BLOW UP THE OLD WAY OF TESTING gDNA

Whole-genome QC now has one workflow.

FULLY AUTOMATED **FRAGMENT ANALYZER™** DOES IT ALL.

- Assesses gDNA concentration up to 40,000 bp
- Generates a user-defined Genomic Quality Number
- Identifies RNA contamination in gDNA
- Works with samples as small as 0.1 µL

More at AATI-US.COM

ADVANCED ANALYTICAL

isothermal detection of RNA

- Rapid detection in minutes
- Single molecule sensitivity
- Little or no hardware requirements
- Easy to use, stable lyophilised reagents

TwistAmp® exo RT

Real-time fluorescent RNA detection

Using TwistDx's RPA technology, the exo RT kit is recommended for detecting RNA targets with a proprietary fluorescent TwistAmp® exo probe in a one-step process.

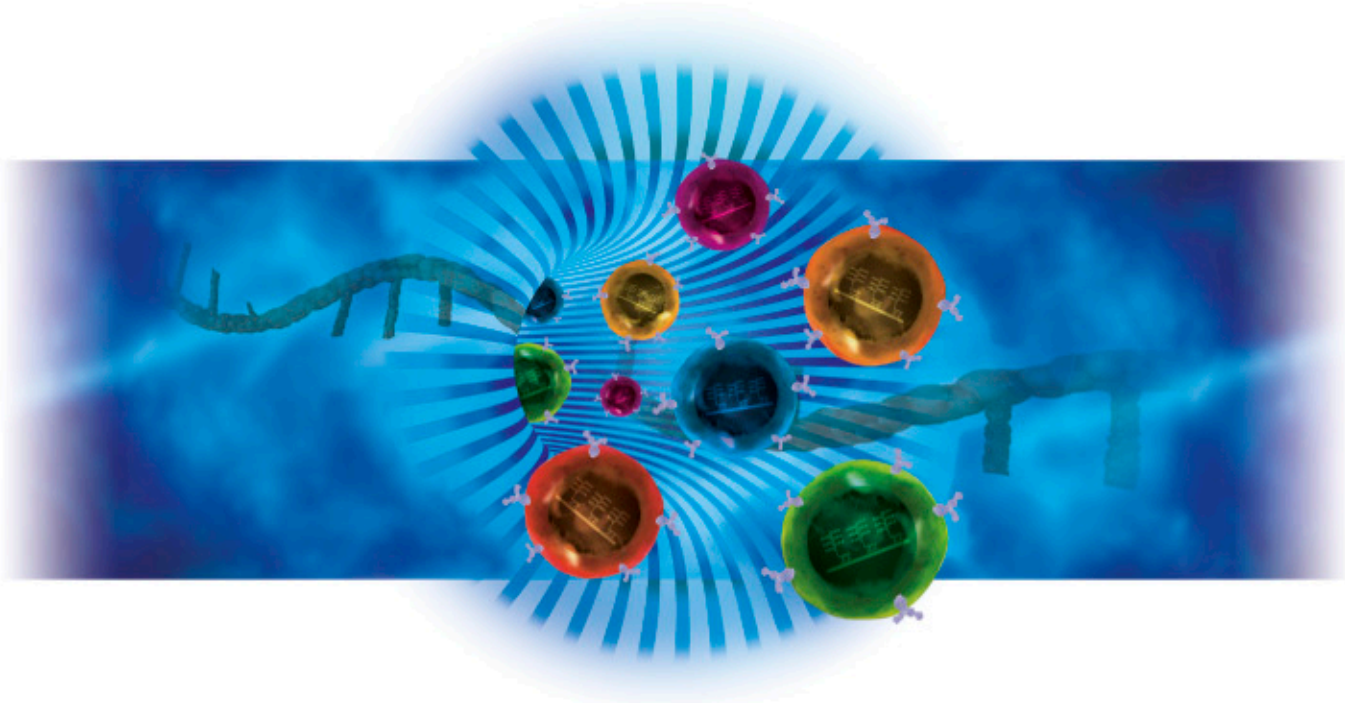
TwistDx

www.twistdx.co.uk

affymetrix
eBioscience

Imagine if you could detect RNA and protein in millions of single cells

Enter a new dimension of single-cell analysis



Detect RNA and protein simultaneously by flow cytometry to:

- See gene expression heterogeneity at the single-cell level
- Compare RNA and protein in the same cell
- Evaluate viral RNA within infected cells
- Detect non-coding RNA in cell subsets
- Analyze mRNA expression levels when antibody selection is limited

Download White Paper

Download your copy of the PrimeFlow™ RNA Assay Validation White Paper at www.ebioscience.com/primeflow-white-paper-genres

Biology for a better world.

NORTH AMERICA: 888.999.1371 ▪ EUROPE: +43 1 796 40 40-305 ▪ JAPAN: +81 (0)3 6430 4020 ▪ INQUIRIES: info@ebioscience.com

eBioscience GeneChip USB

Reduce your NGS Sequencing Costs with Improved Library Complexity

Accel-NGS™ 2S DNA Library kit for Illumina® Platforms

- Broad input range: 10 pg to 1 µg. PCR-free libraries from 10 ng
- Exceptional coverage of AT-rich & GC-rich sequences
- Superior library complexity
- Tremendously efficient adapter technology

Swift BIOSCIENCES

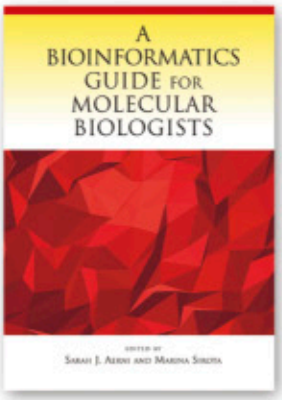
Soar Above. Discover More.

Accel-NGS™

www.swiftbiosci.com

A BIOINFORMATICS GUIDE FOR MOLECULAR BIOLOGISTS

Edited by Sarah Aerni and Marina Sirota, *Biomedical Informatics Program, Stanford University School of Medicine*



Informatics can vastly assist progress in research and development in cell and molecular biology and biomedicine. However, many investigators are either unaware of the ways in which informatics can improve their research or find it inaccessible due to a feeling of "informatics anxiety." This sense of apprehension results from improper communication of the principles behind these approaches and of the value of the many tools available. In fact, many researchers are inherently distrustful of these tools. A more complete understanding of bioinformatics offered in *A Bioinformatics Guide for Molecular Biologists* will allow the reader to become comfortable with these techniques, encouraging their use—thus helping to make sense of the vast accumulation of data. To make these concepts more accessible, the editors approach the field of bioinformatics from the viewpoint of a molecular biologist, (1) arming the biologist with a basic understanding of the fundamental concepts in the field, (2) presenting approaches for using the tools from the standpoint of the data for which they are created, and (3) showing how the field of informatics is quickly adapting to the advancements in biology and biomedical technologies. All concepts are paired with recommendations for the appropriate programming environment and tools best suited to solve the particular problem at hand. It is a must-read for those interested in learning informatics techniques required for successful research and development in the laboratory.

2014, 328 pp, illustrated (64 4C, 26 B&W), index
Hardcover $79
ISBN 978-1-936113-22-4

Contents

MACROGEN

Advancing through Genomics

E-Mail.
info@macrogen.com / ngs@macrogen.com

Website.
dna.macrogen.com

Looking for A Genomic Research Partner?

Next-Generation Sequencing(NGS)
- Whole genome Sequencing (Hiseq X Ten)
- Exome Sequencing
- Trageted Sequencing
- Long Read Sequencing
- Transcriptome Analysis, small RNA
- Epigenomics

Bio Informatics
- Assembly / Mapping
- Variant (SNP / Indel) calling
- CNV & Breakpoints
- Expression Profiles
- DEGs / miRNA
- Enrichment Profiles
- Gene Annotation

Capillary Sequencing

Microarray

Oligonucleotide Synthesis

Genetically Engineered Mouse

Next-Gen Sequencing

Challenged with low-input samples for ChIP-seq?

LIBRARY PREPARATION FOR NEXT-GEN SEQUENCING

Ligation-free ChIP-seq library prep for low-input DNA samples

The New DNA SMART™ ChIP-Seq Kit

that's GOOD science!

Template switching technology, optimized for DNA

The DNA SMART ChIP-Seq Kit generates Illumina® sequencing libraries from as little as 100 pg of either single-stranded or double-stranded DNA. This kit generates sensitive sequencing libraries without using ligation, which streamlines the protocol and improves library yield and complexity. Using a novel version of Clontech's patented SMART® template switching technology compatible with low-input, fragmented DNA templates, the DNA SMART ChIP-Seq Kit generates robust, reproducible ChIP-seq libraries in around 4 hours.

View a webinar at
www.clontech.com/ChIP-Seq-Webinar-Signup
or call 1.800.662.2566

Scan to find out more

TaKaRa Clontech

www.personalis.com/cancer

Personalis @ AACR 2015 | Booth 2156

The Most Advanced Tumor Profiling and Informatics

Accuracy and Content Enhanced (ACE) **Cancer Services** *for*

Cancer Research and Clinical Trials

Personalis® ACE Cancer Services

The Most Complete and Accurate Solutions *for* Tumor Profiling

Personalis' portfolio of cancer research solutions provides increased sensitivity to detect variants in cancer-associated genes, and provides improved resolution for applications such as tumor stratification, therapeutic response association studies, and identification of potential targets for companion diagnostics. Our sequencing capabilities include both high-depth augmented exome sequencing and RNA-Seq. These assays can be performed from a single sample to provide a comprehensive description of the tumor including somatic variants, low abundance SVs, fusion transcripts, and more – all from the same tumor sample.

- Enhanced coverage of 1,300+ cancer genes and 200+ miRNA genes
- Coverage of intronic and intergenic variants
- Analysis of DNA and RNA from a single sample
- Comprehensive coverage of key cancer pathway genes
- High accuracy somatic variant (DNA) and fusion event (RNA) calling

enhanced coverage of

1,300+ cancer genes

and **200+ miRNA genes**

www.personalis.com/cancer

Personalis®

Pioneering Genome-Guided Medicine

www.personalis.com | info@personalis.com

+1 855-GENOME4 (436-6634)

+1 650-752-1300 (outside U.S.)

Power your next big breakthrough.

Sequencing power for every scale.

NEW

HiSeq X™ Series

Population power

Maximum throughput and low cost population- and production-scale human whole-genome sequencing. Series includes the HiSeq X Ten and the new HiSeq X Five Systems.

NEW

HiSeq® Series

Production power

Maximum throughput and lowest cost for production-scale genomics. Series includes the new HiSeq 3000 and HiSeq 4000 Systems.

NEW

NextSeq® Series

Flexible power

Desktop speed and simplicity for everyday genomics. Series includes the NextSeq 500 and the new NextSeq 550 with cytogenomic array scanning.

MiSeq® Series

Focused power

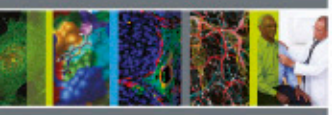
Speed and simplicity for targeted and small-genome sequencing. Series includes the MiSeq and MiSeqDx™ Systems.*

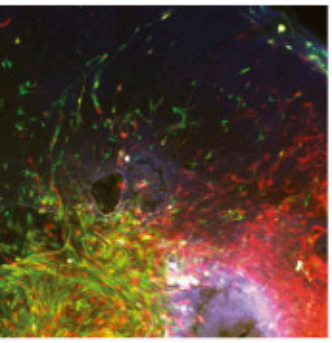
Compare our new systems with our product selector at www.illumina.com/power.

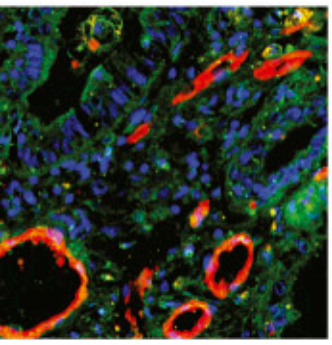
FOR RESEARCH USE ONLY

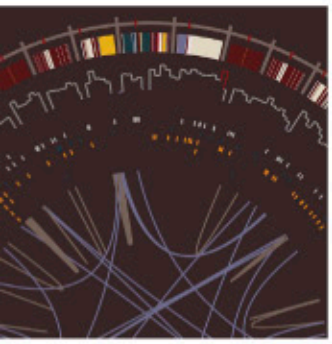
*MiSeqDx™ is a 510(k) cleared, CE-marked instrument. See instructions for use.

illumina®









2015 SCIENTIFIC CONFERENCES

Presenting the most significant research on cancer etiology, prevention, diagnosis, and treatment

AACR Annual Meeting 2015
Program Committee Chairperson: Lewis C. Cantley
April 18-22, 2015 • Philadelphia, PA

Advances in Brain Cancer Research
Co-Chairpersons: Eric C. Holland, Franziska Michor, Martine F. Roussel, and Michael D. Taylor
May 27-30, 2015 • Washington, DC

Metabolism and Cancer
Co-Chairpersons: Ralph J. DeBerardinis, David M. Sabatini, and Almut Schulze
June 7-10, 2015 • Bellevue, WA

Methods in Cancer Biostatistics Workshop: Clinical Trial Designs for Targeted Agents
Chairperson: Steven Piantadosi
June 7-13, 2015 • Lake Tahoe, CA

AACR Precision Medicine Series: Integrating Clinical Genomics and Cancer Therapy
Co-Chairpersons: Charles L. Sawyers, Elaine R. Mardis, and Arul M. Chinnaiyan
June 13-16, 2015 • Salt Lake City, UT

EACR-AACR-SIC Special Conference on Anticancer Drug Action and Drug Resistance: From Cancer Biology to the Clinic
Co-Chairpersons: Richard M. Marais, Pasi Jänne, and Riccardo Dolcetti
June 20-23, 2015 • Florence, Italy

Chromatin and Epigenetics in Cancer
Co-Chairpersons: Peter A. Jones, Sharon Y. R. Dent, and Charles W. M. Roberts
September 24-27, 2015 • Atlanta, GA

CRI-CIMT-EATI-AACR The Inaugural International Cancer Immunotherapy Conference: Translating Science into Survival
September 27-30, 2015 • New York, NY

Advances in Breast Cancer Research
Co-Chairpersons: Matthew J. Ellis, Charles M. Perou, and Jane E. Visvader
October 17-20, 2015 • Bellevue, WA

Advances in Ovarian Cancer
Co-Chairpersons: Kathleen R. Cho, Douglas A. Levine, and Benjamin G. Neel
October 17-20, 2015 • Orlando, FL

Fourth AACR International Conference on Frontiers in Basic Cancer Research
Chairperson: M. Celeste Simon;
Co-Chairpersons: James P. Allison, John E. Dick, Nathanael S. Gray, and Victor E. Velculescu
October 23-26, 2015 • Philadelphia, PA

Basic Science of Sarcomas
Co-Chairpersons: Robert G. Maki, Angelo Paolo Dei Tos, Jonathan A. Fletcher, Lee J. Helman, and Brian Van Tine
November 3-4, 2015 • Salt Lake City, UT

New Horizons in Cancer Research
Co-Chairpersons: Lewis C. Cantley and Carlos L. Arteaga
November 2015 • Shanghai, China

AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics
Scientific Committee Co-Chairpersons: Levi A. Garraway, Lee J. Helman, and Jean-Charles Soria
November 5-9, 2015 • Boston, MA

Pediatric Oncology
Co-Chairpersons: Scott Armstrong, Charles G. Mullighan, Kevin M. Shannon, and Kimberly Stegmaier
November 9-12, 2015 • Fort Lauderdale, FL

Developmental Biology and Cancer
Co-Chairpersons: Hans Clevers, Stuart Orkin, and Suzanne Baker
November 30-December 3, 2015 • Boston, MA

Tumor Metastasis
Co-Chairpersons: Bruce R. Zetter, Melody A. Swartz, and Jeffrey W. Pollard
November 30-December 3, 2015 • Austin, TX

Noncoding RNAs and Cancer
Co-Chairpersons: Howard Y. Chang, Jeannie T. Lee, Joshua Mendell
December 4 - 7, 2015 • Boston, MA

www.AACR.org/Calendar

AACR American Association for Cancer Research

FINDING CURES TOGETHER™

CROPS 2015

improving agriculture through genomics

REGISTER NOW cropsconference.org

May 18 – 21, 2015

HUDSONALPHA INSTITUTE FOR BIOTECHNOLOGY
HUNTSVILLE, AL USA

CROPS 2015 ***provides a discussion forum for what is the next, most difficult challenge for plant genomics: integrating and translating genomic knowledge to improve breeding and crop production.***

Abstract deadline
April 1, 2015

Early Booking deadline
April 17, 2015

Register today at **CROPSconference.org**

KEYNOTE SPEAKERS

Gerald A. Tuskan
Joint Genome Institute

Steve Rounsley
DOW AgroSciences

PRESENTED BY

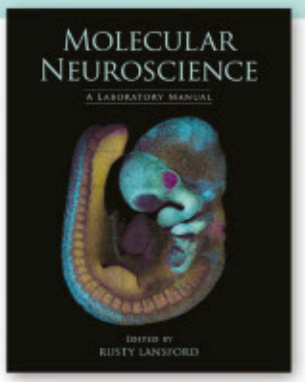
HudsonAlpha Institute for Biotechnology

Institute of Plant Breeding, Genetics & Genomics at UGA

The University of Georgia

MOLECULAR NEUROSCIENCE

A Laboratory Manual



Edited by Rusty Lansford, *California Institute of Technology*

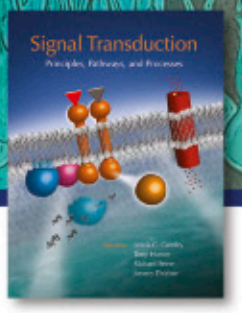
This laboratory manual serves as a comprehensive practical guide to molecular and cellular step-by-step methods for neuroscientists, detailing fundamental and advanced techniques for working with cells, DNA, RNA, gene transfer, and imaging. The techniques included in this manual were developed in the Advanced Techniques in Molecular Neuroscience course offered annually at Cold Spring Harbor Laboratory, as well as protocols drawn from its best-selling lab manuals. It is an essential resource for all neuroscientists, from graduate students upward, who seek to use molecular techniques to probe the complexities of the nervous system.

2014, 648 pp., illus. (64 4C, 50 B&W), index
Hardcover $150 ISBN 978-1-621820-13-0
Paperback $90 ISBN 978-1-621820-14-7

CONTENTS

www.cshlpress.org

SIGNAL TRANSDUCTION



Edited by Lewis Cantley, *Harvard Medical School,* Tony Hunter, *The Salk Institute,* Richard Sever, *Cold Spring Harbor Laboratory,* and Jeremy Thorner, *University of California, Berkeley*

Signal transduction pathways are molecular circuits that define how cells communicate with each other and respond to their environment. This new textbook for the first time provides a comprehensive view of the subject by covering both the basic mechanisms involved and the roles of signal transduction in fundamental biological processes. It starts by describing the basic players—signals, receptors, second messengers, and effectors—before comprehensively mapping the various different signaling pathways that operate in cells. It then goes on to provide detailed descriptions of how signal transduction functions in essential processes such as cell growth and division, metabolism, sensory perception, immunity, and reproduction.

2014, 464 pp., illus., index
Hardcover $165 £110

ISBN 978-0-879699-01-7

Contents (preliminary)

www.cshlpress.org