Bst DNA/RNA Polymerase

For Isothermal Amplification

Bst DNA/RNA Polymerase is a mixture of Bst DNA polymerase and extremely thermostable reverse transcriptase (65℃ tolerant), which is suitable for isothermal amplification reaction of RNA. It can detect low-sensitivity RNA molecules. This enzyme is recommended in isothermal amplification experiments using RNA as a template. In addition, Bst DNA/RNA Polymerase can also perform isothermal amplification of DNA templates.

Quality Assurance

QC Items	Specifications	Results
Concentration	8 KU/ml	☑ Pass
RNase contamination	No degradation under 16 U for 2 μg total RNA at 25°C for 30 min	☑ Pass
DNase contamination	No degradation under 16 U for 2 μg gDNA at 37°C for 60 min	☑ Pass
Inactive	Complete inactive at 85°C for 5 min	☑ Pass

Storage

Store at -20℃ for three years. Avoid multiple freeze-thaw cycles.

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

Our Bst DNA/RNA Polymerase is ideal for:

- DNA/RNA isothermal amplification
- GC-rich rapid sequencing
- Rapid sequencing of micro-template DNA

Ready for this new experience?

Please visit https://www.sbsgenetech.com/store/products/412377

SBS Genetech Co., Ltd.

SBS Genetech is a long-term sponsor of
Cold Spring Harbor Laboratory

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Microbiomics Services

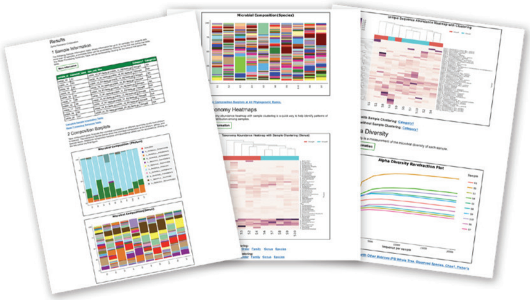
Celebrate Your Discoveries

A Complete Microbiomics Solution

Get data worth celebrating! Zymo Research is proud to offer unbiased microbiome profiling services, from DNA extraction to sequencing and bioinformatics analysis. ZymoBIOMICS® microbiomics services achieve species-level resolution with 16S sequencing and strain-level resolution with shotgun sequencing. All services include publication-ready data.

End-to-End Microbiomics Services, Including Bioinformatics Analysis.

Microbiome Standards → Sample Collection → DNA/RNA Extraction → Library Preparation → NGS Analysis



Comprehensive and User-Friendly Report Includes:

- Composition Bar Plots
- Taxonomy Heatmaps
- Alpha-Diversity
- Beta-Diversity
- Absolute Abundance for 16S/ITS
- Biomarker Discovery (LEfSe)

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for a custom microbiomics services quote.

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NET-CAGE : Native Elongating Transcript Cap Analysis of Gene Expression

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.

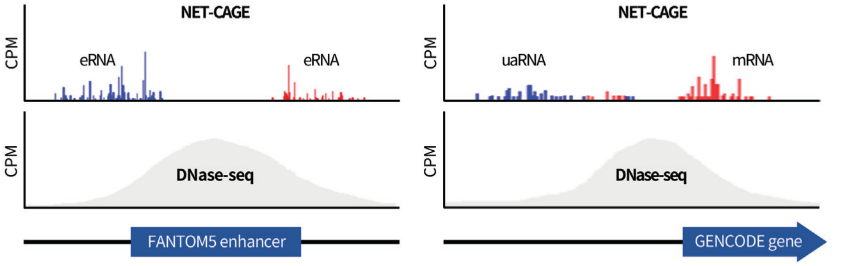


Fig.1. NET-CAGE signals around a region of FANTOM5 enhancer (left) and GENCODE gene (right).

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

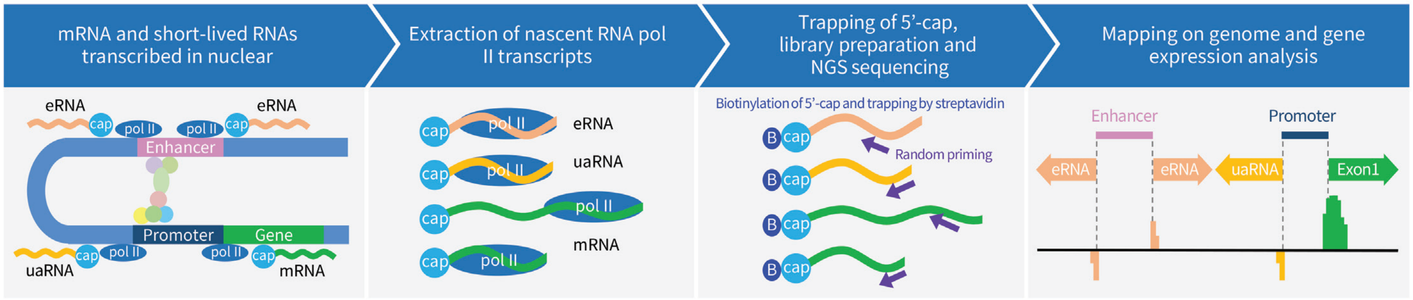
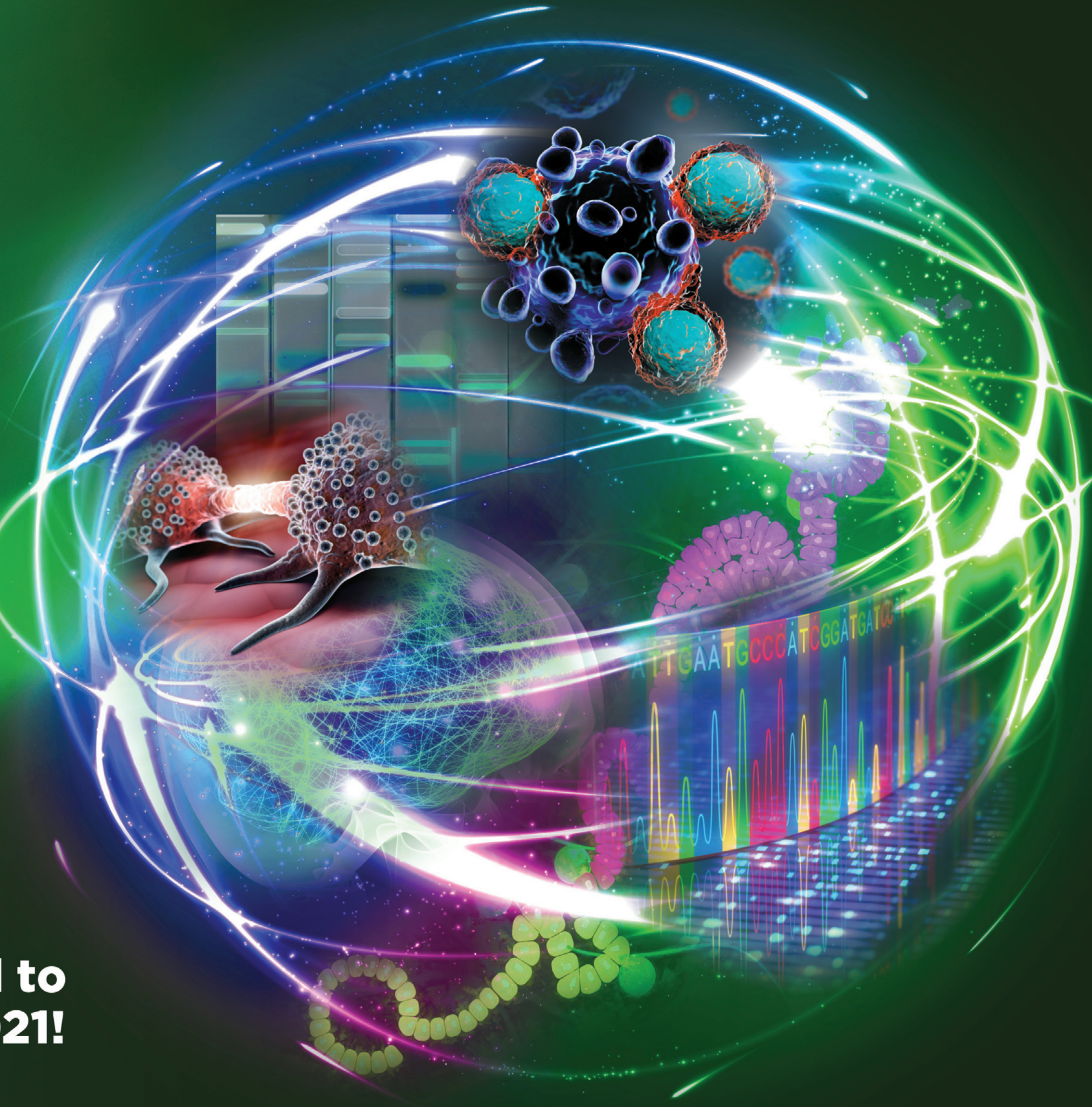


Fig.2. Workflow of the NET-CAGE. NET-CAGE is a unique NGS library preparation method using "cap-trapping" technology.

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

DNAFORM
Precision gene technologies
contact@dnaform.jp



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IONIC®
PURIFICATION SYSTEM

Get 3.5x More DNA and 2x More RNA from FFPE Samples

Automated Nucleic Acid Purification – Pure and Simple

The **IONIC® Purification System** uses isotachophoresis 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.

- **Simple Workflow**
  Extract and purify 8 samples at a time with less than 5 minutes of hands-on time per sample
- **Purify *both* mRNA and miRNA**
  Co-purify both mRNA and miRNA with higher yields than column-based kits
- **Simplify Lysis**
  De-paraffinize, lyse, and de-crosslink in a single reaction without using harsh chemicals
- **Improve Reliability**
  Minimize user-to-user variability, cross-contamination, and sample loss

For more information, contact **info@purigenbio.com**.

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PURE AND SIMPLE™

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BIOSYSTEMS