JUST RIGHT

WHETHER YOU RUN 24, 240 OR EVEN 2,400 SAMPLES A DAY, FRAGMENT ANALYZER™ IS JUST RIGHT.

Qualify and quantify nucleic acids for ANY throughput. Streamline sample analysis for ANY application.

NGS QC - RNA QC - gDNA - SSRs

Learn more at www.aati-us.com/just-right
Unlock the Power of FFPE Samples with Exome Sequencing from 25 ng DNA

Accel-NGS® 2S Hyb DNA Library Kit

* Enabling Targeted Sequencing of Limiting Samples

- Increased library complexity
- 5’ and 3’ repair steps for damaged samples
- No adapter titrations required
- Compatible with all hybridization panels

© 2016, Swift Biosciences, Inc. The Swift logo is a trademark and Accel-NGS is a registered trademark of Swift Biosciences. 16-0866, 05/16
The S is for Simplicity

The new Ion S5™ System. Targeted sequencing has never been simpler.

Simple library prep tools, cartridge-based reagents and automated data analysis have reduced DNA-to-data hands-on time to less than 45 minutes. So you’ll spend less time doing routine molecular biology, and more time informing time-sensitive decisions.

- Ion AmpliSeq™ technology
- As little as 1 ng low-quality DNA sample input for library prep
- Cartridge-based reagents
- Less than 15 minutes of sequencing setup time
- 2.5 to 4 hours of run time
- Fastest run time of any benchtop sequencer

Watch the Ion S5 System in action at
thermofisher.com/IONS5

For Research Use Only. Not for use in diagnostic procedures. © 2015 Thermo Fisher Scientific Inc. All rights reserved. All trademarks are the property of Thermo Fisher Scientific and its subsidiaries unless otherwise specified. C0019129 1015
Next Generation Sequencing (NGS) Services

SBS Genetech provides a wide variety of next generation sequencing suitable for most research needs. We offer comprehensive services including library preparation, sample validation, sequencing, and bioinformatics.

- **Comprehensive NGS Services**
  
  Genomic DNA Sequencing  
  Strand Specific RNA Sequencing  
  miRNA Sequencing  
  PCR Amplicon Sequencing  
  16S Metagenomic Sequencing

- **Sequencing Only Services**  
  HiSeq Sequencing  
  MiSeq Sequencing

- **Specialized Sequencing Services**
  
  Library Generation  
  Project Planning and Consultation

Interested? Please send your inquiries to order@sbsbio.com

Tel: +86-10-82784296/92 +86-10-62969345/46  
Fax: +86-10-82784290  E-mail: order@sbsbio.com  
Website: http://www.sbsbio.com
Echo® ACOUSTIC LIQUID HANDLER

DO MORE with LESS

Using sound energy, the revolutionary Echo liquid handling technology offers a tipless, non-contact, contamination-free alternative for transferring nanoliter scale volumes of liquid to any assay format faster and with better results. Scientists can now meet the ongoing challenges of...

**doing MORE**
- Higher throughput
- Improved data quality
- More flexibility

**with LESS**
- 100-fold reduction of reaction volumes
- Minutes of hand-on time instead of hours
- No pipetting tips, no waste
- Decreased overall operating costs

LABCYTE™
The Future of Science is Sound

@LabcyteInc
info-us@labcyte.com

© 2016 LABCYTE INC. All rights reserved. Labcyte®, Echo®, and the Labcyte logo are registered trademarks or trademarks of Labcyte Inc., in the U.S. and/or other countries.

FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.

MOVING LIQUIDS with SOUND
Extraordinary variation of floral organs in Phalaenopsis orchid is due to differential expression of multiple genes in sepal, petal, and labellum.1


Differential gene expression creates beauty

Differential gene expression plays a significant role in development of many species including orchids.

Phalaenopsis orchids are important species for development and evolutionary studies. Moreover, they are well recognized for their exceptional beauty. The flowers have several organs (i.e. sepal, petal, and labellum), which are significantly different, however together compose conspicuous and harmonious look (view photo). The unique shape of these flower organs is a result of differential expression of multiple genes involved in their development.

Lexogen is focusing on development of accurate and affordable tools for transcriptome analysis with RNA-Seq. QuantSeq is a dedicated kit for expression profiling. It is an easy protocol for producing highly strand-specific next generation sequencing libraries from the 3’ end of polyadenylated RNA. Only one fragment per transcript is produced, directly linking the number of mapping reads to the gene expression values. Restricted length saves sequencing space and allows for high level of multiplexing, enabling cost-efficient and fast RNA-Seq experiment.

Expression Profiling RNA-Seq Library Prep Kit

- Gene expression analysis
- Exact 3’ UTR tagging
- From 100 pg total RNA input including low quality RNA and FFPE samples
- Cost-effective sequencing of up to 96 samples / lane
- Ready-to-sequence libraries in 4.5 hours
- Illumina™ and Ion Torrent™ compatible
- Reduced data analysis time
- Custom solutions available

www.lexogen.com

* Illumina is a registered trademark of Illumina, Inc. Ion Torrent is a registered trademark of Life Technologies.
BD FACSseq™ Cell Sorter and BD™ Precise Assays

Enhanced transcript analysis of single cells

Seamless workflow from sample to digital data

- Acquire protein and transcript information from every cell analyzed
- BD™ Molecular Index technology removes amplification bias, improving gene expression analysis results
- Easily prepare NGS-ready libraries in one tube, in as fast as five hours
- Quickly select and isolate hundreds to thousands of cells

See more at bdbiosciences.com/go/facseq

BD Life Sciences, 2350 Qume Drive, San Jose, CA 95131

bdbiosciences.com

Class 1 Laser Product. For Research Use Only. Not for use in diagnostic or therapeutic procedures.
© 2016 BD, BD, the BD Logo and all other trademarks are property of Becton, Dickinson and Company.
23-17810-01
Empowering Research Through Smart Solutions

The right tools for your bioinformatics analysis needs

**novoAlign**
- The market's leading aligner for accurate and speedy multi-threaded sequence alignment.
- Powerful tool designed for mapping of short reads onto a reference genome.
- Now available on BaseSpace.

**novoSort**
- The fastest multi-threaded sort/merge tools for BAM files.
- Sort and mark duplicates in a flash.

**novoLR package**
- novoLRcleaver
- novoLRcorrector
- novoLRpolish
- Genome assembly prep using hybrid technology for mixed short reads and single molecule long reads.
- Long reads hybrid correction using in-house algorithms for read ranking and correction.
- Post-assembly sequence polishing.

**novoWorx**
A on-site, integrative, customizable workbench that allows users to run an entire pipeline without using command lines interface. The platform mainly utilizes Novocraft's proprietary software; novoAlign for alignment and novoSort for sorting and SAM to BAM conversion. A combination of unique in-house softwares and open source modules to decipher your big data into meaningful results.

**novoClinic**
A patient-centric NGS targeted sequence analysis platform that provides integrated sample tracking for quality control and compliance. The built-in customizable analysis pipeline and straight-forward data reporting system will ease the burden of data mining and interpretation, allowing clinicians to focus on diagnosis and treatment.

NOVOCRAFT TECHNOLOGIES SDN. BHD.
C-23A-05, 3 Two Square, Section 19, 46300 Petaling Jaya, Selangor, Malaysia

+603 7960 0541  office@novocraft.com
+603 7960 0540  http://www.novocraft.com

Novocraft-Technologies-Sdn-Bhd
2016-2017
SCIENTIFIC CONFERENCES

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

EORTC-NCI-EMA-AACR International Conference on Innovation and Biomarkers in Cancer Drug Development
Conference Co-Chairpersons: Denis A. Lacombe and John W. Martens
September 8-9, 2016 • Brussels, Belgium

11th Biennial Ovarian Cancer Research Symposium
Conference Co-Chairpersons: Deborah K. Armstrong, Martin M. Matzuk, Gordon B. Mills, and Saul E. Rivkin
September 12-13, 2016 • Seattle, WA
Co-presented with the Rivkin Center for Ovarian Cancer

Colorectal Cancer: From Initiation to Outcomes
Conference Co-Chairpersons: Ernest T. Hawk, Steven H. Itzkowitz, Kenneth W. Kinzler, and Johanna W. Lampe
September 17-20, 2016 • Tampa, FL

Ninth AACR Conference on The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved
Conference Co-Chairpersons: Rick A. Kittles, Folakemi T. Odedina, Jeffrey N. Weitzel, and Jun J. Yang
September 25-28, 2016 • Fort Lauderdale, FL

CRI-CIMT-EATI-AACR Second International Cancer Immunotherapy Conference: Translating Science into Survival
Conference Co-Chairpersons: James P. Allison, Philip D. Greenberg, Christoph Huber, and Guido Kroemer
September 25-28, 2016 • New York, NY

DNA Repair: Tumor Development and Therapeutic Response
Conference Co-Chairpersons: Robert G. Bristow, Maria Jasin, and Theodore S. Lawrence
November 2-5, 2016 • Montreal, Quebec, Canada

New Horizons in Cancer Research: Delivering Cures Through Cancer Science
Conference Co-Chairpersons: Jose Baselga and Scott A. Armstrong
November 2-5, 2016 • Shanghai, PR, China

Improving Cancer Risk Prediction for Prevention and Early Detection
Conference Co-Chairpersons: Graham A. Coditz, Susan M. Gapstur, Kenneth R. Muir, and Mark E. Sherman
November 16-19, 2016 • Orlando, FL

EORTC-NCI-AACR Molecular Targets and Cancer Therapeutics Symposium
Conference Co-Chairpersons: Jean-Charles Soria, Lee J. Helman, and Levi A. Garraway
November 29-December 2, 2016 • Munich, Germany

San Antonio Breast Cancer Symposium
Symposium Co-Directors: Carlos L. Arteaga, Virginia G. Kaklamani, and C. Kent Osborne
December 6-10, 2016 • San Antonio, TX

Precision Medicine Series: Opportunities and Challenges of Exploiting Synthetic Lethality in Cancer
Conference Co-Chairpersons: René Bernards, William C. Hahn, and Louis M. Staudt
January 4-7, 2017 • San Diego, CA

AACR International Conference on New Frontiers in Cancer Research
Conference Co-Chairpersons: Peter A. Jones and Frank McCormick
January 18-22, 2017 • Cape Town, South Africa

AACR Annual Meeting 2017
Program Committee Chairperson: Kornelia Polyak
April 1-5, 2017 • Washington, DC

Learn more and register at AACR.org/Calendar
Announcing Keystone Symposia’s 2016–2017 RNA Conferences

**Precision Genome Engineering**
Scientific Organizers: J. Keith Joung, Emmanuelle Charpentier and Olivier Danos
January 8–12, 2017 | Breckenridge, Colorado | USA
www.keystone symposia.org/17A2

**Omens Strategies to Study the Proteome**
Scientific Organizers: Alan Saghathel, Chuan He and Ileana M. Cristea
January 29–February 2, 2017 | Breckenridge, Colorado | USA
www.keystone symposia.org/17A8

**Epigenetics and Human Disease: Progress from Mechanisms to Therapeutics**
Scientific Organizers: Johnathan R. Whetstone, Jessica K. Tyler and Rabinder K. Prinjha
January 29–February 2, 2017 | Seattle, Washington | USA
www.keystone symposia.org/17A9

**Noncoding RNAs from Disease to Targeted Therapeutics**
Scientific Organizers: Kevin V. Morris, Arch Fox and Paloma Hoban Glangrande
Joint with **Protein-RNA Interactions: Scale, Mechanisms, Structure and Function of Coding and Noncoding RNPs**
Scientific Organizers: Gene W. Yeo, Jernej Ule, Karla Neugebauer and Melissa J. Moore
February 5–9, 2017 | Banff, Alberta | Canada

**mRNA Processing and Human Disease**
Scientific Organizers: James L. Manley, Siddhartha Mukherjee and Gideon Dreyfuss
March 5–8, 2017 | Taos, New Mexico | USA
www.keystone symposia.org/17C3

**RNA-Based Approaches in Cardiovascular Disease**
Scientific Organizers: Thomas Thum and Roger J. Hajjar
Joint with **Molecular Mechanisms of Heart Development**
Scientific Organizers: Benoit G. Bruneau, Brian L. Black and Margaret E. Buckingham
March 26–30, 2017 | Keystone, Colorado | USA
www.keystone symposia.org/17X8

Submit an abstract to participate fully in the conference via a poster presentation and possible selection for a short talk. Scholarships are available for graduate students and postdoctoral fellows. For full program, speaker, abstract and scholarship details, visit www.keystone symposia.org/genetics
The development of CRISPR–Cas technology is revolutionizing biology. Based on machinery bacteria use to target foreign nucleic acids, these powerful techniques allow investigators to edit nucleic acids and modulate gene expression more rapidly and accurately than ever before.

Authors also describe other applications of the CRISPR–Cas system, including its use for regulating genome activation and repression, and discuss the development of next-generation CRISPR–Cas tools. The book is thus an essential laboratory resource for all cell, molecular, and developmental biologists, as well as biochemists, geneticists, and all who seek to expand their biotechnology toolkits.
Decoding the Language of Genetics

By David Botstein, Lewis-Sigler Institute for Integrative Genomics

In this book, the distinguished geneticist David Botstein offers help and advice to scientists and physicians daunted by the arcane technical terms that flourish in his discipline. The science of gene function has a vocabulary of specialized, sometimes confusing terms to explain how traits and diseases are inherited, how genes are organized and regulated in the genome, and how the genetic code is read and translated by cells. These terms are often a barrier to full understanding of the underlying concepts. Yet, as more and more individuals learn about their genomes, the information these sequences contain cannot be understood or explained without reference to the basic ideas of genetics. Botstein draws on his long experience as a teacher and pioneering scientist to explain and illuminate what many genetic terms mean and how they entered common usage.

2015, 240 pages, illustrated (30 4C, 10 B&W), index
Hardcover $79

Contents

Preface
Acknowledgments

1 The Basics
2 Implicit Experiments and the Functional Gene
3 Recombination and Linkage Mapping
4 Pathway Analysis
5 Regulation of Metabolic Pathways
6 Phage and the Beginning of Molecular Genetics
7 Transcription, Translation, and the Genetic Code
8 Suppression Genetics

9 Functional Suppression
10 The Genetics of Complex Phenotypes
11 Transcriptional Regulation of Gene Expression
12 The Modular Architecture of Genes and Genomes
13 Evolution Conserves Functional Sequences
14 Human Population Genetics
15 Inferring Human Gene Function from Disease Alleles
16 What Is Next in Genetics and Genomics?
Index

www.cshlpress.org
LEARN FROM CANCER GENOMICS DATA

FASTER

The Cancer Genomics Cloud is now open to researchers worldwide.
All The Cancer Genome Atlas data and more than $1,000,000 in funding is available to support your compute and data storage on the system.

CANCER GENOMICS CLOUD
SEVEN BRIDGES

Learn more at cancergenomicscloud.org
Immunoassays for immuno-oncology research
Move confidently across platforms

Immune checkpoints have come to the forefront of cancer therapies as a powerful and promising strategy to stimulate anti-tumor T cell activity. Affymetrix provides a wide range of products for immune-oncology research for the quantification of these important checkpoint proteins. ProcartaPlex® Human Immuno-oncology Checkpoint Panel enables simultaneous quantification of 14 checkpoint modulators. Speed, sensitivity, and specificity make Platinum ELISA the method of choice for biomarker evaluation.

Affymetrix offers multiple immunoassay platforms, providing the freedom to move from a multiplex assay to an ELISA while producing comparable data.

- 98% correlation of antibody pairs across platforms
- Lot-to-lot consistency for reliable reproducibility
- Exceptional scalability between ProcartaPlex® assays and traditional Platinum ELISA

Visit our website to learn more about the ProcartaPlex® Human Immuno-oncology Checkpoint Marker Panel and Platinum ELISA

www.ebioscience.com/immuno-oncology

© 2016 Affymetrix, Inc. All rights reserved. For Research Use Only. Not for use in diagnostic procedures.