

Your *Genome Research* Needs

A black silhouette of a hand with the index finger pointing towards a white, rounded rectangular button. The button has the word 'HELP' written on it in a bold, black, sans-serif font.

HELP

SBS Genetech offers a brand of products to support your genome research

- Muta-direct™ Site-Directed Mutagenesis Kit
- Premium™ Master Assembly Mix
- Topo Cloning Kit
- Scarlet™ Blood Direct PCR Kit
- PrimeSNP™ Genotyping Kit
- GClean™ First Strand cDNA Synthesis Kit
- PrimeTaq™ Probe One-Step RT-qPCR Kit
- SuperGold™ High Fidelity PCR EasyMasterMix
- Bst DNA/RNA Polymerase
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Solutions for Genomic and Epigenomic Research

Now Offering GLP and GCP Compliant Laboratory Services



DNA METHYLATION ANALYSIS

Bisulfite Pyrosequencing

Quantify gene-specific and global methylation levels of individual CpG sites at high resolution and accuracy.

Targeted Bisulfite NGS

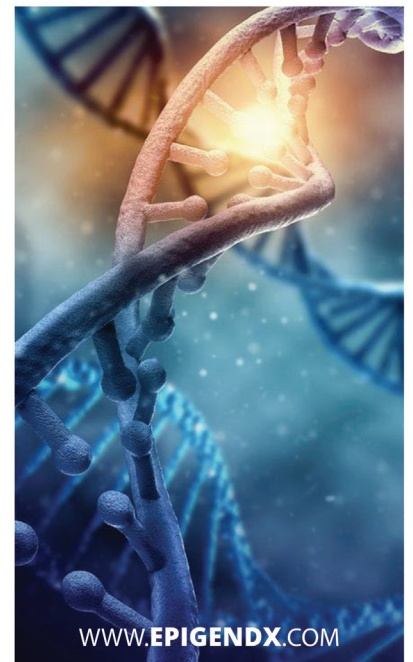
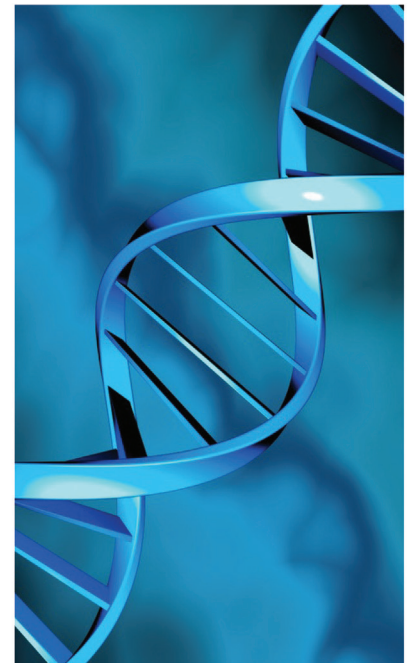
Quantify DNA methylation in multiple targets simultaneously at single basepair resolution.

Custom Assays

Study DNA methylation level at request target genes.

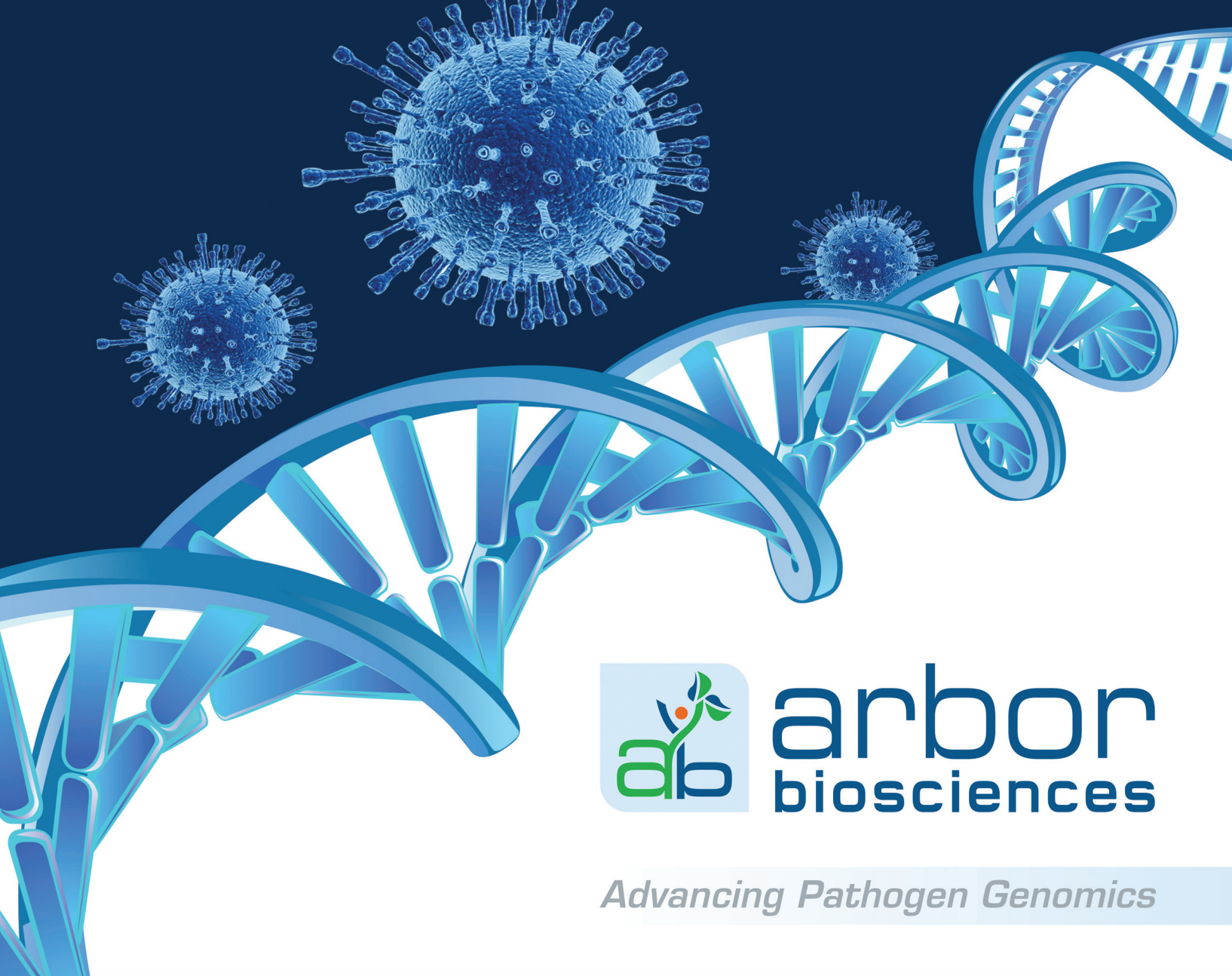
Global DNA Methylation

Genome-wide methylation screening or quantify global methylation level of Line-1 elements.



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arbor
biosciences

Advancing Pathogen Genomics



my Baits®

myBaits® Custom Panels for Pathogen Sequencing

Whole genome enrichment of pathogens from native environments

Generate orders of magnitude enrichment of pathogen DNA or RNA from naturally complex samples, including bacterial, fungal, and viral pathogens, with hybridization-based target capture kits.

- Generate whole genome sequences of bacteria, fungi, and viruses
- Achieve >250-fold enrichment of pathogens from NGS libraries
- Easily detect any type of mutation; SNPs, indels, rearrangements



IONIC™ PURIFICATION SYSTEM

Simple and Reliable Extraction from FFPE Samples

The **Ionic™ Purification System** uses isotachopheresis to extract, purify, and concentrate nucleic acid from biological samples without binding, washing, or stripping from fixed surfaces. Since nucleic acids remain in their native form, not denatured or dehydrated, the Ionic system produces more nucleic acid with higher quality – an ideal solution for low-quality samples or samples with limited starting material.

- **Simplify Lysis**

Deparaffinize, lyse, and de-crosslink in a single reaction without using harsh chemicals

- **Eliminate Bias**

Extract targeted nucleic acid regardless of fragment length or GC content

- **Minimize User Involvement**

Extract and purify 8 samples in one hour with just 3 minutes of hands-on time per sample

- **Improve Reliability**

Minimize user-to-user variability, cross-contamination, and sample loss



For more information, contact info@purigenbio.com.

NUCLEIC ACID PURIFICATION
PURE AND SIMPLE™

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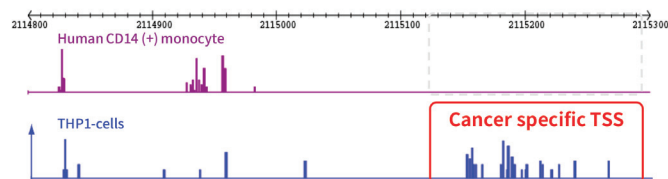
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Promoter / Enhancer Annotation in the NGS era

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 positions 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

Collect. Spin. Load.

Primary tube handling in automated direct sample processing on the QIAasymphony 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



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