New to single-cell sequencing?

that's GOOD science!

Takara Bio has the solutions you need.

- **SMART-Seq® HT kit**—streamlined full-length cDNA library prep
- **SMART-Seq Stranded kit**—complete RNA library prep that captures coding and noncoding RNAs
- **SMARTer® PicoPLEX® Gold kit**—accurate detection of SNVs and CNVs from single cells
- **SMARTer™ ICELL8® system**—automated high-throughput single-cell isolation, selection, and processing

SMARTer NGS

To learn more:
takarabio.com/SMARTerNGS

TaKaRa

Clontech TaKaRa cellartis

Takara Bio USA, Inc.
United States/Canada: +1.800.662.2566 • Asia Pacific: +1.650.919.7300 • Europe: +33.(0)1.3904.6880 • Japan: +81.(0)77.565.6999

For Research Use Only. Not for use in diagnostic procedures.

arbor biosciences

Experts in Targeted Sequencing

INTRODUCING
CRISPR-Powered
Targeted Sequence
Depletion

my NGS Guides™

NEW myNGS Guides™ MitoDeplete Kit

CRISPR-Powered Mitochondrial Sequence Depletion

- Remove up to 95% of mtDNA-derived templates from NGS libraries
- Available for Human, Mouse, and Custom species
- Save 30-70% in ATAC-Seq library sequencing costs
- One-step, single-tube incubation prior to sequencing

ArborBiosci.com | info@arborbiosci.com | +1 734-998-0751 | *Follow us on Twitter:* @ArborBio

Collect. Spin. Load.

Primary tube handling in automated direct sample processing on the QIAsymphony SP for ccfDNA purification

Streamlined protocols for the PAXgene Blood ccfDNA System

- Eliminate manual plasma transfer
- Lower risk of sample mixup
- Minimize risk of blood exposure
- Save time, cut costs, reduce waste

For Research Use Only.
Not for use in diagnostic procedures.
Explore more at **www.preanalytix.com**

PreAnalytiX
A QIAGEN / BD Company

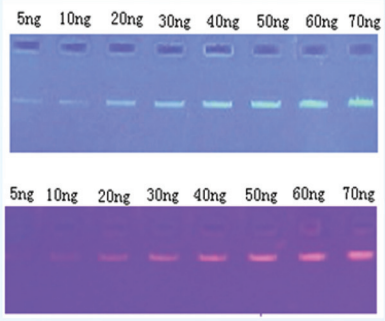
SBS Genetech Co., Ltd.

GoodView™ Nucleic Acid Stain

——An alternative to EB

GoodView™ is a safer nucleic acid stain, an alternative to the traditional ethidium bromide (EB) stain for detecting nucleic acid in agarose gels. It emits green fluorescence when bound to DNA or RNA. This new stain has two fluorescence excitation maxima when bound to nucleic acid, one centered at 268 nm and another at 294 nm. In addition, it has one visible excitation at 491 nm. The Fluorescence emission of GoodView™ bound to DNA is centered at 530 nm.

Comparative sensitivity test of GV and EB



Sensitivity test result of GV at UV 300nm.

Sensitivity test result of EB at UV 300nm.

The result of electrophoresis demonstrates GV is almost as sensitive as EB.

The Test Report from Institute for Environmental Health and Related Product Safety of Chinese Center for Disease Control and Prevention concludes that:

- Acute Oral Toxicity Test: GoodView™ Nucleic Acid Stain belongs to nontoxic.
- Mouse Marrow Chromophilous Erythrocyte Micronucleus Test: Negative. There is no significant difference in the incidence of micronuclei between test and control groups.
- Ames Test: Negative. No mutagenicity was observed.
- In Vitro Mammalian Cell Chromosome Aberration Test: Negative. No increasing aberration rate was observed.

GoodView Nucleic Acid Stain is included on New Products, Science Magazine, January 11, 2019.
Please visit: http://science.sciencemag.org/content/363/6423/193

Beijing SBS Genetech Co., Ltd.
Phone: +86-10-82784296 Fax: +86-10-82784290
Email: order@sbsbio.com Website: www.sbsbio.com

MilliporeSigma

Design Engineer Innovate

with MISSION™ CRISPR

Be confident in your genome editing.

The SygRNA® synthetic, crRNA:tracrRNA and one-part sgRNA systems accelerate genome editing. Pair with Cas9 protein, mRNA, or established Cas9 expressing cell lines. Deliver by a variety of methods including microinjection, electroporation, and lipofection.

Guaranteed performance with MISSION™ CRISPR predesigned knockout gRNAs

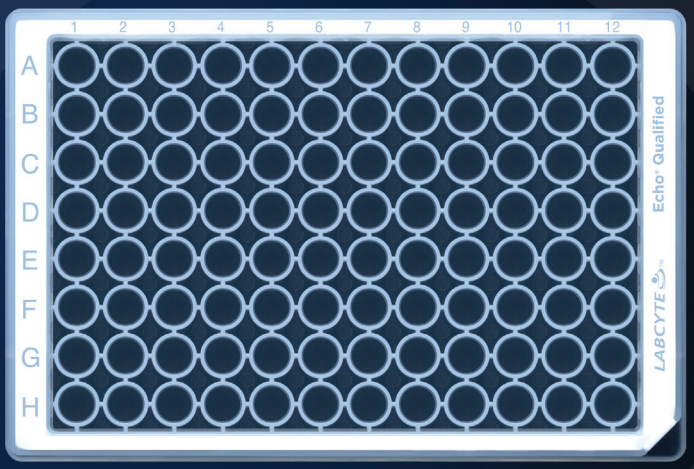
To find out more, visit
SigmaAldrich.com/SygRNA

2019 - 19308 1/2019

The life science business of Merck KGaA, Darmstadt, Germany operates as MilliporeSigma in the U.S. and Canada.

Sigma-Aldrich®
Lab & Production Materials

Coming soon...



96 New Reasons to Buy an Echo® Liquid Handler

Introducing the Echo® Qualified 96-well Microplate

A favorite for genomics applications, the Echo® 525 Liquid Handler saves reagents, sample, and time. Transfer of nanoliter volumes with high accuracy and precision enables assay miniaturization while maintaining data quality. Coming soon, Echo Qualified 96-well Microplates will link the unsurpassed performance of the Echo System with upstream sample preparation steps performed in a 96-well format.

- **Qualified by Labcyte for reproducible acoustic performance**
- **High transparency with high contrast well locators for quick sample identification**
- **Compatible with the Echo 525 Liquid Handler**

For more information, visit www.labcyte.com/**echo-525.**

LABCYTE™

The Future of Science is Sound

info-us@labcyte.com

CSHL Meetings & Courses


aerial view of CSHL sandspit and inner harbor during meeting social

2019 Meetings

Microbiome
July 18 - 21

Cell Death
August 13 - 17

Eukaryotic mRNA Processing
August 20 - 24

Mechanisms of Eukaryotic Transcription
August 27 - 31

Eukaryotic DNA Replication & Genome Maintenance
September 3 - 7

Microbial Pathogenesis and Host Response
September 10 - 14

Stem Cell Biology
September 17 - 21

Biology of Cancer: Microenvironment & Metastasis
September 24 - 28

Neurobiology of *Drosophila*
October 1 - 5

Genome Engineering: Frontiers of CRISPR/Cas
October 10 - 13

Yeast Research: Origins, Insights, Breakthroughs
October 23 - 26

Genome Informatics
November 6 - 9

Single Cell Analyses
November 13 - 16

Zebrafish Neural Circuits & Behavior
November 20 - 23

Plant Genomes, Systems Biology & Engineering
December 4 - 7

Development & 3D Modeling of the Human Brain
December 9 - 12

meetings.cshl.edu

2019 Fall Courses

Workshop on Cereal Genomics
October 15 - 21

Programming for Biology
October 15 - 30

X-Ray Methods in Structural Biology
October 15 - 30

Advanced Sequencing Technologies & Applications
November 5 - 17

The Genome Access Course
November 11 - 13

Scientific Writing Retreat
November 13 - 17

Computational Genomics
December 4 - 11

Preview of our early 2020 Meetings

Systems Bio: Global Regulation of Gene Expression
March 11 - 14

Neuronal Circuits
March 18 - 21

The PARP Family & ADP-ribosylation
April 1 - 4

Gene Expression & Signaling in the Immune System
April 14 - 18

Protein Homeostasis in Health & Disease
April 21 - 25

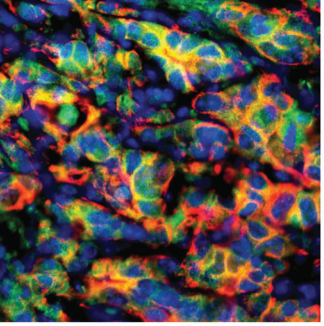
Genome Organization & Nuclear Function
April 28 - May 2

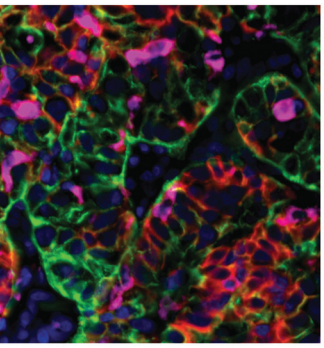
The Biology of Genomes
May 5 - 9

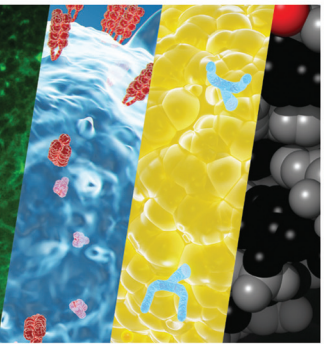
Regulatory & Non-Coding RNAs
May 12 - 16

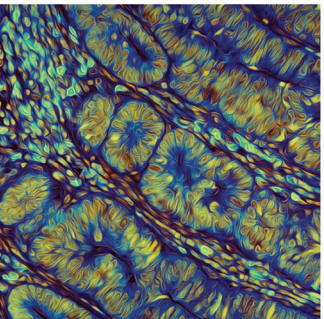
Retroviruses
May 18 - 23

meetings.cshl.edu









2019–2020 SCIENTIFIC CONFERENCES

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

Pancreatic Cancer: Advances in Science and Clinical Care
Conference Cochairs: Dafna Bar-Sagi, Luis A. Diaz, Elizabeth M. Jaffee, Ben Z. Stanger, and Brian M. Wolpin
September 6-9, 2019 | Boston, MA

Advances in Ovarian Cancer Research
Conference Cochairs: Carol Aghajanian, David D. L. Bowtell, George Coukos, Alan D. D'Andrea, and Karen H. Lu
September 13-16, 2019 | Atlanta, GA

Advances in Pediatric Cancer Research
Conference Cochairs: Crystal Mackall, David Malkin, Stefan Pfister, and Kimberly Stegmaier
September 17-20, 2019 | Montreal, QC, Canada

12th AACR Conference on The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved
Conference Chair: Laura Fejerman
September 20-23, 2019 | San Francisco, CA

Fifth CRI-CIMT-EATI-AACR International Cancer Immunotherapy Conference: Translating Science into Survival
Conference Cochairs: Christoph Huber, Guido Kroemer, Ellen Puré, and Giorgio Trinchieri
September 25-28, 2019 | Paris, France

Cancer Research UK-AACR Joint Conference: Engineering and Physical Sciences in Oncology
Conference Cochairs: Sangeeta N. Bhatia, Kevin M. Brindle, Joe W. Gray, and Molly Stevens
October 15-17, 2019 | London, England

AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics
Organizing Committee Cochairs: Elizabeth M. Jaffee, James H. Doroshow, and Denis A. Lacombe
October 26-30, 2019 | Boston, MA

AACR International Conference: Infection and Cancer
Conference Chair: Tak W. Mak
November 8-10, 2019 | Hong Kong

Tumor Immunology and Immunotherapy
Conference Cochairs: Timothy A. Chan, Charles G. Drake, Marcela V. Maus, and Arlene H. Sharpe
November 17-20, 2019 | Boston, MA

San Antonio Breast Cancer Symposium
Codirectors: Carlos L. Arteaga, Virginia G. Kaklamani, and C. Kent Osborne
December 10-14, 2019 | San Antonio, TX

Advancing Precision Medicine Drug Development: Incorporation of Real World Data and Other Novel Strategies
Conference Cochairs: David M. Hyman, Elaine R. Mardis, Lillian L. Siu, and Eliezer M. Van Allen
January 9-12, 2020 | San Diego, CA

Sixth AACR-IASLC International Joint Conference: Lung Cancer
January 11-14, 2020 | San Diego, CA

Advances in Liquid Biopsies
Conference Cochairs: Luis A. Diaz Jr., Maximilian Diehn, Irene M. Ghobrial, and Nicholas C. Turner
January 13-16, 2020 | Miami, FL

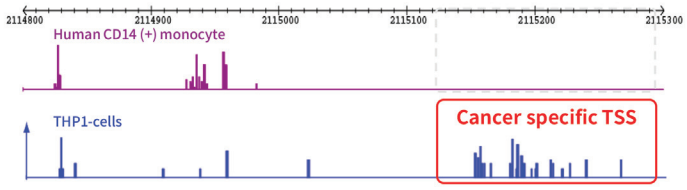
Learn more and register at
AACR.org/Calendar

AACR American Association for Cancer Research®
FINDING CURES TOGETHER®

Promoter / Enhancer Annotation in the NGS era

Cap Analysis of Gene Expression (CAGE) is a new NGS library preparation method using "cap-trapping" technology which enables you to detect and quantify **transcription start site (TSS)** of RNA pol II transcripts including **mRNAs**, **lincRNAs** and **enhancer RNAs**.

- **Accurate promoter annotation**—reliable estimation of promoter posions and their activities based on precise TSS information
- **Estimation of transcription factor binding sites**—genome-wide motif search around TSS which have different expression profiles among samples
- **Detection of active enhancers**—identify active enhancers by detection of bidirectional enhancer RNAs
- **Development of new biomarkers**—TSS variants are valuable candidate of biomarkers even in the case that there are no difference at the gene expression level
- **Accurate quantification of gene expression**—PCR-free library preparation process without fragmentation allow for more reliable quantification of gene expression than RNA-seq



CAGE expression pattern of a histone H3 methyltransferase gene of human CD14(+) monocytes and THP-1 leukemia monocytic cells.

CAGE library preparation & analysis services	
Library preparation for Illumina sequencers	500 USD/sample
Sequencing (Illumina HiSeq/ NextSeq)	250 USD/sample
Bioinformatics analysis	250 USD/sample
CAGE library preparation kit	
8 samples (Cat. 52003-8)	2,000 USD
48 samples (Cat. 52003-48)	10,000 USD

More than 250 papers using CAGE have been published!
Learn more at **cage-seq.com**

DNAFORM
Precision gene technologies
contact@dnaform.jp

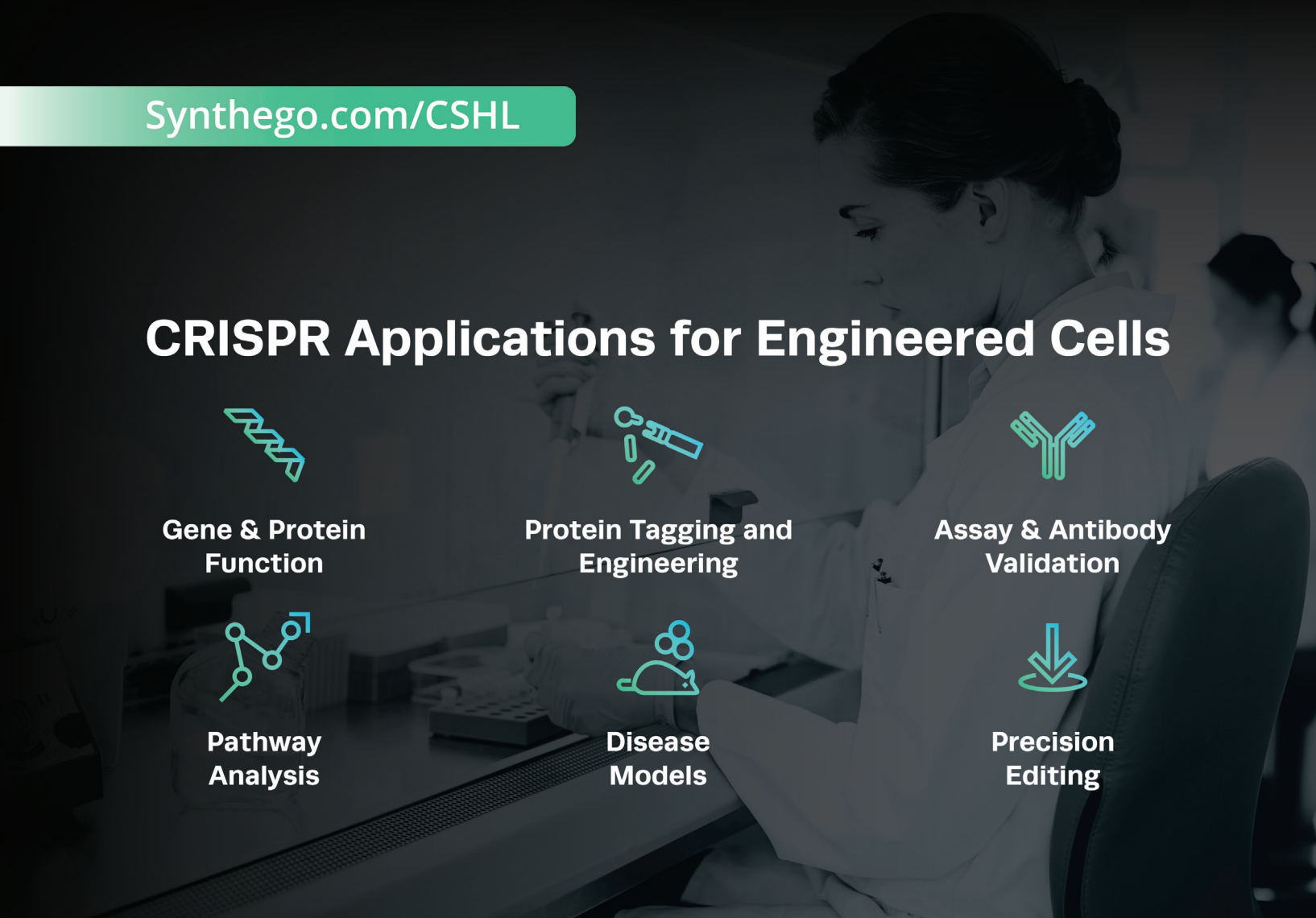
SYNTHEGO | Full Stack Genome Engineering

AUTOMATE YOUR GENOME ENGINEERING

CRISPR Done for You

Engineered Cells products deliver your desired edit in your preferred cell type with guaranteed results. We've optimized CRISPR. You focus on the discoveries.

Synthego.com/CSHL



CRISPR Applications for Engineered Cells

- Gene & Protein Function
- Protein Tagging and Engineering
- Assay & Antibody Validation
- Pathway Analysis
- Disease Models
- Precision Editing