

PrimeTaq™ Probe One-Step RT-qPCR Kit

Enables reliable detection and measurement

PrimeTaq™ Probe One-Step RT-qPCR Kit provides rapid real-time quantification of RNA targets. The kit contains optimized components that allow both reverse transcription and PCR amplification to take place. With this kit, all steps can be performed in a single tube. PrimeTaq™ Probe One-Step RT-qPCR Kit is intended for molecular biology applications.

Easy-to-use



Features

- **High specificity and sensitivity:**

Specificity is not only dependent on PCR primers, but also specific binding and degradation of probes and target genes to generate fluorescent signals. The detection sensitivity and specificity are usually significantly higher than those of the methods using fluorescent dyes such as SYBR Green.

- **Multiple detection:**

In a single reaction, different genes correspond to different probes and different probes correspond to different fluorescent markers, which can be used for multiple fluorescent quantitative PCR detection. PrimeTaq™ Probe One-Step RT-qPCR Kit can be used for the detection of 2-3 genes at the same time after optimization of primers and probes.

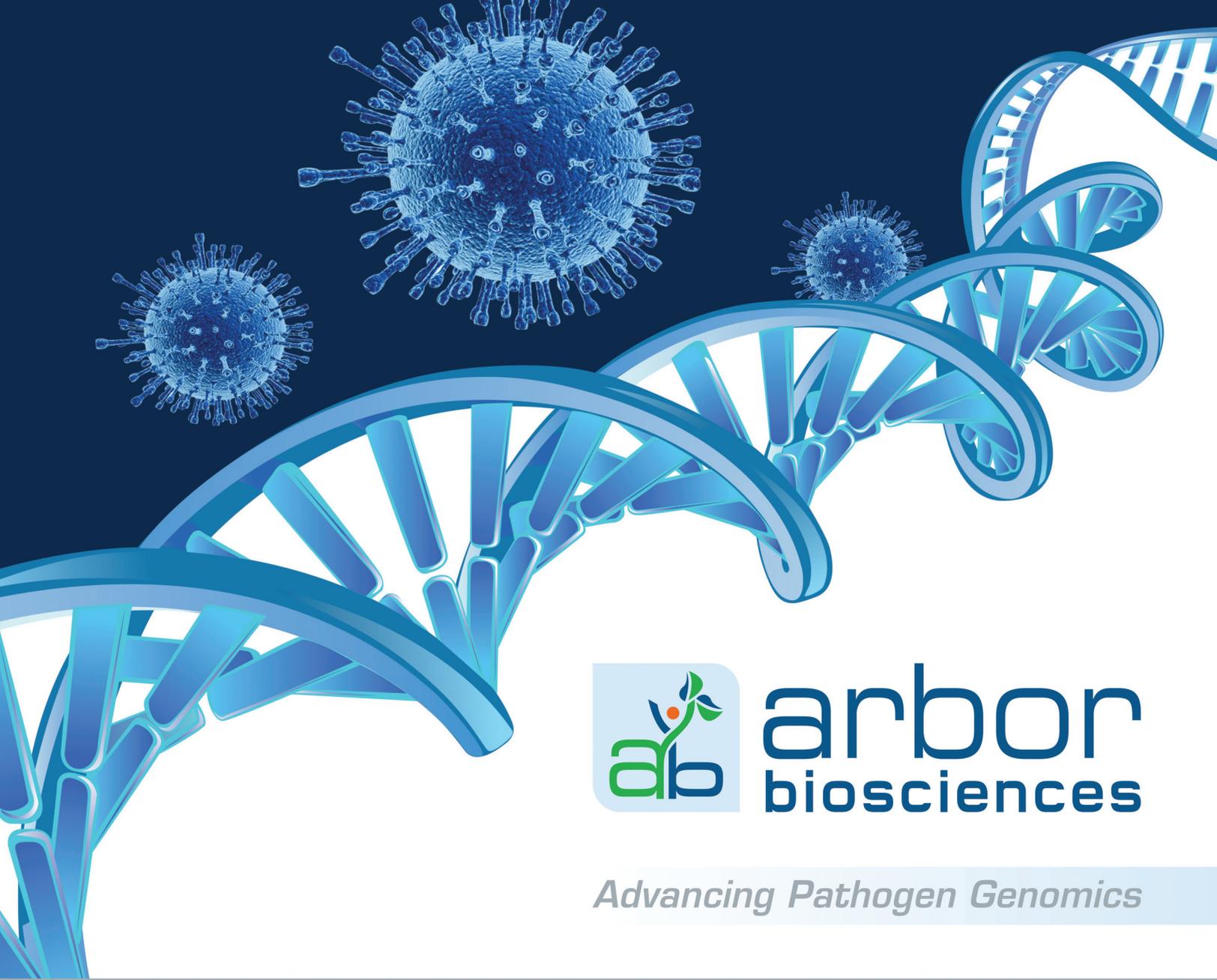
It's easier. It's faster. And it's more efficient.

PrimeTaq™ Probe One-Step RT-qPCR Kit gives you a totally new experience for RT-qPCR. You can have reliable detection and measurement of products generated during each cycle of PCR process.

Ready for this new experience?

Please visit <https://www.sbsgenetech.com/products>

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Advancing Pathogen Genomics



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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

A novel solution for Genome-wide Enhancer / Promoter Annotation

NET-CAGE is a new NGS library preparation method using “cap-trapping” technology which enables you to detect **transcription start site** and **instantaneous transcriptional activity** of RNA pol II transcripts including **short-lived transcripts** such as **eRNAs** and **uaRNAs**.

- **Genome-wide High-resolution detection of active enhancers**—identify precise position of active enhancers by detection of bidirectional enhancer RNAs (eRNAs).
- **Detection of instantaneous gene expression**—detect accurate transcriptional activity at a given moment by quantifying nascent RNA pol II transcripts.
- **Accurate quantification of gene expression**—PCR-free library preparation process without fragmentation allows for more reliable quantification of gene expression than RNA-seq.
- **Applicable for cryopreserved cells and tissue samples**—The protocol does not contain any incorporation process for labeling.

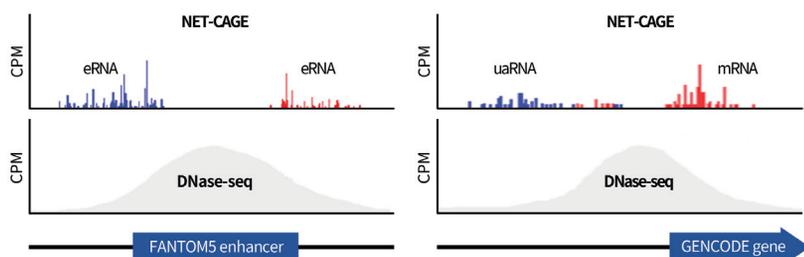


Fig.1. NET-CAGE signals around a region of FANTOM5 enhancer (left) and GENCODE gene (right).

NET-CAGE library preparation /analysis services	
NET-RNA extraction	100 USD/sample
CAGE library preparation for Illumina sequencers	500 USD/sample
Sequencing (Illumina HiSeq/ NextSeq)	250 USD/sample
CAGE bioinformatics analysis	250 USD/sample

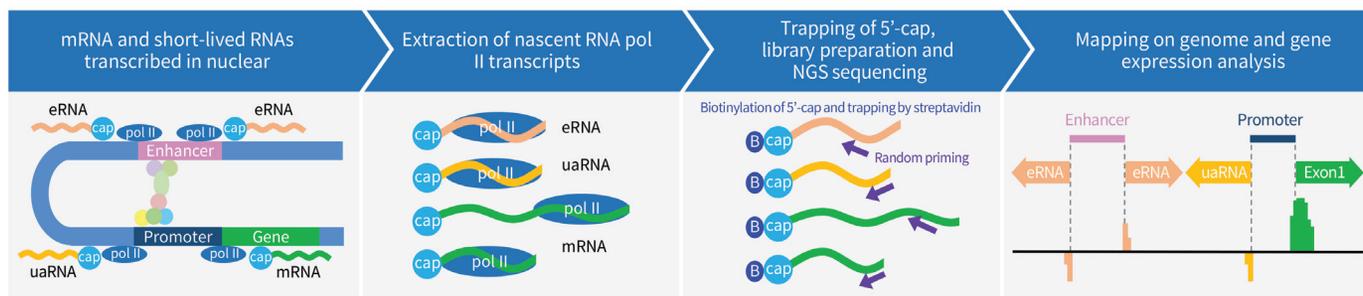


Fig.2. Workflow of the NET-CAGE. NET-CAGE is a unique NGS library preparation method using “cap-trapping” technology.



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DNA METHYLATION ANALYSIS

Bisulfite Pyrosequencing

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

Targeted Bisulfite NGS

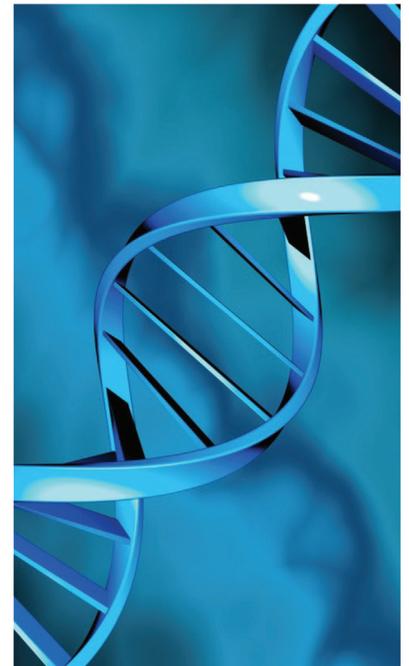
Quantify DNA methylation in multiple targets simultaneously at single basepair resolution.

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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