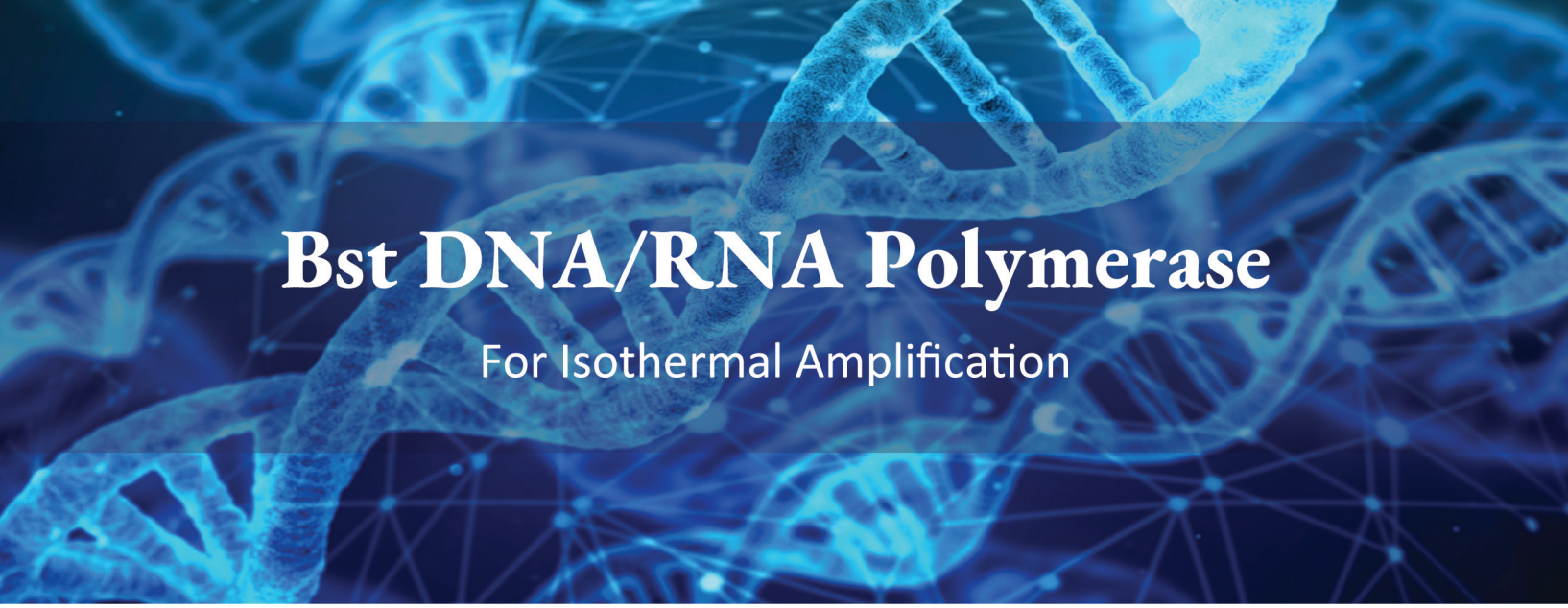


Bst DNA/RNA Polymerase

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.

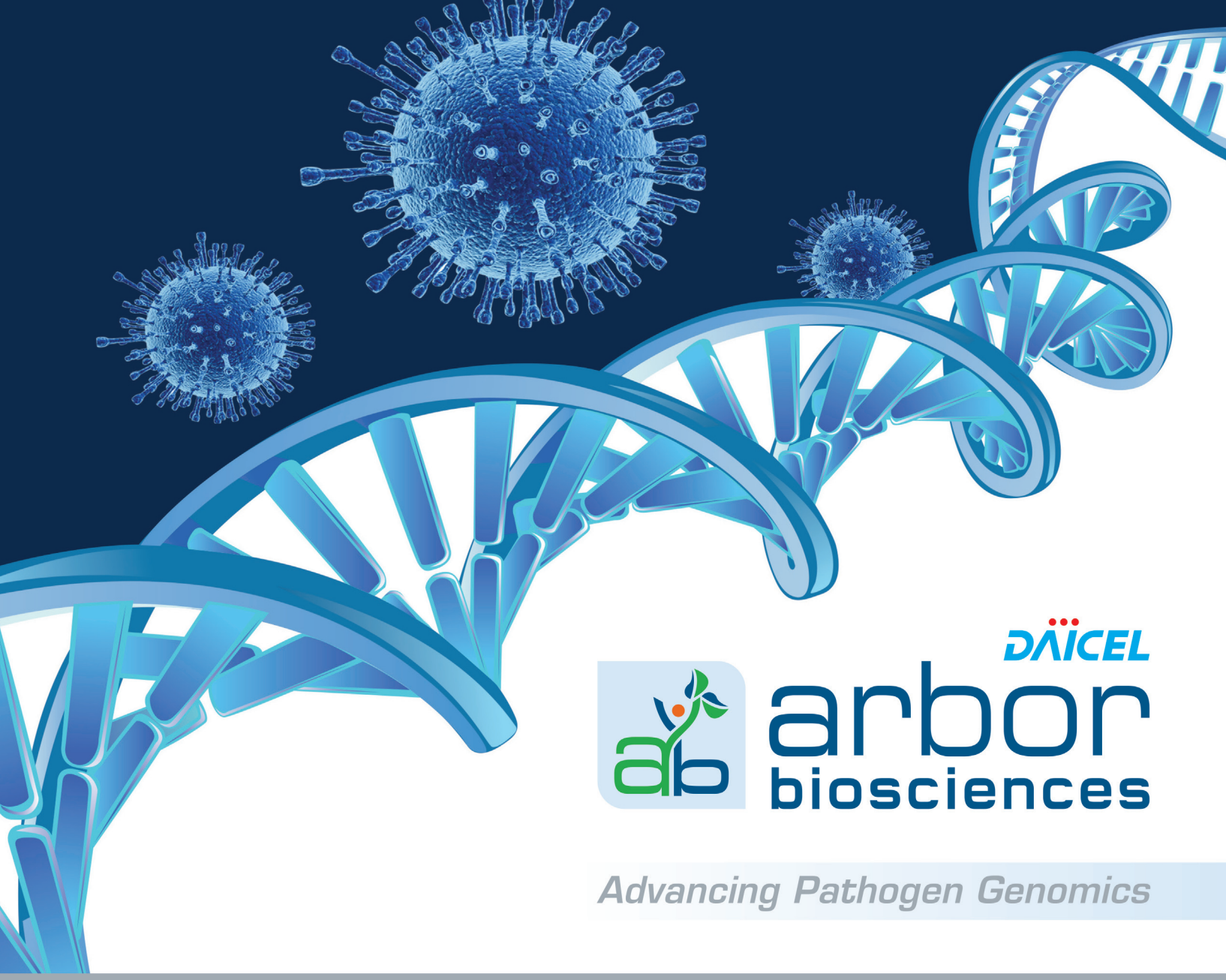
It's easier. It's faster. And it's more efficient.

Our Bst DNA/RNA Polymerase is ideal for:

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

sbs 赛百盛
SBS Genetech Co., Ltd.

Ready for this new experience?
Please visit https://www.sbsgenetech.com/store/products/412377



DAICEL

arbor biosciences

Advancing Pathogen Genomics

myBaits®

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

ArborBiosci.com | info@arborbiosci.com | +1 734-998-0751 | *Follow us on Twitter:* @ArborBio

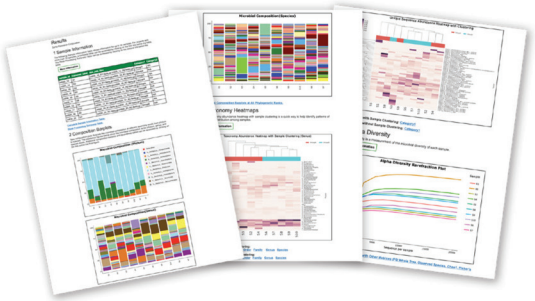
Microbiomics Services

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.



Comprehensive and User-Friendly Report Includes:

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

Visit **www.zymoresearch.com/pages/zymobiomic-services**
for a custom microbiomics services quote.

ZYMO RESEARCH

www.zymoresearch.com | info@zymoresearch.com | Toll Free: (888) 882-9682

Collect. Spin. Load.

Primary tube handling in automated direct sample processing on the QIAsymphony 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

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

PreAnalytiX
A QIAGEN / BD Company

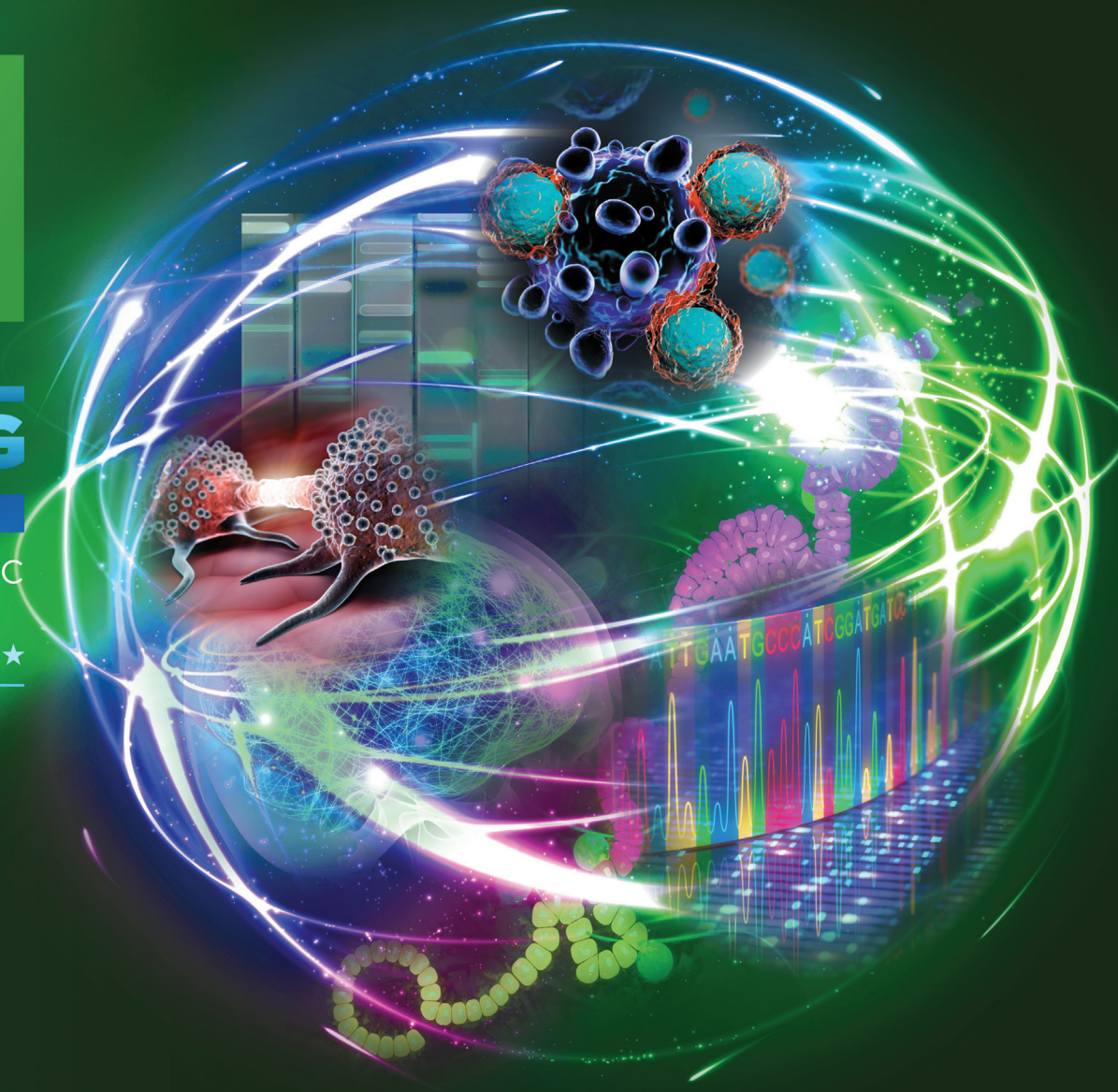
AACR
American Association for Cancer Research®

ANNUAL MEETING

APRIL 9-14, 2021

WASHINGTON ★ DC
#AACR21

★ ★ ★ ★ ★ ★ ★



Submit your scientific findings to the world's most comprehensive annual meeting dedicated to the research, prevention, detection, and treatment of cancer.

★ **Abstract Submission Deadline:** Thursday, November 19, 2020

★ **Late-Breaking and Clinical Trials Abstract Submission Deadline:** Monday, January 11, 2021

★ **Become a Member!**
Join the AACR and receive a discount on registration.

VISIT AACR.ORG/AACR2021 FOR MORE INFORMATION AND TO SUBMIT AN ABSTRACT!

We look forward to seeing you!

ABIM CME MOC ACCREDITED

Continuing Medical Education Activity - *AMA PRA Category 1 Credits™* available

DISCOVERY SCIENCE *DRIVING* CLINICAL BREAKTHROUGHS

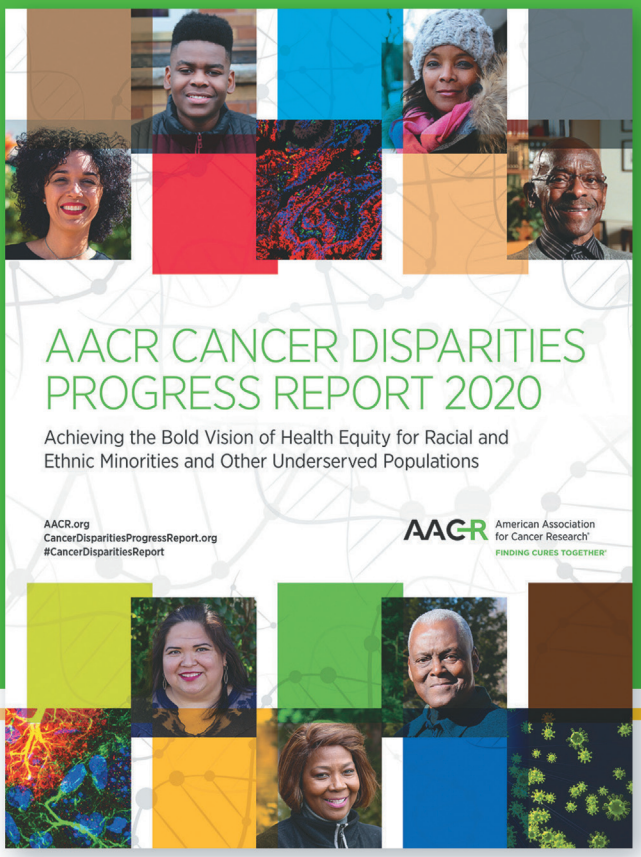
AACR.ORG ★ #AACR21

AACR.ORG/AACR2021

2001015Aa

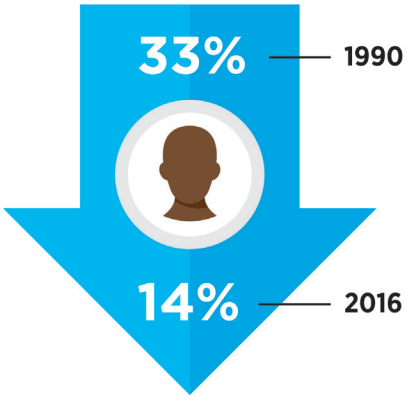
AACR CANCER DISPARITIES PROGRESS REPORT 2020

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

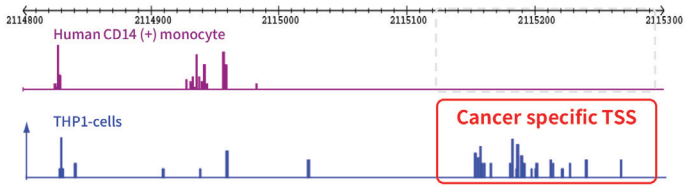
CancerDisparitiesProgressReport.org

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

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
48 samples (Cat. 52003-48)	10,000 USD

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

DNAFORM
Precision gene technologies
contact@dnaform.jp

www.purigenbio.com/**ffpe**

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**.

NUCLEIC ACID PURIFICATION
PURE AND SIMPLE™

PURIGEN™ BIOSYSTEMS

FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.