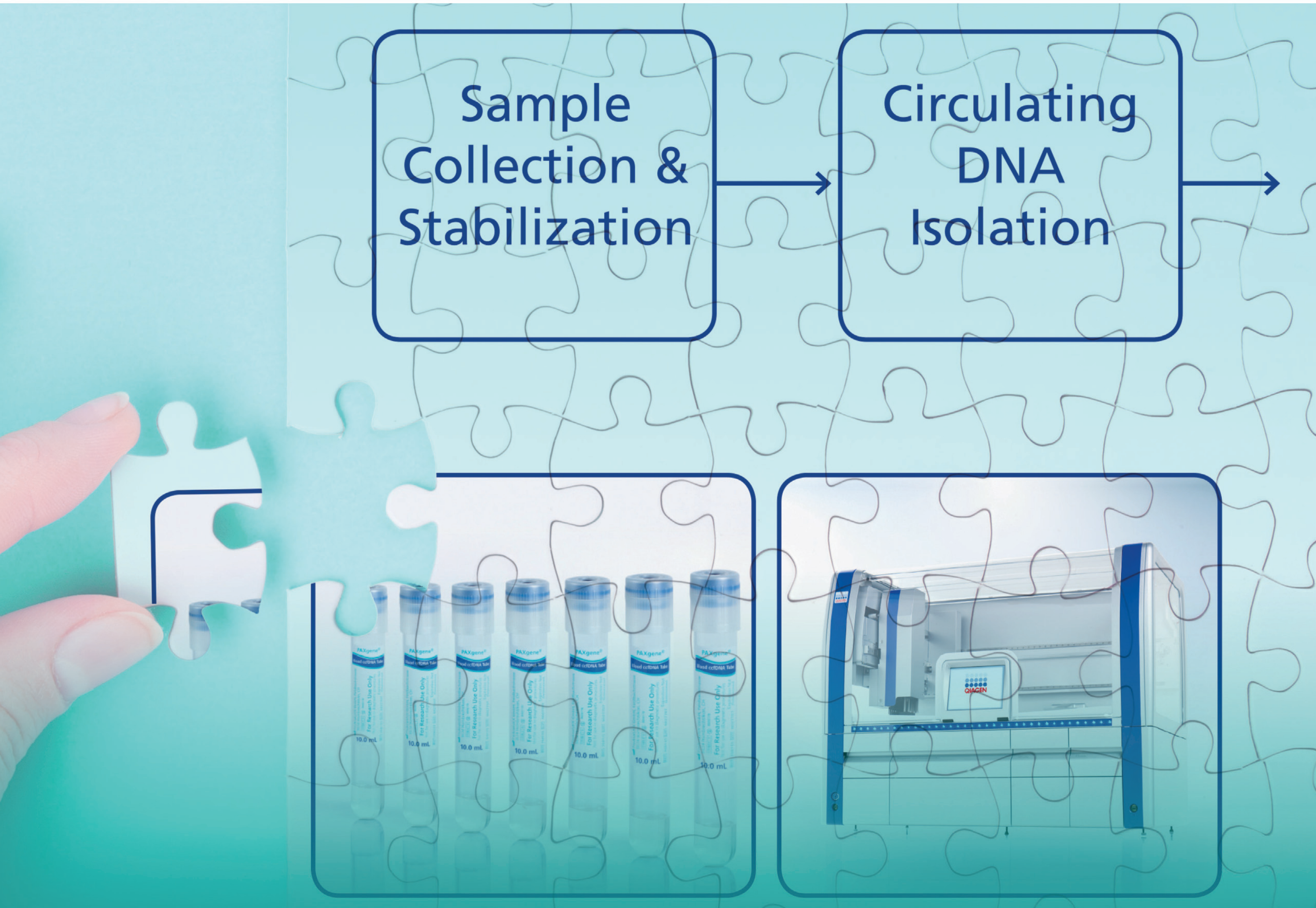
All the pieces are in place

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



- **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**

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

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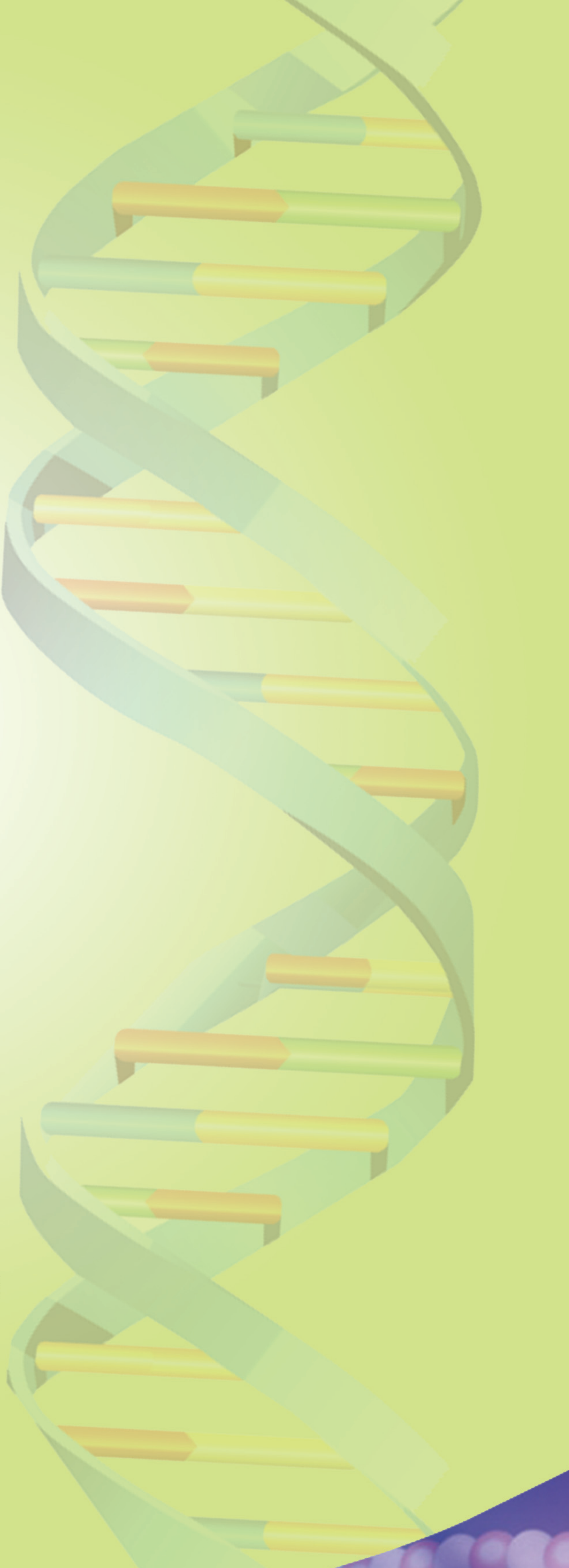

Custom Oligonucleotides

- ◆ Regular oligos
- ◆ Long oligos
- ◆ Phosphorothioated oligos (S-Oligos)
- ◆ Modified oligos
- ◆ Fluorescent oligos
- ◆ Taqman probes
- ◆ Molecular beacon
- ◆ Oligo pool & microarray

Custom Peptide Synthesis

- ◆ Purities from desalt to 98%
- ◆ Acetylation/Amidation
- ◆ Phosphorylatd peptides
- ◆ Fluorescein/Biotin labeled peptides
- ◆ Specialty peptides with unnatural amino acids
- ◆ Cyclic peptides
- ◆ KLH/BSA/OVA Conjugation
- ◆ Multiple Antigenic Peptides
- ◆ Peptide nucleic acid (PNA)

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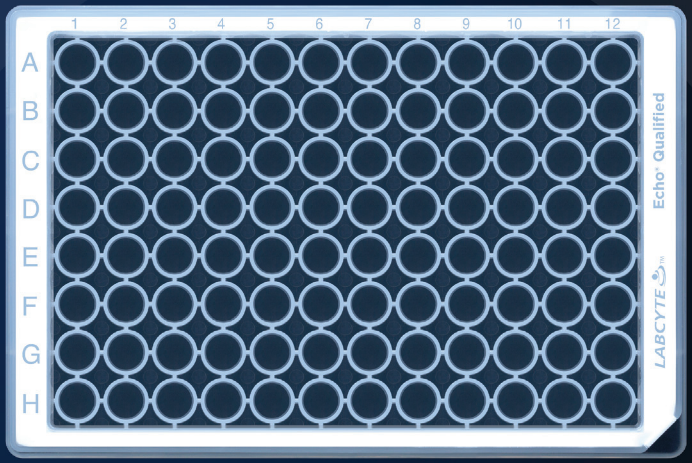
Coming soon...



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**

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CSHL Meetings & Courses

aerial view of CSHL sandspit and inner harbor during meeting social

2019 Meetings

Ubiquitins, Autophagy & Disease April 23 - 27
Telomeres & Telomerase April 30 - May 4
The Biology of Genomes May 7 - 11
Mechanisms of Metabolic Signaling May 14 - 18
Retroviruses May 20 - 25
84th Symposium: RNA Control & Regulation May 29 - June 3
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

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

meetings.cshl.edu

Preview of our early 2020 Meetings

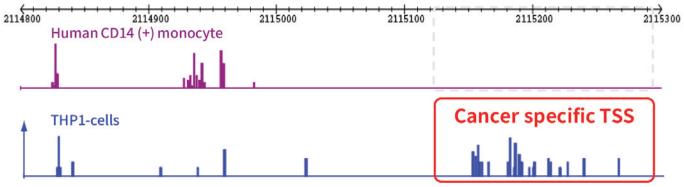
Systems Biology: Global Regulation of Gene Expression March 11 - 14
Neuronal Circuits March 18 - 21
The PARP Family & ADP-ribosylation April 1 - 4
Gene Expression & Signaling in the Immune System April 14 - 18
Protein Homeostasis in Health & Disease April 21 - 25
Genome Organization & Nuclear Function April 28 - May 2
The Biology of Genomes May 5 - 9
Regulatory & Non-Coding RNAs May 12 - 16
Retroviruses May 18 - 23

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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