

Bst DNA/RNA Polymerase

For Isothermal Amplification

Bst DNA/RNA Polymerase is a mixture of Bst DNA polymerase and extremely thermostable reverse transcriptase (65°C 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 | <input checked="" type="checkbox"/> Pass |
| RNase contamination | No degradation under 16U for 2 µg total RNA at 25°C for 30 min | <input checked="" type="checkbox"/> Pass |
| DNase contamination | No degradation under 16 U for 2 µg gDNA at 37°C for 60 min | <input checked="" type="checkbox"/> Pass |
| Inactive | Complete inactive at 85°C for 5 min | <input checked="" type="checkbox"/> Pass |

Storage

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

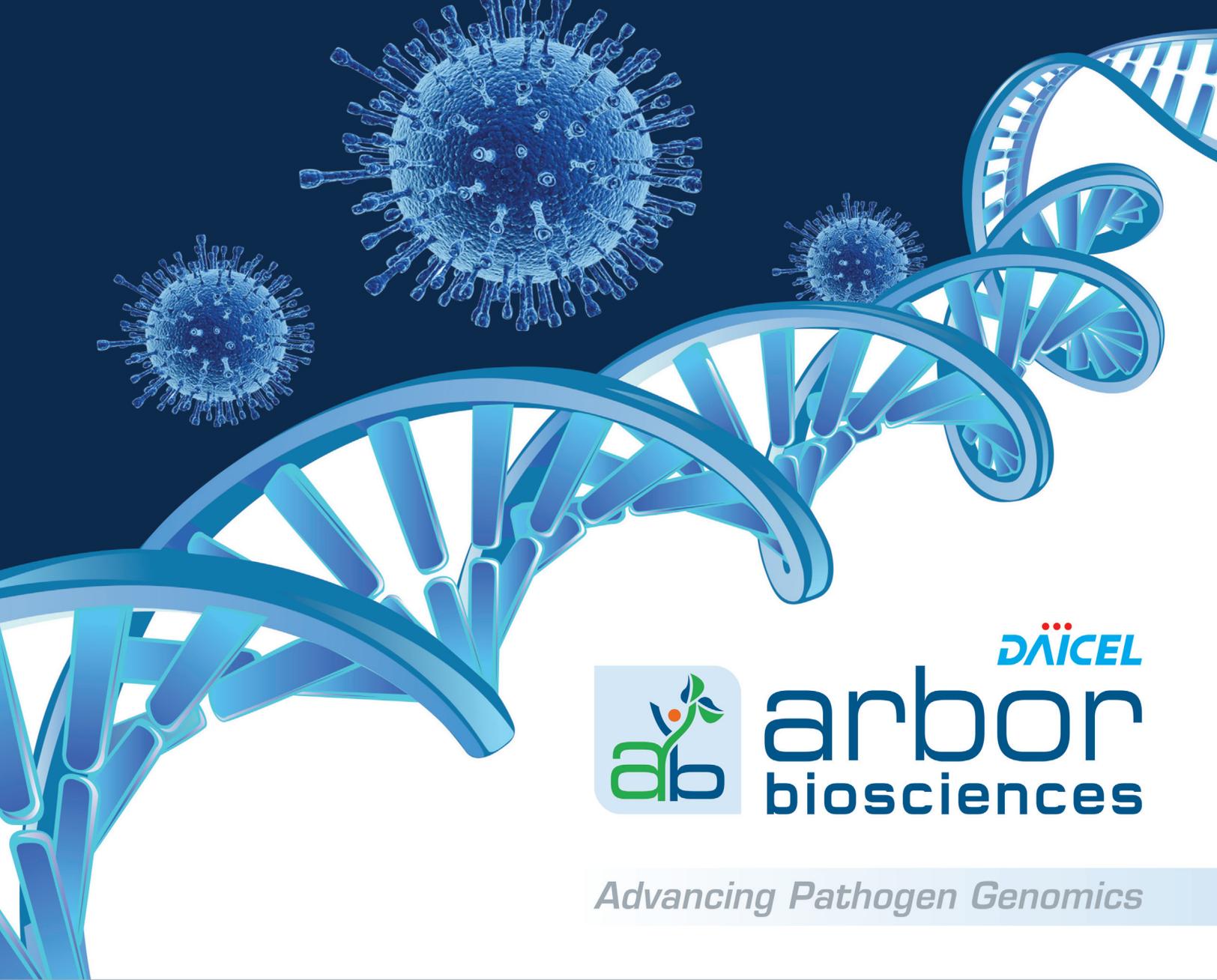
It's easier. It's faster. And it's more efficient.

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>



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

Microbiomics Services

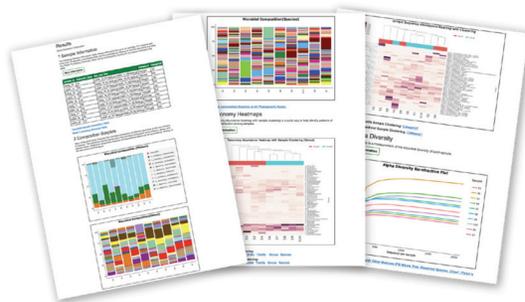
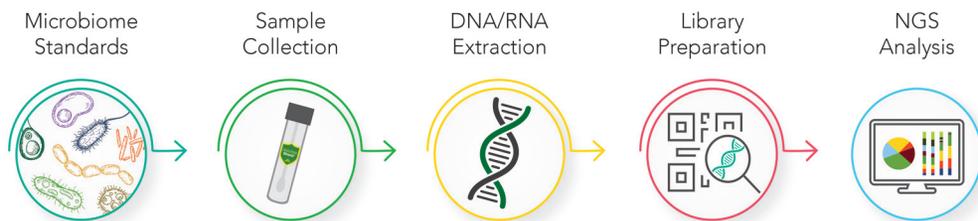
Celebrate Your Discoveries



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.

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- Taxonomy Heatmaps
- Alpha-Diversity
- Beta-Diversity
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- Biomarker Discovery (LEfSe)

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Collect. Spin. Load.

Primary tube handling in automated direct sample processing on the QIASymphony SP for ccfDNA purification



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- ❖ Eliminate manual plasma transfer
- ❖ Lower risk of sample mixup
- ❖ Minimize risk of blood exposure
- ❖ Save time, cut costs, reduce waste



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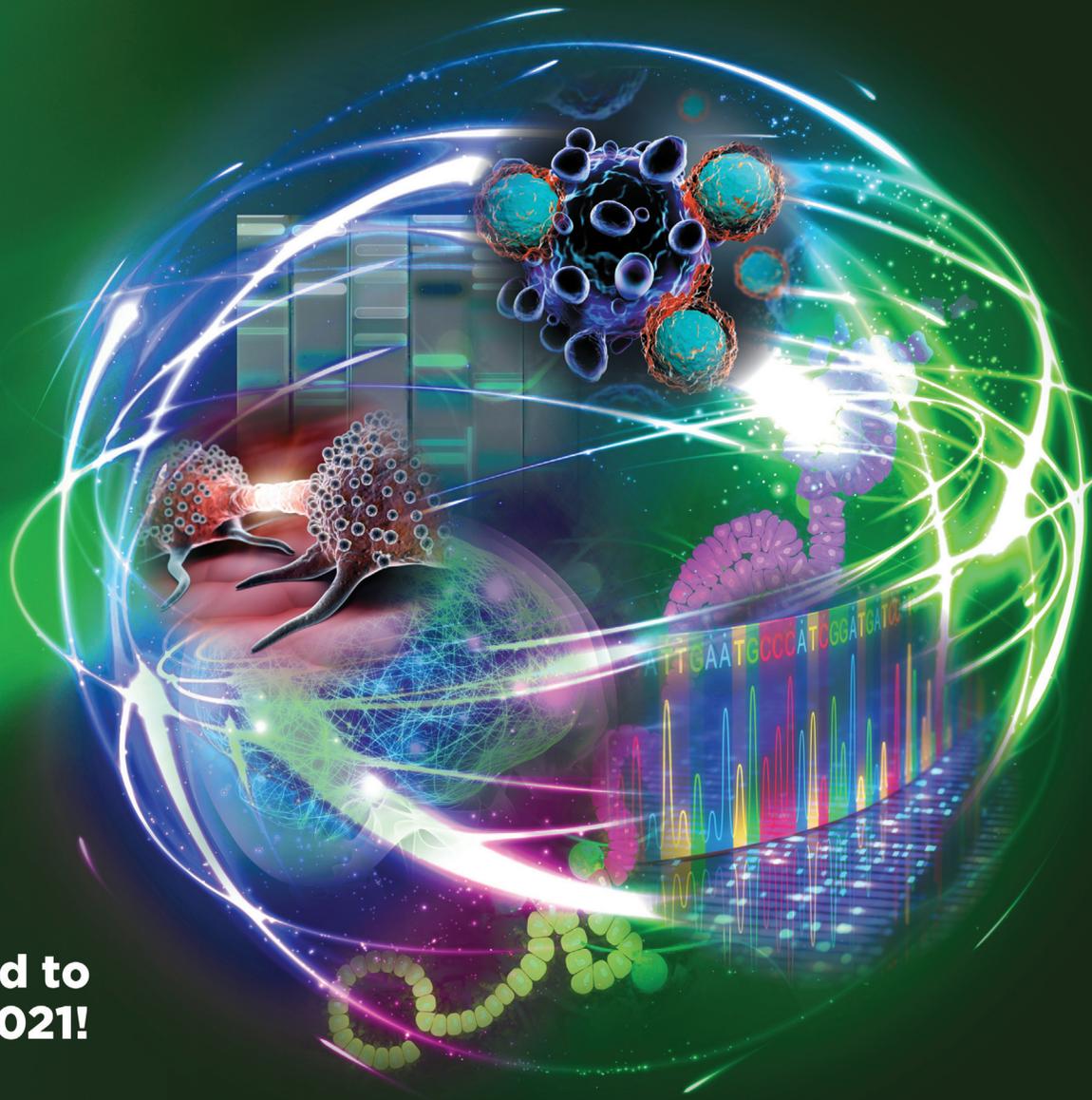
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2021

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Submission Deadline: Monday, January 11, 2021

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**VISIT [AACR.ORG/AACR2021](https://aacr.org/aacr2021) FOR MORE
INFORMATION AND TO SUBMIT AN ABSTRACT!**

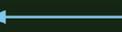
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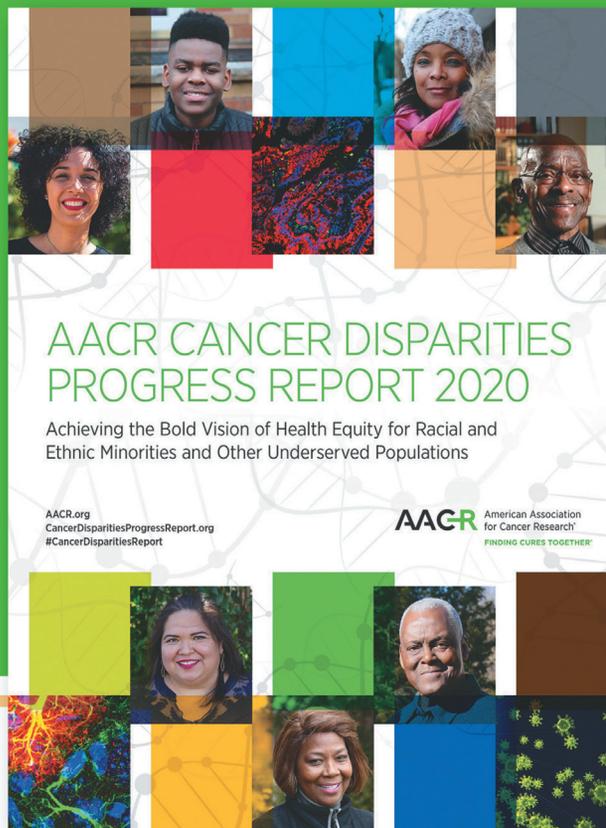


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AACR CANCER DISPARITIES PROGRESS REPORT 2020

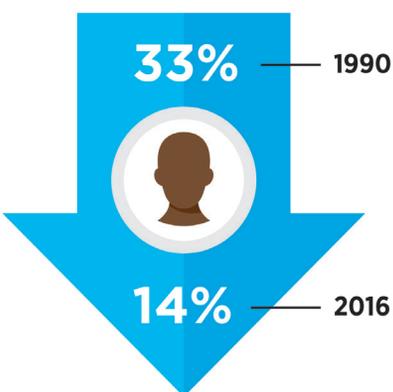
Achieving the Bold Vision of Health Equity for Racial and Ethnic Minorities and Other Underserved Populations



The American Association for Cancer Research is proud to announce the release of the inaugural *AACR Cancer Disparities Progress Report 2020*.

This report highlights the current disparities in the burden of cancer within the United States and the research that aims to mitigate these challenges. Some of the recent advances you will learn about include:

Decline in Disparity for Overall Cancer Death Rate between African Americans and Whites



The National Cancer Institute recently revised its eligibility criteria for cancer clinical trials to expand access for previously excluded patients.

Get your FREE copy of the full report by visiting

[CancerDisparitiesProgressReport.org](https://www.aacr.org/cancer-disparities-progress-report-2020)



so that you can learn about the many ways in which research is transforming lives.

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.

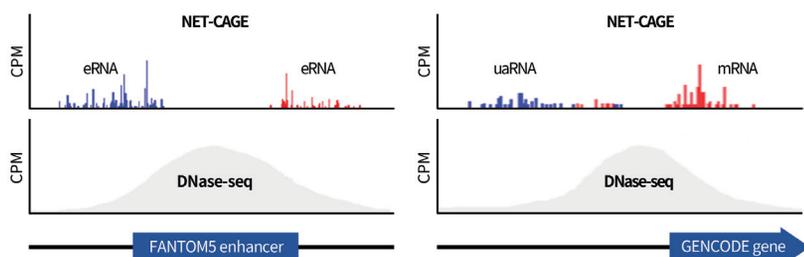


Fig.1. NET-CAGE signals around a region of FANTOM5 enhancer (left) and GENCODE gene (right).

| 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 |

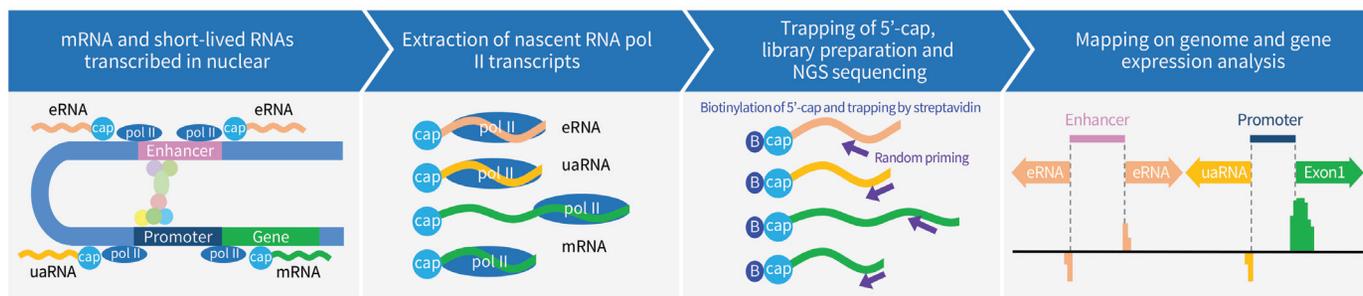


Fig.2. Workflow of the NET-CAGE. NET-CAGE is a unique NGS library preparation method using “cap-trapping” technology.



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

Automated Nucleic Acid Purification – Pure and Simple

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.

- **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.



NUCLEIC ACID PURIFICATION
PURE AND SIMPLE™

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