ZYMO RESEARCH

CELEBRATING 25 YEARS

Reveal a Microbiome's True Nature

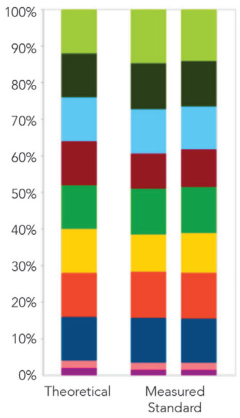
with Mock Microbial Community Standards

The ZymoBIOMICS® Microbial Community Standard

From beautiful lakes to raw sewage, the microbial composition of environmental samples can vary between collection sites and is often unknown.

Standards are needed to ensure unbiased characterization of all microbes in a sample. Zymo Research provides a mock community standard, composed of easy-to-lyse and tough-to-lyse microbes used to assess profiling accuracy of microbiomics workflows.

Well-Defined Microbial Community



Species	Avg. GC (%)	Gram Stain	gDNA Abun. (%)
■ *Pseudomonas aeruinosa*	66.2	-	12
■ *Escherichia coli*	56.8	-	12
■ *Salmonella enterica*	52.2	-	12
■ *Lactobacillus fermentum*	52.8	+	12
■ *Enterococcus faecalis*	37.5	+	12
■ *Syaphylococcus aureus*	32.7	+	12
■ *Listeria monocytogenes*	38.0	+	12
■ *Bacillus subtilis*	43.8	+	12
■ *Saccharomyces cerevisiae*	38.4	Yeast	2
■ *Cryptococcus neoformans*	48.2	Yeast	2

Precise Composition

	ZymoBIOMICS® Microbial Community Standard	Supplier A
Abundance Variation	< 15%	< 1,000%
Foreign Contaminants	< 0.01%	< 10%
Includes both Bacteria and Fungi	✓	✗
Strict manufacturing QC	✓	✗

To learn more, visit

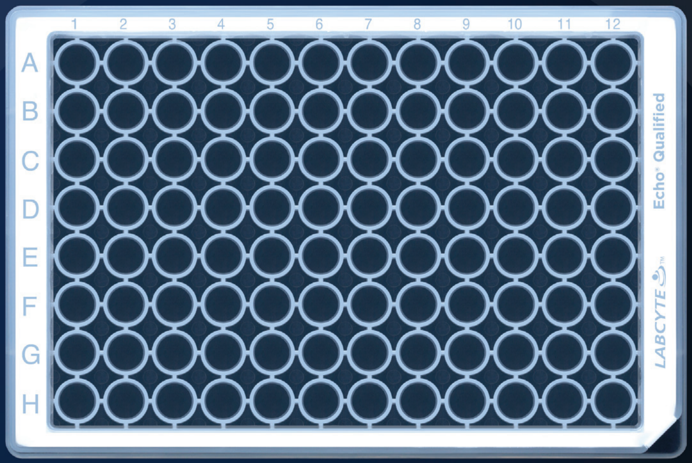
www.zymoresearch.com/pages/microbiome-standards

✉ info@zymoresearch.com

www.zymoresearch.com

☎ Toll Free: (888) 882-9682

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.**

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◎ M-MLV (H-) Reverse Transcriptase US$1.5 per KU for more than 1,000 KU

- H minus Moloney Murine Leukemia Virus (M-MLV) Reverse Transcriptase is a recombinant M-MLV reverse transcriptase. RNase H activity has been eliminated by a point mutation in the RNase H domain of M-MLV RTase,ensuring high yields.
- Deficient RNase H activity to reduce RNA template degradation during the first-strand cDNA synthesis.
- cDNA up to 12 kb.

◎ RNasin (RNase inhibitor) US$10 per KU for more than 100 KU

RNasin is a ribonuclease inhibitor extracted from human placenta with a molecular weight 51 kDa. It inhibits the activity of RNase by specifically binding up to RNase with a non-covalent bond. RNasin, free of RNase or Nickase, can maintain its activity at pH from 5 to 8, and the highest one at pH7.8.

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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.

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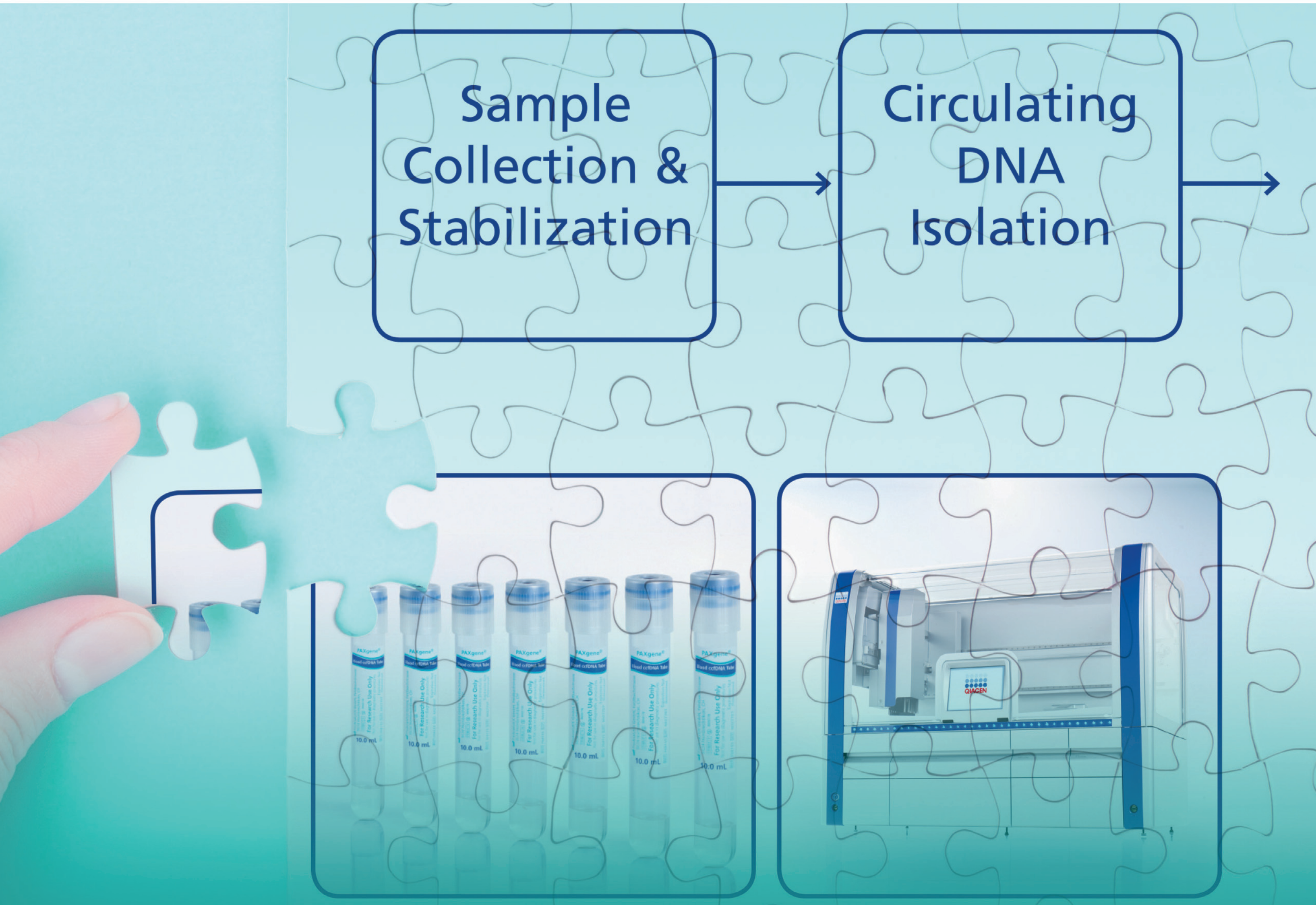
All the pieces are in place

Discover the **PAXgene® Blood ccfDNA System**: a complete, integrated preanalytical workflow solution for circulating cell-free DNA



Sample Collection & Stabilization → Circulating DNA Isolation →

- **Non-crosslinking preservation** of ccfDNA levels
- **Seamless integration** with proven ccfDNA isolation kits
- Streamlined with **primary tube sampling** during automated processing
- Designed for sensitive research assays, including analysis of **circulating tumor DNA** and **non-invasive prenatal testing**

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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

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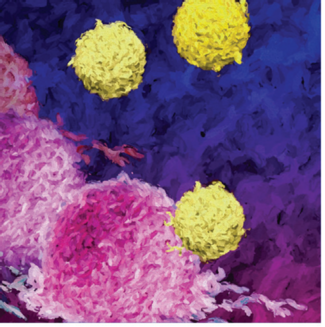

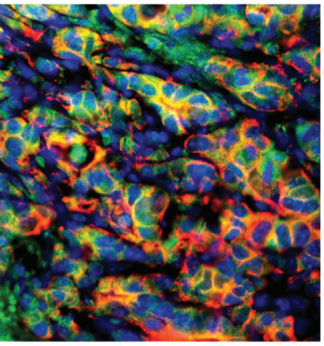

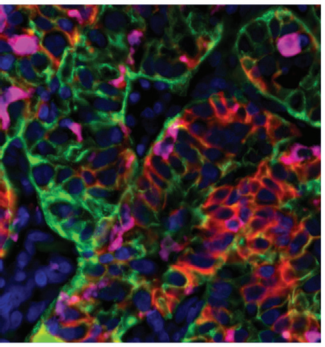

2019
SCIENTIFIC CONFERENCES

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

Immune Cell Therapies for Cancer: Successes and Challenges of CAR T Cells and Other Forms of Adoptive Therapy
Conference Cochairs: Crystal L. Mackall and Patrick Hwu
July 19-22, 2019 | San Francisco, CA

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

Learn more and register at
AACR.org/Calendar

AACR American Association for Cancer Research®
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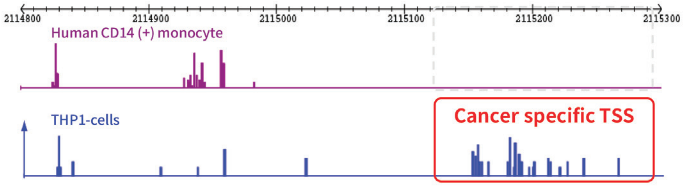
CAGE 5’-RNA sequence service/library preperation kit

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
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