Forefront of Gene Therapy Manufacturing

FROM BENCH TO BEDSIDE

AFFORDABLE

Providing low-cost, high-quality vectors for use in cells, small/large animal models and in the clinic. Scalable proprietary transfection process, providing the benefit of higher cost-effectiveness.

RESEARCH TOOLS

High Titer, High Purity. Rapid turn around times. Additional research tools include AAV Biosensors - GCaMP, RCaMP, CaMPARi, jRGECO1; ORF clones, ZIKA, viral controls.

PRE-CLINICAL/CLINICAL

Providing custom, on-demand virus for pre-clinincal and clinical applications. Additional services: Master and Working cell banking, Aseptic filling, QC testing. Compliant with US FDA and EU EMA regulatory requirements.

Feature Viral Vector Application Note.

Discover the advantage of Vigene's viral-tools and technologies to help meet your basic, preclinical, and/or clinical application needs. Specializing in **AAV**, **Adenovirus** and **Lentivirus** gene delivery.

DOWNLOAD FREE APPLICATION NOTE **vigenebio.com/virus-manufacturing**

Vigene Biosciences
Excellence in Gene Delivery

1-800-485-5808
vigenegmp.com
vigenebio.com

Whole genome and exome sequencing just got a

supercharged workflow.

Meet our newest addition to the Swift portfolio: *Swift 2S Turbo*

Swift 2S Turbo DNA Library Kits are a simple, easy and cost-effective library prep solution. A revolutionary workflow offering fast, robust enzymatic fragmentation prep and flexible adapter options to produce high quality libraries for production scale sequencing. Swift 2S Turbo is a universal library prep kit, compatible with a variety of applications such as whole genome and exome sequencing for simple and complex genomes.

Contact 734.330.2568 or info@swiftbiosci.com for *Early Access Promotion.*

Swift BIOSCIENCES™

swiftbiosci.com

© 2018, Swift Biosciences, Inc. The Swift logo is a trademark of Swift Biosciences. This product is for Research Use Only. Not for use in diagnostic procedures. 18-2239, 8/18

ion torrent

Gene panels on demand, how and when you want them

Ion AmpliSeq On-Demand Panels help you get more from targeted next-generation sequencing

- **Now more selection**—build custom panels from a growing catalog of **over 5,000 pretested genes** most relevant in inherited disease research*
- **Now more sizes**—order the exact quantity you need: 8, 24, 32, and 96 reactions per pack

With practical pack sizes that help lower up-front cost, and a powerful content selection engine that automates optimal gene selection, Ion AmpliSeq™ On-Demand Panels help you do targeted sequencing in your own lab, your own way.

Do targeted sequencing your way at **ampliseq.com**

Learn more at **thermofisher.com/ampliseqondemand**

ThermoFisher SCIENTIFIC

For Research Use Only. Not for use in diagnostic procedures. © 2017 Thermo Fisher Scientific Inc. All rights reserved.
All trademarks are the property of Thermo Fisher Scientific and its subsidiaries unless otherwise specified. **COL05650 1217**

sbs 赛百盛

Beijing SBS Genetech Co., Ltd.

Ultra-pure dNTPs at unbeatable prices

Description

dNTPs contain dATP, dCTP, dGTP and dTTP (monosodium salts) at a concentration of 10mM or 100mM each in sterile deionized water at pH7.5, whose purity is up to 99.5% (HPLC). It is free of RNase and DNase, and suitable for any molecular biology application that requires pure deoxynucleotides, such as PCR, DNA sequencing, cDNA synthesis and nick translation.

Stability

All of our dNTPs are very stable – we guarantee 100% stability for 2 years from the date of purchase.

Features

·Ultra-pure: >99% by HPLC
·Reliable, consistent results
·Available both as ready-to-use mix and a set

Applications

·PCR and qPCR
·cDNA synthesis
·Primer extension
·DNA sequencing
·DNA labeling
·Mutagenesis

Quality control

·Purity assay (HPLC) >99%
·Free of pyrophosphate, DNA and RNA
·DNase, RNase and nickase free
·Tested for PCR, qPCR and RT-PCR

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

GO EXPONENTIAL

Accelerate the pace of discovery with the power of Linked-Reads

In a world of incremental improvements, true breakthroughs are born from massive leaps forward. The genomics community is not about shifting paradigms but shattering them. With Linked-Read sequencing data, we can achieve a comprehensive understanding of genomic variation. Power your next discovery with Chromium™ Solutions that uncover the genome and exome data you've been missing. Now, you can resolve ambiguous single nucleotide variants, obtain phasing and haplotype information, identify structural variants, and assemble genomes without breaking a sweat.

Biology is challenging. Research is a race. Get there faster.
Learn more at **go.10xgenomics.com/linked-reads**

10x GENOMICS®

arbor biosciences

Experts in Targeted Sequencing

INTRODUCING
v4 Chemistry & Streptavidin Beads Included in Kit

myBaits®

TARGETED SEQUENCING KITS

- Complimentary Probe Design Service
- Compatible with Any NGS Library Prep
- Predesigned Kits for Immediate Shipment
- Custom Kits for Unique Organisms

myReads®

NGS SERVICES FOR TARGETED SEQUENCING

- Experimental Design Services
- Project Management by Dedicated Scientists
- Best-in-Class Library Preparation and Enrichment
- Sequencing on Illumina® and PacBio®

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

Arbor Biosciences, myBaits and myReads are trademarks of Arbor Biosciences. Illumina and PacBio are trademarks of Illumina and Pacific Biosciences respectively.

Echo® Acoustic LIQUID HANDLING
for **GENOMICS**

Reduce Library Prep Costs

100-Fold

Echo® Liquid Handlers enable library preparation in low microliter volumes for a range of sequencing methods. Dramatically reduce reagent costs, conserve samples, and eliminate steps – all while improving library quality.

Echo acoustic liquid handling allows...

- 100-fold reduction of library prep reaction volumes
- 30-fold reduction of sample pooling turnaround time
- Increased sample throughput
- Automation of workflow to easily prepare thousands of samples
- Improved accuracy of results

Comparison of Liquid Handling Methods*

	Manual Pipetting	Echo® Liquid Handler
Amount of DNA	50 ng	0.06 – 2.0 ng
DNA volume (Rxn)	25 µL	200 nL
Library prep volume (Rxn)	25 µL	300 nL
Total volume	50 µL	0.5 µL
Reactions per kit	96	9600
Cost per reaction	$72.91	**$0.73**

For more information, visit www.labcyte.com/**sequencing.**

** Low-Cost, High-Throughput Sequencing of DNA Assemblies Using a Highly Multiplexed Nextera Process. Shapland et al. ACS Synth. Biol., 2015*

LABCYTE™
The Future of Science is Sound

© **2018 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.

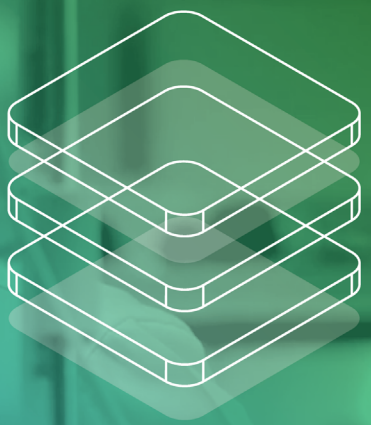
@LabcyteInc
info-us@labcyte.com

Introducing

Engineered Cells

SYNTHEGO

Full Stack Genome Engineering



Synthego.com/cshl

30th Anniversary AACR Special Conference

CONVERGENCE: ARTIFICIAL INTELLIGENCE, BIG DATA AND PREDICTION IN CANCER

October 14-17, 2018 | Newport Marriott | Newport, RI

Register Online or Onsite!

CONFERENCE COCHAIRS

Phillip A. Sharp
David H. Koch Institute for Integrative Cancer Research at MIT, Cambridge, MA

William C. Hahn
Dana-Farber Cancer Institute, Boston, MA

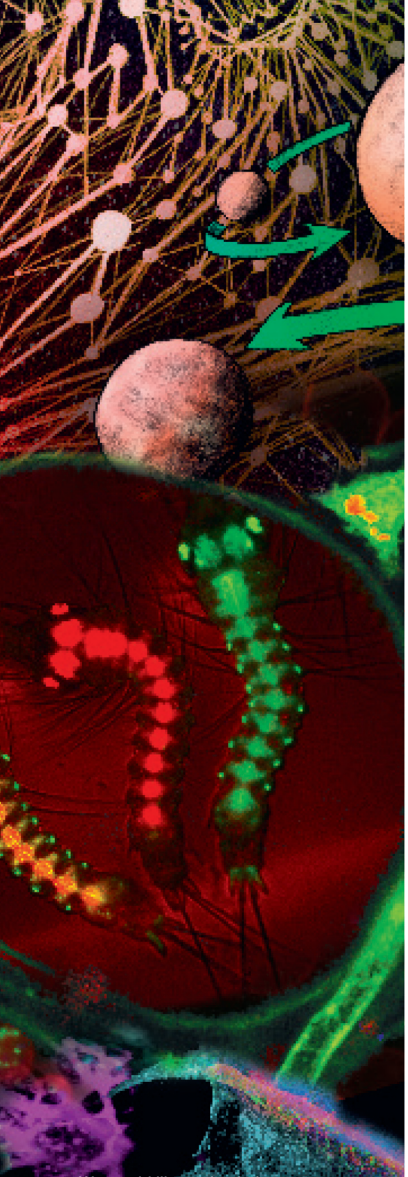
ABOUT THIS CONFERENCE

Information technologies have transformed many aspects of society, but to date they have had a modest impact on diagnosis, prevention, or treatment of cancer. One of the first points of intersection of information technologies on advancing the understanding and control of cancer is the ability to predict the development, progression, and malignancy of the disease in both populations and individuals. New, transformative technologies are emerging that collect large sets of high-resolution data at levels of single molecules, single cells, specific tissues, organisms, and populations. Extracting insights from these big data sets requires development of new methods in information technologies and machine learning and new concepts. It is this interface of cancer biology, computation, and clinical oncology that will most likely produce the future breakthroughs in control of cancer. This AACR Special Conference will cover the state of the art in understanding the disease of cancer from incident to early diagnosis, prevention, and treatment, with an emphasis on approaches that use big data and new computational methods such as machine learning.

Learn more and register at
AACR.org/AIBDP18

#AACR30SC18

AACR American Association for Cancer Research®
FINDING CURES TOGETHER®



EMBL 2019 PREVIEW

Courses and Conferences

JANUARY

14 – 18 Jan • EMBL Course
Advanced Training with Oxford Nanopore Technologies

21 – 25 Jan • EMBL Course
Bioinformatics for Discovery

29 – 31 Jan • EMBL Course
Data Carpentry

FEBRUARY

3 – 8 Feb • EMBL Course
Analysis and Integration of Transcriptome and Proteome Data

4 – 8 Feb • EMBL Course
Metabolomics Bioinformatics for Life Scientists

6 – 8 Feb • EMBL Industry Workshop
Cryo-EM in Industry and Academia

11 – 15 Feb • EMBL Course
Introduction to Multiomics Data Integration

26 – 28 Feb • EMBL Course
Bioinformatics Resources for Protein Biology

MARCH

4 – 8 Mar • EMBL Course
Single-Cell Immunology

7 – 9 Mar • EMBL–Wellcome Genome Campus Conference
Proteomics in Cell Biology and Disease Mechanisms

11 – 15 Mar • EMBL Course
Target Engagement in Biology and Drug Discovery

13 – 15 Mar • EMBO Workshop
Visualizing Biological Data (VIZBI 2019)

17 – 20 Mar • EMBO | EMBL Symposium
Synthetic Morphogenesis: From Gene Circuits to Tissue Architecture

17 – 22 Mar • EMBL Course
Genome Engineering: CRISPR/Cas

19 – 20 Mar • EMBL Course
Exploring Human Genetic Variation

25 – 29 Mar • EMBL Course
Optogenetics: From Design to Cell Signalling to Tissue Morphogenesis

25 – 29 Mar • EMBL Course
Introduction to Metabolomics Analysis

27 – 28 Mar • EMBL Course
Transgenic Animals - Micromanipulation Techniques

31 Mar – 3 Apr • EMBO | EMBL Symposium
Reconstructing the Human Past - Using Ancient and Modern Genomics

31 Mar – 5 Apr • EMBL Course
Techniques for Mammary Gland Research

APRIL

1 – 5 Apr • EMBL Course
Statistical Methods in Bioinformatics with R/Bioconductor

1 – 5 Apr • EMBL Course
Introduction to Next Generation Sequencing

7 – 12 Apr • EMBO Practical Course
High–Accuracy CLEM: Applications at Room Temperature and *in Cryo*

8 – 12 Apr • EMBL Course
Advanced RNA–Seq Analysis

10 – 13 Apr • EMBO | EMBL Symposium
Probing Neural Dynamics with Behavioural Genetics

MAY

1 – 4 May • EMBO Workshop
Chromatin and Epigenetics

2 – 4 May • EMBL Course
Techniques for Studying Iron in Health and Disease

5 – 10 May • EMBL Conference
8th Congress of the International BioIron Society

5 – 10 May • EMBL Course
Quantitative Proteomics: Strategies and Tools to Probe Biology

12 – 18 May • EMBL Course
Single-Cell Omics

13 – 17 May • EMBL Course
Fundamentals of Widefield and Confocal Microscopy and Imaging

13 – 17 May • EMBL Course
Networks and Pathways

13 – 24 May • EMBL Course
Computational Molecular Evolution

15 – 18 May • EMBO | EMBL Symposium
The Identity and Evolution of Cell Types

19 – 24 May • EMBL Course
Advanced Fluorescence Imaging Techniques

28 – 30 May • EMBL Conference
BioMalPar XV: Biology and Pathology of the Malaria Parasite

JUNE

2 – 8 Jun • EMBL Course
Extracellular Vesicles: From Biology to Biomedical Applications

3 – 4 Jun • EMBL Conference
Biological Solutions for the Global CO_2 Challenge

3 – 7 Jun • EMBL Course
Whole Transcriptome Data Analysis

4 – 6 Jun • EMBL Course
Managing a Bioinformatics Core Facility

4 – 6 Jun • EMBL Course
Bioinformatics for Principal Investigators

10 – 14 Jun • EMBL Course
Metagenomics Bioinformatics

12 – 19 Jun • EMBL Course
Microbial Metagenomics: A 360° Approach

17 – 21 Jun • EMBL Course
Cancer Genomics

24 – 28 Jun • EMBL Course
Summer School in Bioinformatics

30 Jun – 5 Jul • EMBL Course
Proteomics Bioinformatics

JULY

1 – 5 Jul • EMBL Course
Shift Your DNA and RNA Sequencing Library Preparation into Hyper–Drive

2 – 4 Jul • EMBL Course
Microinjection in Zebrafish & Medaka: From Transgenesis to CRISPR

3 – 6 Jul • EMBO | EMBL Symposium
Mechanical Forces in Development

7 – 12 Jul • EMBL Course
Super-Resolution Microscopy

7 – 12 Jul • EMBL Course
***In Silico* Systems Biology**

9 – 12 Jul • EMBO | EMBL Symposium
New Approaches and Concepts in Microbiology

15 – 19 Jul • EMBL Course
Bioinformatics Resources for Immunologists

29 Jul – 2 Aug • EMBL Course
Hands-On Flow Cytometry - Learning by Doing!

SEPTEMBER

1 – 6 Sep • EMBL Course
Chromatin Signatures During Differentiation: Integrated Omics Approaches to Neuronal Development

4 – 7 Sep • EMBL Conference
Protein Synthesis and Translational Control

8 – 17 Sep • EMBO Practical Course
Current Methods in Cell Biology

11 – 13 Sep • EMBO | EMBL Symposium
Multiomics to Mechanisms - Challenges in Data Integration

14 – 22 Sep • EMBO Practical Course
Synthetic Biology in Action: Bridging Natural/Non-Natural

16 – 20 Sep • EMBL Course
Structural Bioinformatics

22 – 25 Sep • EMBO Workshop
Creating is Understanding: Synthetic Biology Masters Complexity

23 – 27 Sep • EMBL Course
Introduction to Next Generation Sequencing

23 – 28 Sep • EMBL Course
Liquid Biopsies

29 Sep – 2 Oct • EMBO | EMBL Symposium
Systems Genetics: From Genomes to Complex Traits

30 Sep – 4 Oct • EMBL Course
Whole Transcriptome Data Analysis

OCTOBER

7 – 9 Oct • EMBL Conference (Hamburg)
Tools for Structural Biology of Membrane Proteins

8 – 10 Oct • EMBL Course
Exploring Biological Sequences

9 – 12 Oct • EMBO | EMBL Symposium
Seeing is Believing – Imaging the Molecular Processes of Life

16 – 18 Oct • EMBL Course
Computing Skills For Reproducible Research: Software Carpentry

16 – 19 Oct • EMBO | EMBL Symposium
The Non-Coding Genome

21 – 25 Oct • EMBL Course
Analysis of High-Throughput Sequencing Data

24 – 25 Oct • EMBL Science and Society Conference
Science as Storytelling: From Facts to Fictions

29 – 30 Oct • EMBL Course
Microinjection into Adherent Cells

NOVEMBER

3 – 8 Nov • EMBL Course
Humanized Mice in Biomedical Research: Challenges and Innovations

4 – 7 Nov • EMBL Conference
Cancer Genomics

11 – 15 Nov • EMBO Practical Course
The Fundamentals of High-End Cell Sorting

14 – 16 Nov • EMBL Conference
Precision Health: Molecular Basis, Technology and Digital Health

17 – 22 Nov • EMBL Course
Circular RNAs

20 – 23 Nov • EMBO | EMBL Symposium
Metabolism Meets Epigenetics

28 – 30 Nov • EMBL Conference
21st EMBL PhD Symposium

DECEMBER

1 – 7 Dec • EMBL Course
Measuring Translational Dynamics by Ribosomal Profiling

8 – 10 Dec • EMBL–Wellcome Genome Campus Conference
Target Validation Using Genomics and Informatics

We would like to thank the members of the EMBL ATC Corporate Partnership Programme:

FOUNDER PARTNERS:
Leica Microsystems, Olympus

CORPORATE PARTNERS:
10x Genomics, BD, Boehringer Ingelheim, Eppendorf, GSK, Sartorius, Thermo Fisher Scientific

ASSOCIATE PARTNERS:
Merck, New England Biolabs, Nikon, Promega, Roche, Sanofi

CONFERENCES are held at the EMBL Advanced Training Centre Heidelberg, Germany (unless indicated otherwise)

COURSE LOCATIONS:
Heidelberg | Hinxton

TRAIN ONLINE!

- free online courses and webinars
- created by our tools and resource experts
- learn at your own pace

www.ebi.ac.uk/training/online

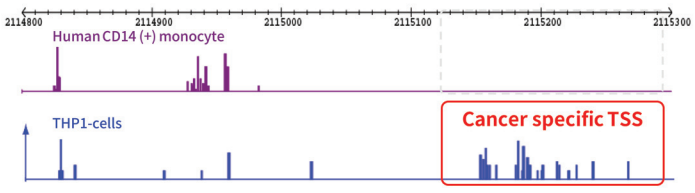
For further details visit our website:
www.embl.org/events
@emblevents

EMBL

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 precise **transcription start site (TSS)** of RNA pol II transcripts including **mRNAs**, **lincRNAs** and **enhancer RNAs** and to quantify their expression accurately.

- **Accurate promoter annotation** — reliable estimation of promoter positions and their activities based on precise TSS information
- **Estimation of transcription factor binding sites** — search transcription factor binding motif 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.

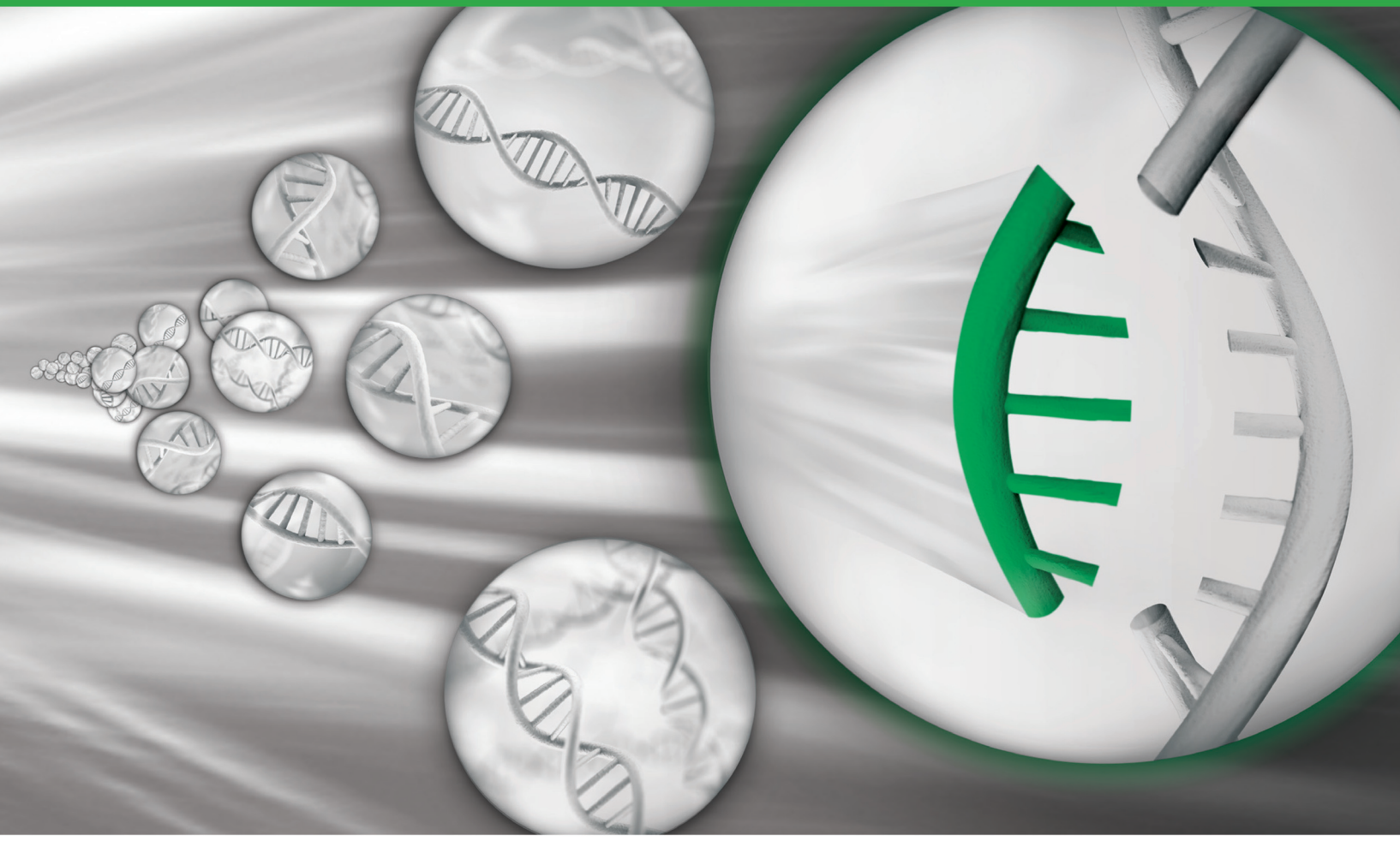
CAGE library preparation & analysis services	
Library preparation for Illumina sequencers	500 USD/sample
Sequencing (Illumina HiSeq/ NextSeq)	250 USD/sample
Bioinformatics analysis	250 USD/sample
CAGE library preparation kit	
8 samples (Cat. 52003-8)	2,000 USD
48 samples (Cat. 52003-48)	10,000 USD

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

DNAFORM
Precision gene technologies
contact@dnaform.jp

GENOME EDIT DETECTION

FAST. SIMPLE. PRECISE.
DROPLET DIGITAL™ PCR



Accelerate genome editing with ddPCR™ Genome Edit Detection Assays.

Droplet Digital PCR (ddPCR) enables rapid quantification of genome editing events. Design and order ddPCR Assays to detect NHEJ and HDR edits, for any target of interest, on Bio-Rad's easy-to-use Digital Assay Site. Use these assays to detect editing events with ultra-high sensitivity using minimal amounts of input DNA or to easily distinguish between homozygous and heterozygous edits in clonal populations.

Find out how Droplet Digital PCR can accelerate your genome editing research at www.bio-rad.com/GenomeEditDetection

BIO-RAD