MiSeq. Next-generation sequencing for all you seek.

You want amazing accuracy and performance on your benchtop. Illumina delivers—yet again. The MiSeq Personal Sequencer is the only fully integrated, truly end-to-end benchtop solution around. It's just one more example of why Illumina solutions generate a remarkable 90% of all the world's sequencing data. Discover what's possible.

www.illumina.com/iseek

illumina®

I AM A SPECIMEN IN A CANCER STUDY. GENETIC RESEARCHERS WANT TO

KNOW

MORE ABOUT ME THROUGH WHOLE TRANSCRIPTOME ANALYSIS. I AM READY TO HELP IDENTIFY IMPORTANT BIOMARKERS. THAT'S WHY I'M ON THE WAY TO EXPRESSION ANALYSIS.

EVERY SPECIMEN HAS A STORY. LET YOURS BE HEARD AT **GENOMICKNOWHOW.COM**

GENOMIC KNOW-HOW®

ion torrent

by life technologies™

PGM™ for genes. Proton™ for genomes.

Sequencing for all.

Powered by fast, simple, scalable semiconductor chips, the Ion PGM™ Sequencer introduced an entirely new approach to sequencing, making it dramatically faster and more accessible.

The new Ion Proton™ Sequencer will go even further. With chip densities up to 1,000 times greater than the Ion PGM™ Sequencer, the Ion Proton™ Sequencer will put whole-genome sequencing within reach of every lab.

Find fast, affordable benchtop sequencing at
lifetechnologies.com/ionsequencing

life technologies™

Mutation Discovery | Genotyping | Gene Expression

Get There Faster

Reach your scientific destinations faster with our LCGreen® Plus+ Reagents and LightScanner® Systems

Our LCGreen Plus+ melting reagents and LightScanner systems will take your lab to the next level with highly sensitive mutation screening and genotyping capabilities. As pioneers in the PCR industry, we continue to offer superior systems, software, and chemistry for melting analysis.

LightScanner Express >>> Arrivals

EASILY GENOTYPE SAMPLES AT A FRACTION OF THE COST.

RAPIDLY VISUALIZE MELTING PEAKS WITH SUPERIOR SOFTWARE.

AFFORDABLY DETECT MUTATIONS WITH UNLABELED PROBES.

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

Request a FREE sample of our LCGreen Plus+ Melting Reagent by visiting www.hiresmelting.com

Idaho Technology is now BIOFIRE®
BioFireDX.com

multiply your research power with instant collaboration

The new DNAnexus

An instant cloud-based DNA data management and analysis platform

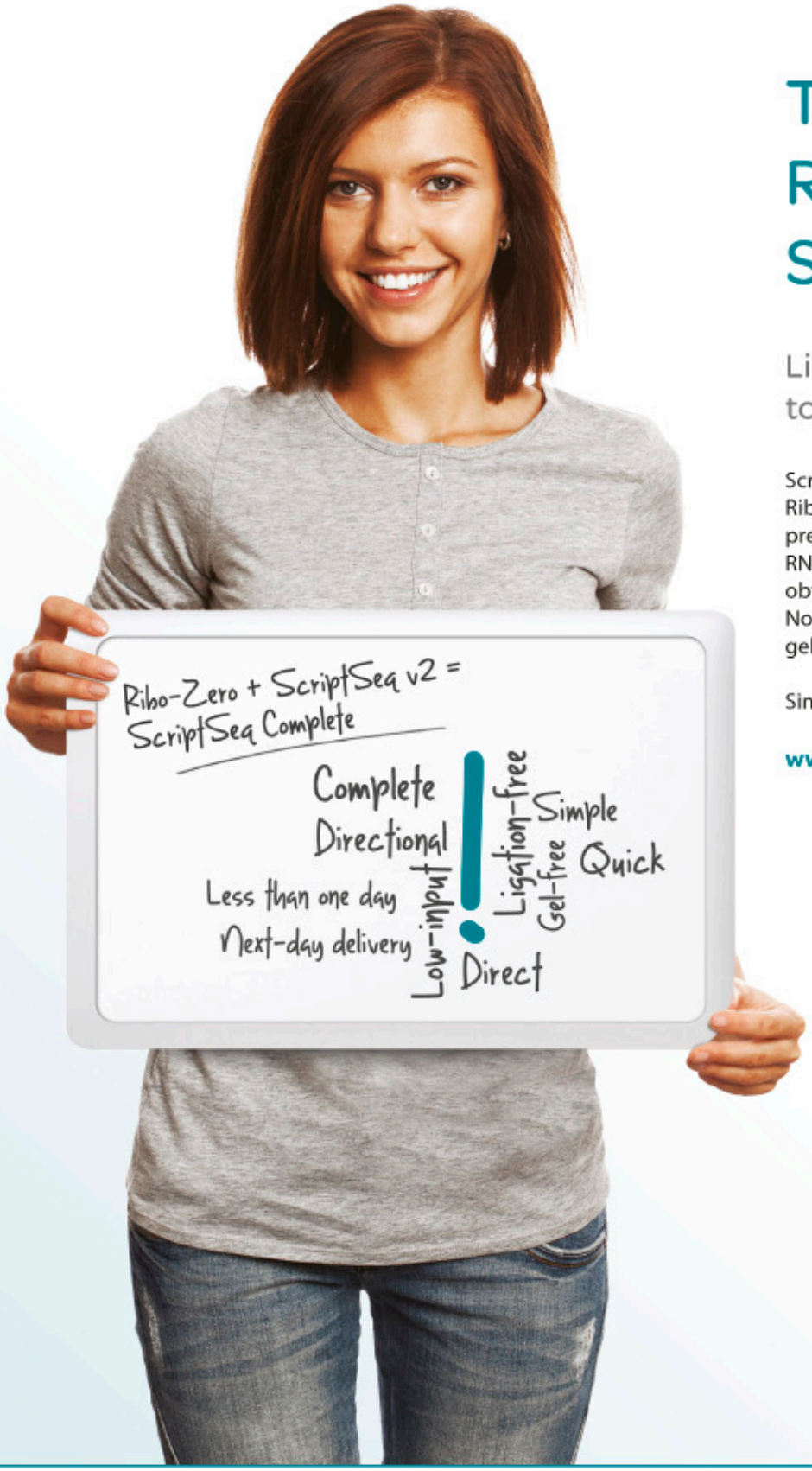
Leverage an ever-expanding cloud-based community-powered ecosystem!

- Accelerated results
- Unlimited compute and storage
- Easy and powerful collaboration
- Instant security and compliance

DNAnexus

Powering the Genomics Revolution™

Learn more at DNAnexus.com/results



The *Complete* RNA-Seq Solution.

Libraries in 1 day from 100 ng total RNA

ScriptSeq™ Complete kits combine proven Ribo-Zero™ technology with ScriptSeq library preparation to offer a complete solution for RNA-Seq. Starting with 100 ng of total RNA, obtain sequencer-ready libraries the same day. No cDNA fragmentation, adaptor ligation, or gel size-selection.

Simplify your RNA-Seq.

www.epicentre.com/complete

epicentre®
an Illumina® company

Oligo Modifications?

Your wish is our command.

All Modifications & 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.

Oligo Synthesis

Omni-Pure

PURE & SIMPLE. ANY DNA.

Omni-Pure™ & Omni-Clean™ Purification Systems

- Purify plasmid DNA, genomic DNA & RNA from almost any source
- Purify DNA and RNA from agarose gels
- Ultra Purified High Yield
- No Toxic Reagents
- Rapid Purification Protocols
- Suitable for All Molecular Biology Applications
- Convenient Optimized Reagents
- Easy Spin Column Format

Gene Link. Results you can rely on.

Genetic Tools & Reagents

Gene Detection Made Easy.

Gene Link is the leader in triple repeat disorder genotyping using non-radioactive based methods

We have more than a decade of expertise and have developed non-radioactive detection methods for safe, sensitive, and reliable genotyping of human genetic disorders.

Take a look at our simple agarose & polyacrylamide gel based systems, chemiluminescent Southern blot detection methods, and fluorescent systems for genotyping of triple repeat disorders.

Gene Link. Results you can rely on.

Gene Detection System

RNA interference

Specializing in the design & synthesis of siRNA, miRNA, siRNA-Aptamer & RNA oligos with challenging combinations of modifications

SmartBase™ siRNA modifications to specifically increase duplex stability, nuclease resistance and cell permeation.

SmartSeed™ siRNA modifications that assist to minimize the off-target effects induced by seed region complementarity.

Guaranteed RNAi Explorer™ Simply give us the accession number and Gene Link designs, synthesizes and supplies 3 siRNA.

Gene Link. Results you can rely on.

RNA Interference

*Not every siRNA can effectively down regulate a gene. The process of RNA interference varies by individual siRNA while some do not exhibit any interference at all.

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

Gene Link™ | 190 Saw Mill River Road | Hawthorne, NY 10532 | tel: 914-769-1192 | email: support@genelink.com

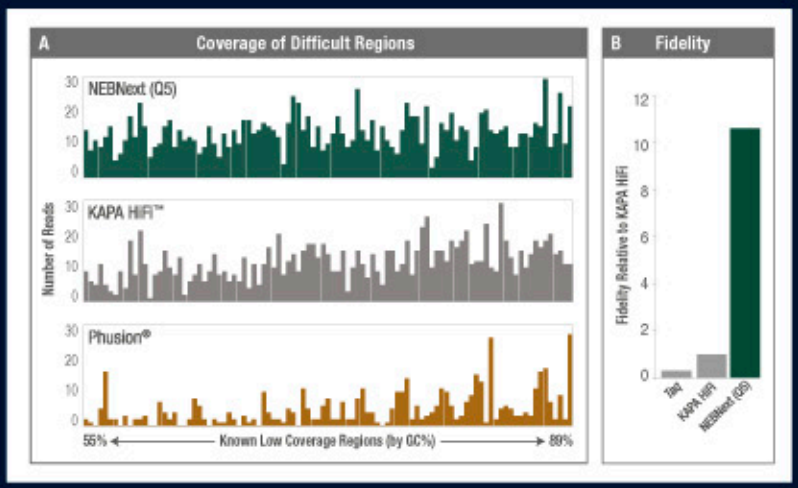
NEW ENGLAND BioLabs® Inc.
enabling technologies in the life sciences

The Right Balance.

NEBNext®
High-Fidelity 2X PCR Master Mix

A formulation of Q5™ High-Fidelity DNA Polymerase, this new master mix is specifically optimized for robust high-fidelity amplification of NGS libraries. With an ultra-low error rate and even coverage, including for GC-rich amplicons, the NEBNext High-Fidelity 2X PCR Master Mix strikes the right balance for NGS library preparation.

NEBNext High-Fidelity 2X PCR Master Mix minimizes GC-bias and error rate.

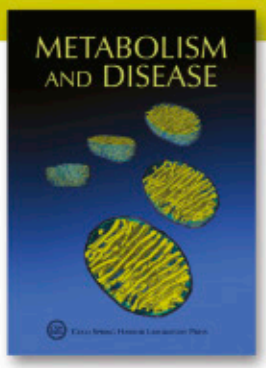


A. Indexed human IMR90 DNA libraries were split and amplified using 8 cycles of PCR with Phusion High-Fidelity PCR Master Mix with HF Buffer, KAPA HiFi HotStart ReadyMix or NEBNext High-Fidelity 2X PCR Master Mix, followed by sequencing on an Illumina HiSeq™ 2000. 180 million reads were randomly extracted from each data set and the number of reads overlapping distinct low coverage regions of the human genome (Aird et al. Genome Biology, 2011) are shown for each library.

B. Fidelity measurements of Taq DNA Polymerase (in Standard Taq Buffer), KAPA HiFi HotStart ReadyMix and NEBNext High-Fidelity 2X PCR Master Mix were measured, side-by-side, in a PCR-based mutation screening assay using a lacZ method. Values ($n \geq 2$) are expressed relative to KAPA HiFi HotStart ReadyMix.

METABOLISM AND DISEASE

Cold Spring Harbor Symposia on Quantitative Biology LXXVI



Edited by Terri Grodzicker, *Cold Spring Harbor Laboratory,* Bruce Stillman, *Cold Spring Harbor Laboratory,* and David Stewart, *Cold Spring Harbor Laboratory*

This volume is based on presentations by world-renowned investigators who gathered at the 76th Cold Spring Harbor Symposium on Quantitative Biology. It reviews the latest advances in our understanding of metabolism and disease, including research on fat, exercise and rhythms; insulin resistance and sensitivity; lifespan, aging and cancer; regulation and dysregulation of metabolism; signaling and gene regulation; environment and sensing; metabolic reprogramming; clocks and intermediary metabolism; metabolism and cancer; and autophagy, timing and small RNAs.

2012, 422 pp., illus., index

Hardcover $318 (Hardcover edition includes online access; call for information and registration) **ISBN 978-1-936113-56-9**

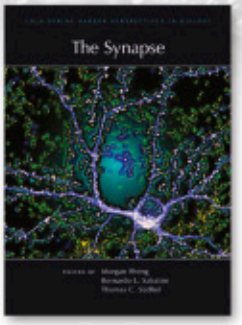
Paperback $129 (Paperback edition does not include online access) **ISBN 978-1-936113-57-6**

CONTENTS

www.cshlpress.org

The Synapse

Edited by Morgan Sheng, *Genentech Research Group;* Bernardo Sabatini, *Harvard Medical School,* and Thomas C. Südhof, *Stanford University School of Medicine*



Synapses are specialized cell contacts where two neurons communicate. Neurotransmitter molecules released from the presynaptic terminal of one neuron diffuse to the postsynaptic terminal on the other, binding to receptors that lead to propagation or modulation of the signal.

Written and edited by experts in the field, this collection from *Cold Spring Harbor Perspectives in Biology* examines the highly complex structures and functions of the pre- and postsynaptic regions, as well as the trafficking mechanisms that transport vesicles containing neurotransmitters. The contributors discuss how long-term potentiation (LTP) and long-term depression (LTD) of synaptic transmission form the basis of learning and memory. The roles of calcium signaling in regulating synaptic and cell function and techniques to study such signaling events are also covered.

This volume also includes discussions of synaptic dysfunction in disorders such as autism and Alzheimer's disease. It is an indispensable reference for neurobiologists, cell and developmental biologists, and anyone wishing to understand how the basic building blocks of the brain are put together and communicate.

2012, 397 pp., illus., index
Hardcover $135

ISBN 978-1-936113-02-6

Contents

www.cshlpress.org

Handcuffed to your pipette?

Free yourself!

The Apollo 324™ system automates library preparation for all major NGS systems, so you can spend your time on more important things. Setting up and starting a run takes only 15 minutes of hands-on time.

Then you are free.

Our PrepX™ reagent kits generate consistent, quality libraries for Ion Torrent PGM™, Roche 454™ GS FLX Titanium™, FLX+ and GS Junior™, and all Illumina® platforms. Color-coded reagent kits — for DNA, RNA and ChIP-seq applications — minimize errors and simplify instrument setup. Pre-aliquoted strips let you set up full or partial runs with no reagent waste.

integenX

For more info visit: www.integenx.com • 888 371 4749

Shaping Epigenetics Discovery.

Chromatin, DNA methylation, RNA analysis.

With EMD Millipore, epigenetics technology has never been more accessible or easier to use. From highly specific antibodies, to rapid bisulfite kits, to industry leading ChIP and next generation sequencing kits, we simplify epigenetics applications to allow you to design the most ambitious experiments to interrogate gene regulation.

With our legacy of expertise from Chemicon and Upstate, we are committed to molding sophisticated yet simple solutions for understanding epigenetic regulation.

To learn more visit www.millipore.com/EPIC

EMD Millipore is a division of Merck KGaA, Darmstadt, Germany

EMBL-EBI

The Ensembl Project is a leading-edge international database providing genomic annotation to the scientific community as part of the Vertebrate Genomics Team at the European Bioinformatics Institute (EMBL-EBI) located on the Wellcome Trust Campus, Hinxton near Cambridge in the UK. EMBL-EBI is now seeking to recruit an exceptionally talented and motivated

Project Leader
Ensembl Regulation Team

to drive our efforts to understand whole genome regulation - developing and applying new methods to identify and classify regulatory elements leading to Ensembl's evidence-based, cell-type specific genome regulatory annotation. In addition to setting the direction and priorities of the Ensembl Regulation team, the Project Leader will participate in major functional and epigenomics projects including the EU-funded Blueprint project and ENCODE.

The Regulation Project Leader will represent Ensembl and the Regulation Team at internal and external meetings, working with the webteam and users to develop effective data displays, hiring and training staff, and participating in the overall leadership of the Ensembl Project.

To view a full description and apply please visit our jobs page www.ebi.ac.uk/jobs

As a world-leading bioinformatics centre, at EMBL-EBI we regularly recruit high quality bioinformaticians, database curators, scientific programmers, and web and software developers – please visit our website to sign up for our job alert emails.

Closing date for applications: 1st October 2012

Center for Personal Cancer Genomics and Therapeutics Faculty Search
Texas Children's Cancer Center - Baylor College of Medicine

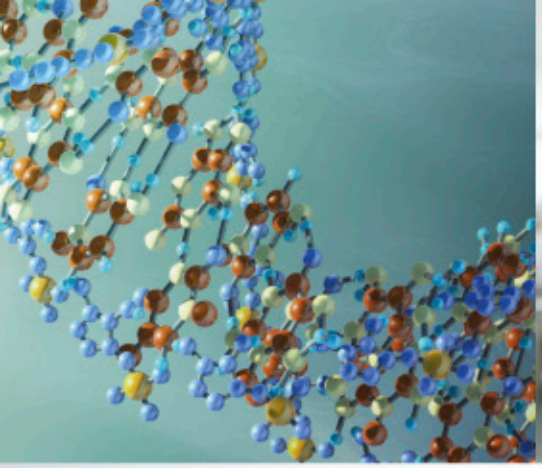
We are seeking full time research faculty at all academic levels for the newly formed **Center for Personal Cancer Genomics and Therapeutics** designed to exploit the latest in genome-scale technology to better understand childhood cancer and identify novel targets to improve therapy and outcomes. The Texas Children's Cancer Center is the largest children's cancer center in the US, with over $21 million annually in federal funding. Candidates with research programs that foster development of new bioinformatics tools, innovative mouse models of cancer or use of model organisms and tissue culture models to carry out functional analyses of large-scale datasets, are encouraged to apply. Previous research experience, including a relevant publication record and history of successful peer-reviewed grant funding, are important. Salary and start-up package will be commensurate with qualifications and prior experience. Interested candidates should submit curriculum vitae, a summary of past work, a brief research plan, and the names of at least three references. Applications will be accepted until the positions are filled and should be submitted to Sharon Plon, MD, PhD by email at splon@bcm.edu.

Baylor College of Medicine is an Equal Opportunity/Affirmative Action/Equal Access Employer.

www.txch.org

Texas Children's Cancer Center

BCM Baylor College of Medicine



The Future of Genomic Medicine VI

Thursday, March 7, and Friday, March 8, 201 3 • Scripps Seaside Forum • La Jolla, California

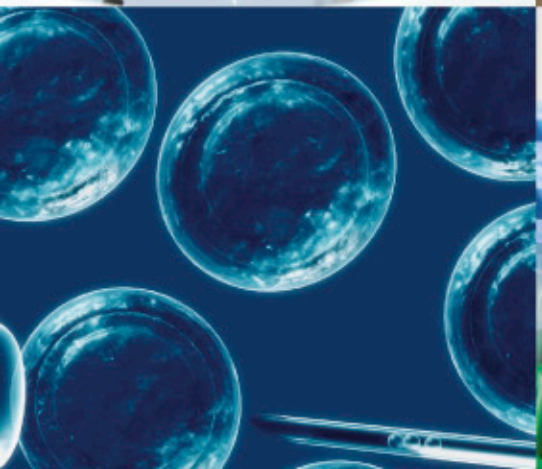
Presented in partnership with the AAAS/Science Translational Medicine

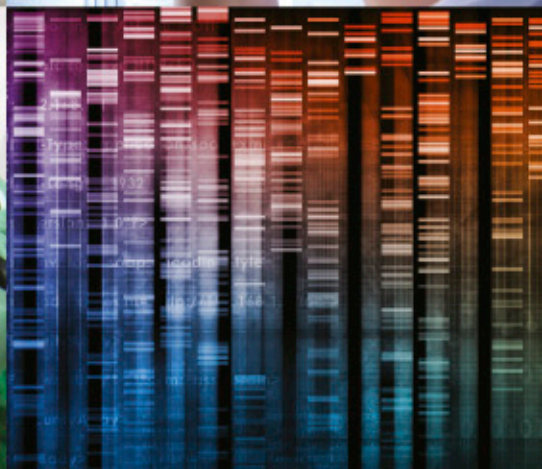
For conference information and to register, visit
http://bit.ly/KWBbK9 or call **858-652-5400**.
You may alco contact Scripps Conference Services
& CME at 11025 North Torrey Pines Road,
Suite 200, La Jolla, CA 92037.

Science Translational Medicine AAAS

Scripps Translational Science Institute





THE RNA INSTITUTE

Employment Opportunities

www.albany.edu/rna/employment.shtml

TWO TENURE TRACK ASSISTANT PROFESSOR POSITIONS with research interests in RNA science, biomedical applications and/or technology development

- Bioinformaticist/Computational Chemist
- Crystallography

THREE RESEARCH STAFF POSITIONS

Supervise use and support users of instrumentation for RNA and RNA interactions

- Bioinformaticist/Computational Research Associate
- Two Biochemistry/Cell & Molecular Biology Research Associates

EIGHT POSTDOCTORAL POSITIONS

- FOUR positions in biochemistry, cell and molecular biology within various research projects, including RNA imaging, and collaborations, including Public-Private Partnerships) in the newly constructed RNA Institute
- FOUR positions in cell biology, virology, and chemistry with new or existing faculty

COLLEGE OF ARTS AND SCIENCES
UNIVERSITY AT ALBANY
State University of New York

Life Sciences Research Building, Room 1085, 1400 Washington Avenue, Albany, NY 12222
PH: 518-437-4443 ■ **FX:** 518-437-4456 ■ **EMAIL:** rna@albany.edu ■ **www.albany.edu/rna**

Announcing Keystone Symposia's 2013 Genome Research Meetings

Nutrition, Epigenetics and Human Disease

February 19–24, 2013 • Hilton Santa Fe/Historic Plaza • Santa Fe, New Mexico • USA
Scientific Organizers: **Robert A. Waterland, David S. Rosenblatt** and **Patrick J. Stover**

Keynote Speaker:
Ezra S. Susser, Columbia University

Session Topics:
Nutrition and Epigenetics in Development and Disease of the CNS • Nutrient Regulation of the Epigenetic Machinery • Nutrition and Epigenetics in Obesity • Nutrient, Methyl Metabolism and Epigenetic Interactions • Nutrition and Developmental Epigenetics in the Endocrine Pancreas • Nutrients and Allelic Targeting of Epigenetic Signatures • Nutritional Modulation of Stem Cell Programming • Present and Future: Pressing Issues in Environmental Epigenetics

Abstract & Scholarship Deadline: October 17, 2012 / **Early Registration Deadline:** December 17, 2012
www.keystonesymposia.org/13B5

Genomic Instability and DNA Repair

joint with **DNA Replication, Recombination and DNA Repair**
March 3–8, 2013 • Fairmont Banff Springs • Banff, Alberta • Canada
Scientific Organizers: **Stephen P. Jackson, Alan D. D'Andrea** and **Susan M. Gasser**

Keynote Speakers:
Frederick W. Alt, HHMI/Children's Hospital Boston and Immune Disease Institute
Kenneth J. Marians, Memorial Sloan-Kettering Cancer Center

Session Topics:
Mechanisms and Control of DNA Repair/Mechanisms of Homologous Recombination • Chromosomal Stability, Instability and Nuclear Architecture • Controlling DNA Damage Responses by Ubiquitylation and Sumoylation • Replication, Chromatin and Genome Instability • Genome Instability, Telomeres, Disease and Aging • DNA Damage and Links to Transcription, RNA Metabolism and Other Processes • Genomic and Genome-Wide Studies • Diagnostic and Therapeutic Applications

Abstract & Scholarship Deadline: November 7, 2012 / **Early Registration Deadline:** January 7, 2013
www.keystonesymposia.org/13X6

Human Genomics and Personalized Medicine

June 17–21, 2013 • Clarion Hotel Sign • Stockholm • Sweden
Organized in collaboration with the Knut and Alice Wallenberg Foundation and Science for Life Laboratory – Stockholm
Scientific Organizers: **Kelly A. Frazer** and **Geoffrey S. Ginsburg**

Keynote Speaker:
John Bell, University of Oxford

Session Topics:
Breakthroughs in Genomic and Personalized Medicine • Genomes and Biology • Cancer Genomics and Applications • Advances and Challenges in the Field • Pharmacogenomics • Personalized Genomes • Policy • Translating Biomarkers to Personalized Medicine

Abstract & Scholarship Deadline: February 20, 2013 / **Early Registration Deadline:** April 16, 2013
www.keystonesymposia.org/13E3

Information shown is current as of May 7, 2012 but subject to change. Please visit the meeting web pages for the most current program information. And visit Keystone Symposia's website at www.keystonesymposia.org/meetings for details on more than 50 other conferences taking place in 2013.

KEYSTONE SYMPOSIA™
on Molecular and Cellular Biology
Accelerating Life Science Discovery