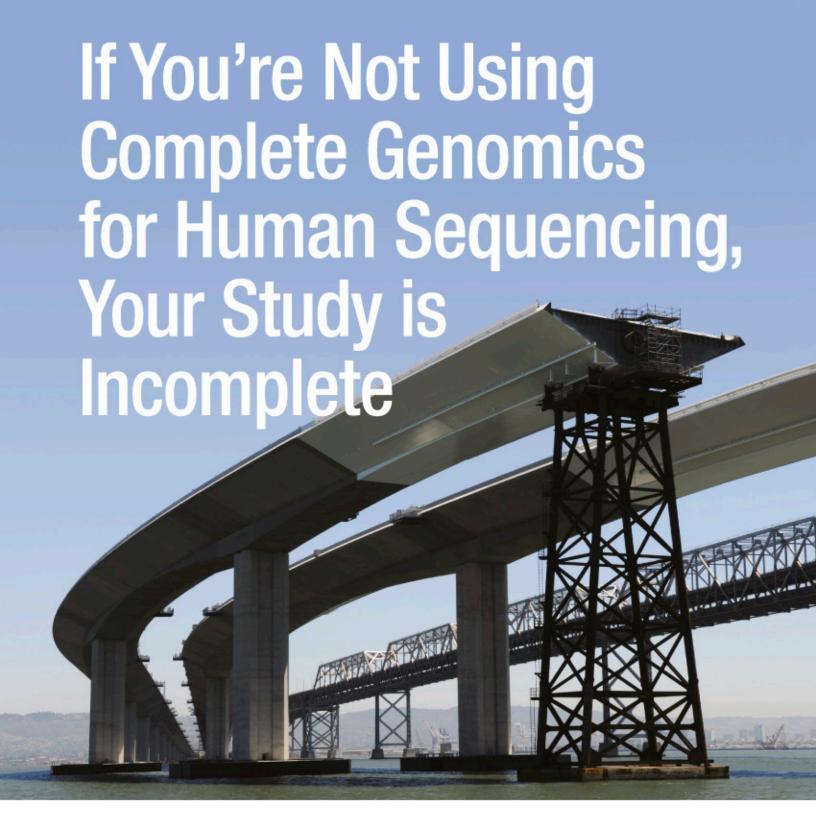
High cost, slow systems

First

(lass

Get on board at www.hiresmelting.com





When researching disease-associated variants, approaches like low-pass and exome-only sequencing leave you with incomplete data. As the world's leading provider of complete human genome sequencing, Complete Genomics delivers:

- More informative data—including non-coding variants
- Comprehensive CNV and SV data—information unavailable with exome sequencing
- Higher quality exome data than selection methods

Recent published studies have shown how non-coding variants are implicated in disease.

And finally, Complete Genomics has made whole genome human sequencing cost-effective.

Find out more at www.completegenomics.com





When Zero Really Matters.

No more wasted RNA-Seq reads.

Superior rRNA removal for RNA-Seq. That's the Ribo-Zero™ performance guarantee. Our kits remove >99% of the rRNA from a variety of total RNA samples. They deliver outstanding results with samples that other kits won't even touch, like partially degraded or FFPE RNA. For better RNA-Seq results without wasted rRNA reads, try Ribo-Zero kits today.

Single-pass method. Intact or degraded RNA. Performance guaranteed.

www.epicentre.com/ribozero







Discover More, Sequence Less

More exomes per lane

Choose the NimbleGen SeqCap EZ Exome Library with more than two million empirically rebalanced DNA probes for highly optimized performance.

Minimize sequencing cost, maximize results

Achieve uniform coverage across the exome to sequence more exomes per lane with up to eight exomes in a single lane!

Focus on what matters

 Cover more than 98% of RefSeq coding regions with an extremely efficient 44 Mb capture target.

Capture and sequence more difficult exons

 High density tiling and empirical rebalancing significantly improve coverage for high GC regions, such as first exons.

Discover more

www.nimblegen.com/exomes

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

Coverage of the Exome

Comparison of SeqCap EZ Human Exome Library v2.0 and Company A kit. The same Illumina PE library from HapMap sample NA12878 was used for both exome enrichment technologies, and each enriched DNA sample was sequenced with one HiSeq lane. SeqCap EZ Exome outperforms Company A based on number of raw sequences needed to achieve greater than 8X coverage for 90% of RefSeq coding regions. Only 4 Gb sequencing is needed for SeqCap EZ Exome, compared to 8 Gb for Company A exome capture.

Roche NimbleGen, Inc Madison, WI USA





The Mammary Gland as an Experimental Model The Mammary Gland as an Experimental Model

Edited by Mina J. Bissell, Lawrence Berkeley National Laboratory, Kornelia Polyak, Harvard Medical School, Jeffrey M. Rosen, Baylor College of Medicine

tudies of mammary gland biology are critically important given the prevalence of breast cancer in the population. There are many other reasons to study this organ, however. It represents an excellent model system for research into developmental mechanisms, gene regulation, tissue organization, hormonal action, secretion, and

stem cell biology, revealing general principles that can be extended to other organs and tissues. Moreover, many in vitro, ex vivo, and in vivo techniques have been developed using the mammary gland model and may be applied to other systems. This book therefore provides valuable lessons for all cell, developmental, and cancer biologists.

2011, 325 pp., illus. (54 color, 5 b/w), index Hardcover \$135

Contents

Preface

SECTION I: HISTORICAL BACKGROUND

Of Mice and Women: A Short History of Mouse Mammary Cancer Research with an Emphasis on the Paradigms Inspired by the Transplantation Method Daniel Medina

A Compendium of the Mouse Mammary Tumor Biologist: From the Initial Observations in the House Mouse to the Development of Genetically Engineered Mice

Robert D. Cardiff and Nicholas Kenney

Choosing a Mouse Model: Experimental Biology in Context—The Utility and Limitations of Mouse Models of Breast Cancer Alexander D. Borowsky

SECTION II: STEM CELLS

Murine Mammary Epithelial Stem Cells: Discovery, Function, and Current Status Jane E. Visvader and Gilbert H. Smith

Stem Cells in the Human Breast Ole William Petersen and Kornelia Polyak

SECTION III: SIGNALING

516-422-4097

Hormone Action in the Mammary Gland Cathrin Brisken and Bert O'Malley

Mammary Gland Growth Factors: Roles in Normal Development and in Cancer Nancy E. Hynes and Christine J. Watson

Cell-Matrix Interactions in Mammary Gland Development and Breast Cancer John Muschler and Charles H. Streuli

Mammary Gland ECM Remodeling, Stiffness, and Mechanosignaling in Normal Development and Tumor Progression

Pepper Schedin and Patricia J. Keely

Oncogene and Tumor Suppressor Genes Eva Y.H.P. Lee and William B. Muller

SECTION VI: MAMMARY GLAND DEVELOPMENTAL BIOLOGY AND CANCER

The Role of the Microenvironment in Mammary Gland Development and Cancer

Kornelia Polyak and Raghu Kalluri

Molecular Mechanisms Guiding Embryonic Mammary Gland Development Pamela Cowin and John Wysolmerski

TGF- Biology in Mammary Development and Breast Cancer Harold Moses and

Mary Helen Barcellos-Hoff

ISBN 978-0-879699-06-2

with Function Rama Khokha and Zena Werb

Leukocytes in Mammary Development and Cancer

Mammary Gland Reprogramming:

Metalloproteinases Couple Form

Lisa M. Coussens and Jeffrey W. Pollard

SYSTEM BIOLOGY AND GENOMICS

Systems Biology and Genomics of Breast Cancer

Charles M. Perou and Anne-Lise Børresen-Dale

Using Functional Genetics to Understand Breast Cancer Biology

Alan Ashworth and Rene Bernards

Chromatin Remodeling in Mammary Gland Differentiation and Breast Tumorigenesis

Tim H.-M. Huang and Manel Esteller

In Vivo Imaging in Cancer John Condeelis and Ralph Weissleder

Afterword

Index

www.cshlpress.com

To order or request additional information, please visit our website or:

Call: 1-800-843-4388 (Continental US and Canada) 516-422-4100 (All other locations)

E-mail: cshpress@cshl.edu

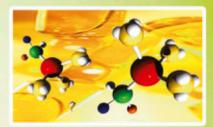
Write: Cold Spring Harbor Laboratory Press, 500 Sunnyside Blvd., Woodbury, NY 11797-2924





Custom Oligonucleotides

- Regular oligos
- Long oligos
- Phosphorothioated oligos (S-Oligos)
- Modified oligos
- ◆ Dual-labeled fluorescent oligos
- ◆ Oligonucleotide-peptide conjugation
- · OPC, PAGE, HPLC purification





Custom Peptide Synthesis

- Purities from desalt to 98%
- ◆ Acetylation/Amidation free of charge
- Phosphorylatd peptides
- · Fluorescein/Biotin labeled peptides
- · Specialty peptides with unnatural amino acids
- Cyclic peptides
- ♦ KLH/BSA/OVA Conjugation
- ♦ Multiple Antigenic Peptides





Tel:+86-10-82784296/92;010-62969345/46

Fax:+86-10-82784290 Email:info@sbsbio.com

Website: www.sbsbio.com



SKILLED AND ACCOMPLISHED CAPABILITIES

All Modifications and Oligo Types Synthesized

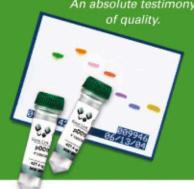
- Long oligos up to 250 mer
- Fluorescent Molecular Probes
- * Ultra-Modified, DNA, RNA, Chimeric, Fluorescent, and Antisense Oligos
- Specializing in the design and synthesis of challenging combinations of modifications

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

Gene Link. Results you can rely on.

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

An absolute testimony of quality.



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



CAREER TRACKS

Dedicated entirely to Employment, Conferences, Meetings, Fellowships, and Grants



University of Massachusetts Medical School Program in Bioinformatics and Integrative Biology

The newly established Program in Bioinformatics and Integrative Biology continues to invite applications for **tenure-track or senior tenured professor positions**. We are seeking innovative, energetic and collaborative individuals who plan to develop strong computational research programs to tackle problems in one of the following areas: regulatory genomics, comparative genomics, systems biology, RNA biology, evolutionary biology, statistical genetics, or proteomics. Exceptionally strong candidates in other computational biology areas will also be considered. Wet bench research space can be arranged for individuals who are interested in performing experiments to augment their computational efforts.

The Program in Bioinformatics and Integrative Biology is housed in a state-of-the-art research building with the neighboring Departments of Biochemistry and Molecular Pharmacology, Neurobiology, Cancer Biology, Medicine, and the Program in Gene Function and Expression. The Program has high-performance computing facilities and a full-time Bioinformatician to support the research activities of its faculty. Salary and start-up package will be competitive and commensurate with the high level of accomplishment expected for successful applicants.

Applicants should submit a cover letter explaining their interest in the Program, a curriculum vitae that includes honors, publications, and a succinct research plan to http://www.academicjobsonline.org. To expedite the review process, applicants should invite three individuals who are familiar with your work and potential for success to upload their recommendation letters at the same web address. Inquiries, but not application materials, may be directed to Professor Zhiping Weng at zhiping.weng@umassmed.edu.

As an equal opportunity and affirmative action employer, UMMS recognizes the power of a diverse community and encourages applications from individuals with varied experiences, perspectives and backgrounds.



Sharing Ideas at the Frontiers of Science

There has never been a better time to experience a Gordon Research Conference! Our high quality, cost-effective meetings are widely recognized as the world's premier scientific conferences.

Aging, Biology of
The Genetic, Epigenetic,
Inflammatory, and
Metabolic Origins of Aging
February 12-17, 2012
Ventura, CA
A GRS* will be held in
conjunction with this
meeting (Feb 11-12)

Reprogramming Cell Fate *NEW!*Feb 26 - Mar 2, 2012
Galveston, TX

Genes & Behavior
Contribution of
Sequenced Genomes
to Understanding
Behavior
March 18-23, 2012
Galveston, TX
A GRS* will be held in
conjunction with this
meeting (Mar 17-18)

DNA Damage, Mutation & Cancer March 25-30, 2012 Ventura, CA

Chromatin Structure & Function May 6-11, 2012 Lucca (Barga), Italy Post-Transcriptional Gene Regulation, The Biology of July 15-20, 2012 Newport, RI

Single Molecule Approaches to BiologyJuly 15-20, 2012
West Dover, VT

Mutagenesis August 19-24, 2012 Newport, RI

^{*} A Gordon Research Seminar (GRS) is a two-day seminar for graduate students and post-docs that precedes an associated GRC.