www.purigenbio.com

IONIC™ PURIFICATION SYSTEM

Finally, get what you need from your FFPE samples

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 is ideal for challenging samples with limited starting material or low-quality material.

Simplified FFPE Workflow

< 3 minutes of hands-on time per sample

FFPE SAMPLE

No need to de-paraffinize

1 **LYSE**

Simplified lysis procedure uses a programmable thermomixer to process up to 24 samples in a single run. No separate steps are required to de-paraffinize or de-crosslink samples.

2 **PURIFY**

Using the Ionic Purification System

3 **COLLECT**

Pure and native nucleic acid

Higher yield, higher quality, and better data

NUCLEIC ACID PURIFICATION
PURE AND SIMPLE™

PURIGEN™ BIOSYSTEMS

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

info@purigenbio.com | www.purigenbio.com/info

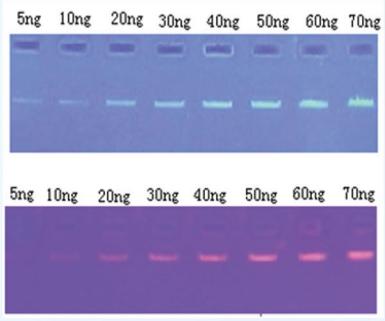
SBS Genetech Co., Ltd.

GoodView™ Nucleic Acid Stain

——An alternative to EB

GoodView™ is a safer nucleic acid stain, an alternative to the traditional ethidium bromide (EB) stain for detecting nucleic acid in agarose gels. It emits green fluorescence when bound to DNA or RNA. This new stain has two fluorescence excitation maxima when bound to nucleic acid, one centered at 268 nm and another at 294 nm. In addition, it has one visible excitation at 491 nm. The Fluorescence emission of GoodView™ bound to DNA is centered at 530 nm.

Comparative sensitivity test of GV and EB



Sensitivity test result of GV at UV 300nm.

Sensitivity test result of EB at UV 300nm.

The result of electrophoresis demonstrates GV is almost as sensitive as EB.

The Test Report from Institute for Environmental Health and Related Product Safety of Chinese Center for Disease Control and Prevention concludes that:

- Acute Oral Toxicity Test: GoodView™ Nucleic Acid Stain belongs to nontoxic.
- Mouse Marrow Chromophilous Erythrocyte Micronucleus Test: Negative. There is no significant difference in the incidence of micronuclei between test and control groups.
- Ames Test: Negative. No mutagenicity was observed.
- In Vitro Mammalian Cell Chromosome Aberration Test: Negative. No increasing aberration rate was observed.

GoodView Nucleic Acid Stain is included on New Products, Science Magazine, January 11, 2019.
Please visit: http://science.sciencemag.org/content/363/6423/193

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Phone: +86-10-82784296 Fax: +86-10-82784290
Email: order@sbsbio.com Website: www.sbsbio.com

bionano GENOMICS

DISCOVER NEXT

REVEAL STRUCTRUAL VARIATION LIKE NEVER BEFORE WITH BIONANO GENOME IMAGING

The Saphyr System images and analyzes ultra-long, linearized DNA molecules labeled at specific sequence motifs for ultra-sensitive, ultra-specific structural variant detection.

Unparalleled Structural Variation Detection
Genome-wide detection of SVs >500 bp to chromosome-arm length at up to 99% sensitivity and <2% false positive rate

Powerful Complement to Sequencing
Discover novel disease-associated SVs missed by NGS and long-read sequencers with sensitivities down to 1% allele frequency

Confident Answers
High concordance to SVs reported by FISH, karyotyping and chromosomal microarrays

Comprehensive Workflow
Robust and streamlined assay, automated for a short turnaround time as little as 4 days

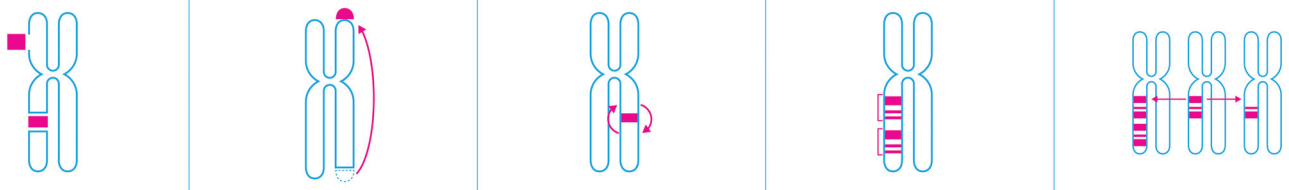
VISIT US AT AACR BOOTH #637

Attend our workshop at AACR to see how Genome imaging is a new breakthrough genomics tool for evaluating the molecular basis of cancer and for studying ecDNA

MONDAY, APRIL 27 | 10:00AM – 11:00 AM

SPOTLIGHT THEATER C

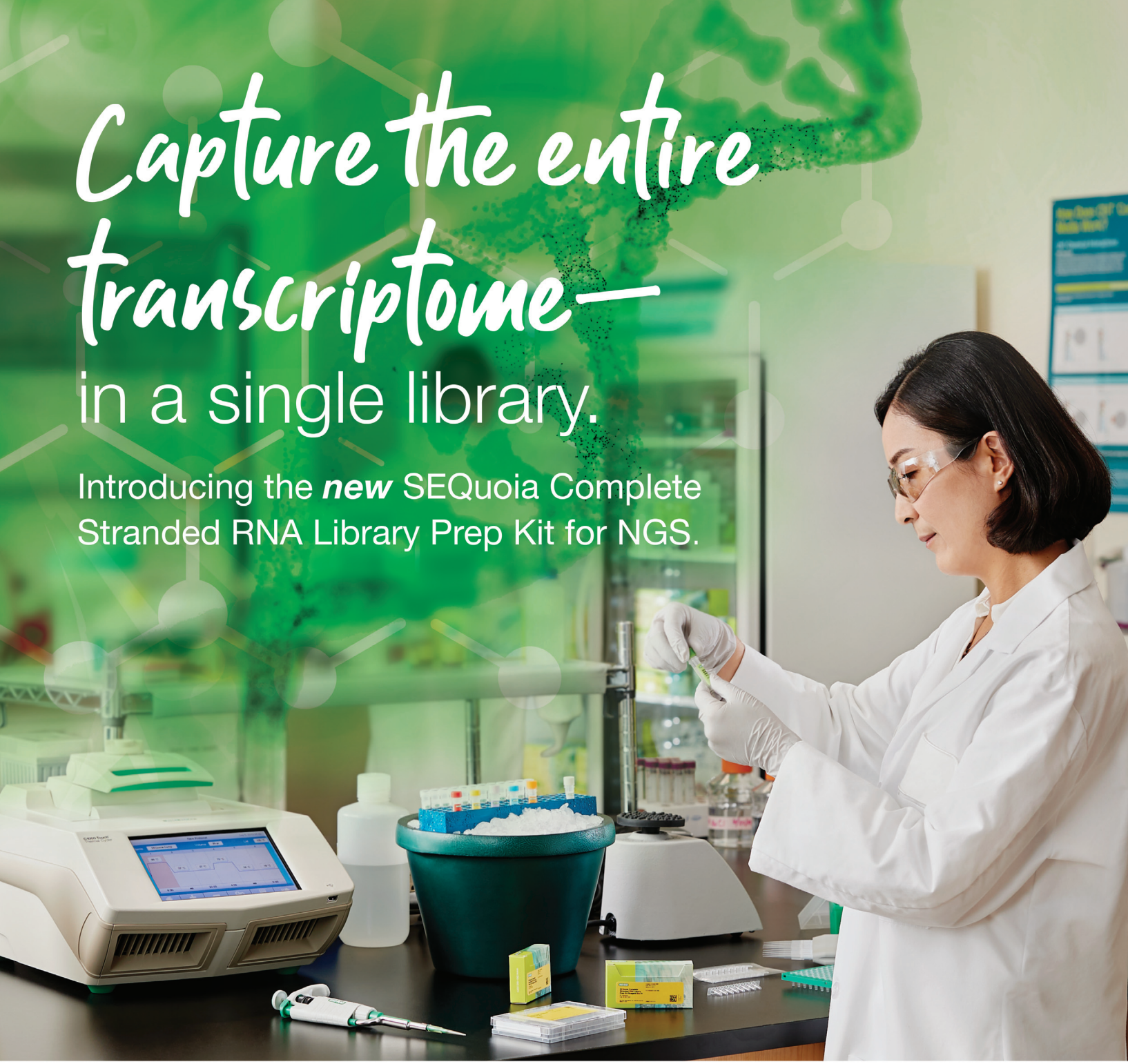
SAPHYR SYSTEM DETECTS VARIANTS OTHER TECHNOLOGIES MISS



Homozygous insertions/deletions larger than 500 bp	**Balanced and unbalanced translocations** larger than 50 kbp	**Inversions** large than 30 kbp	**Duplications** larger than 30 kbp	**Copy number variations** larger than 500 kbp
99% sensitivity	**95% sensitivity**	**99% sensitivity**	**97% sensitivity**	**97% sensitivity**

False-positive as low as 2%

Learn more at **www.bionanogenomics.com**.



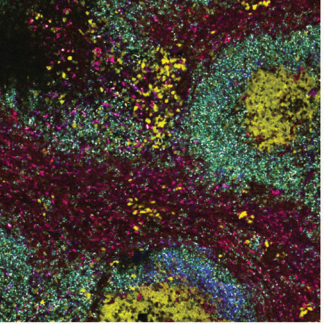
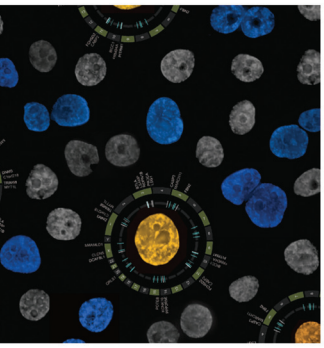
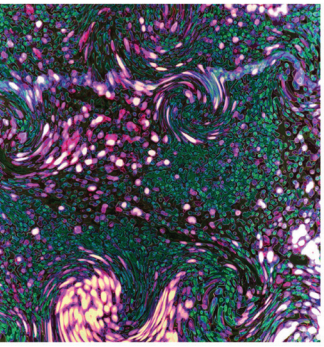
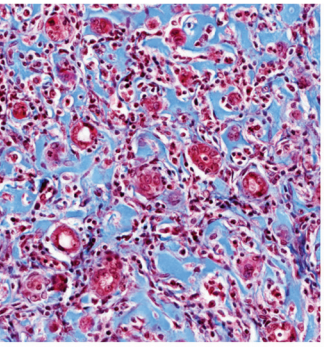
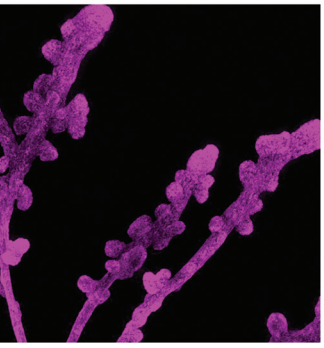
It's new. It's different. And it's only from Bio-Rad.

The SEQuoia Complete Stranded RNA Library Prep kit gives you a truly holistic view of the transcriptome, capturing all types of RNAs (long, short, and everything in between) from all types of samples in less than 4 hours. With unparalleled uniformity of coverage, strandedness, and efficiency, what you will discover will definitely surprise you.

Are you ready for a new approach to transcriptomics?
Get the details at bio-rad.com/SEQuoiaCompleteRNA

#ScienceForward

BIO-RAD


2020 SCIENTIFIC CONFERENCES

Presenting the most significant research on cancer etiology, prevention, diagnosis, and treatment

Seventh JCA-AACR Special Joint Conference on the Latest Advances in Pancreatic Cancer Research: From Basic Science to Therapeutics
Organizing Committee: Kohei Miyazono, Masanobu Oshima, Hiroshi Seno, Elizabeth M. Jaffee, Anirban Maitra, and Rosalie C. Sears
June 9-11, 2020 | Kyoto, Japan

Second AACR International Meeting: Advances in Malignant Lymphoma: Maximizing the Basic-Translational Interface for Clinical Application In cooperation with the International Conference on Malignant Lymphoma (ICML)
Scientific Committee Chair: Ari M. Melnick
June 25-28, 2020 | Boston, MA

Tumor Heterogeneity: From Single Cells to Clinical Impact
Conference Cochairs: Nicholas E. Navin, Kornelia Polyak, Alexander K. Shalek, and Charles Swanton
September 10-13, 2020 | Philadelphia, PA

CRI-ENCI-AACR Sixth International Cancer Immunotherapy Conference: Translating Science into Survival
Conference Cochairs: Özlem Türeci, E. John Wherry, and Jedd D. Wolchok
September 14-17, 2020 | New York, NY

13th Biennial Ovarian Cancer Research Symposium
Conference Cochairs: Douglas A. Levine, Ursula A. Matulonis, Barbara Norquist, and Kunle Odunsi
September 26-28, 2020 | Seattle, WA

Pancreatic Cancer
Conference Cochairs: Dafna Bar-Sagi, Elizabeth M. Jaffee, Ben Z. Stanger, and Brian M. Wolpin
September 29-October 2, 2020 | Philadelphia, PA

Myeloma and Plasma Cell Dyscrasias
Conference Cochairs: Kenneth C. Anderson and Irene Ghobrial
October 2-5, 2020 | Boston, MA

13th AACR Conference on The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved
Conference Chair: John D. Carpten
October 2-5, 2020 | Miami, FL

Advances in Breast Cancer Research
Conference Cochairs: Jason Carroll, Jenny C. Chang, and Jane E. Visvader
October 9-12, 2020 | San Diego, CA

Epigenetics and Metabolism
Conference Cochairs: Chi Van Dang, Kimberly Stegmaier, Craig B. Thompson, and Matthew G. Vander Heiden
October 15-18, 2020 | Baltimore, MD

Tumor Immunology and Immunotherapy
Conference Cochairs: Timothy A. Chan, Charles G. Drake, Marcela V. Maus, and Arlene H. Sharpe
October 16-19, 2020 | Boston, MA

Learn more and register at
AACR.org/Calendar

AACR American Association for Cancer Research®
FINDING CURES TOGETHER®

Postdoctoral Positions

About SCISSOR
Single-Cell In Situ Spatial Omics at subcellular Resolution (SCISSOR) is a well-supported multidisciplinary program that aims to introduce new paradigms for cancer biology and diagnostics, using spatial and non-spatial omics technologies. Our team comprises of computational biologists (lead: Shyam Prabhakar), oncologists (lead: Iain Tan), biotechnologists (lead: Kok Hao Chen), and pathologists (lead: Tony Lim) with a track record of combining cutting-edge computational and experimental approaches to infer disease mechanisms and develop clinical applications (Chen et al., Science 2015; Li et al., Nat Genet 2017; Sun et al., Cell 2016; Fukawa et al., Nat Med 2016; del Rosario et al., Nat Methods 2015; Kumar et al., Nat Biotechnol 2013; Ku et al., Lancet Oncol 2012).

We are looking for bright, motivated individuals who are interested in working on cutting-edge research projects that leverage single cell and spatial omics. Our interdisciplinary team combines experimental biology, technology development and computational biology to address major questions in cancer biology.

Position 1
Postdoctoral fellow: Machine Learning and Mathematical Analysis of Spatial Transcriptomics Data

Successful candidates will develop and apply algorithms for the analysis of large-scale cancer data. This will be a unique opportunity to lead computational analysis of new types of data in the nascent field of spatial transcriptomics.

Requirements:

- Strong programming skills
- Expertise in mathematics, computer science, statistics, engineering, machine learning, signal processing, computational genomics, or a related field
- General quantitative intuition
- Strong publication record
- Strong communication skills
- The ability to work closely with clinicians and experimental biologists

Position 2
Postdoctoral fellow: Assay Development, Cancer Markers and Mechanisms

Successful candidates will have the opportunity to lead experimental design and execution for a spatial transcriptomics study looking at DNA and RNA changes in a variety of human cancers at subcellular resolution.

Requirements:

- Expertise in cancer biology, immunology, genomics or related fields
- Skilled in molecular and cellular assays
- Strong publication record
- Team player and strong communication skills (oral and written)
- The ability to work closely with clinicians and computational biologists

Benefits:
The Genome Institute of Singapore offers a competitive salary and a complete benefits package that ensures a very high living standard in one of the most modern cities in the world.

About the Organisation
The Genome Institute of Singapore (GIS), A*STAR Research Entities is the national flagship program for genomic science in Singapore. GIS is located within the Biopolis, the biomedical research hub of Singapore, which houses in close proximity research institutes under the Agency of Science, Technology and Research (A*STAR), biotech startups and international pharmaceutical corporations. The applicant would have the opportunity to interact with scientists, bioinformaticians, clinicians, engineers and other professionals from all over the world in a vibrant, intellectually stimulating and scientifically curious setting. You will be part of a vibrant scientific community where you will have the opportunity to share your ideas and demonstrate your skills and passion for scientific research. You can find out more about the Genome Institute of Singapore online: https://www.a-star.edu.sg/gis/.

Why Singapore?
Singapore, a city-state with one of the highest standards of living in the world, is an international hub for the biomedical sciences. Singapore is a tropical city with a rich Asian heritage and modern style of living, and is an ideal gateway to explore Asia providing a unique experience and an excellent quality of life.

How to Apply
To apply, please email your CV and names of references to: prabhakars@gis.a-star.edu.sg, arulrayan@gis.a-star.edu.sg

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.

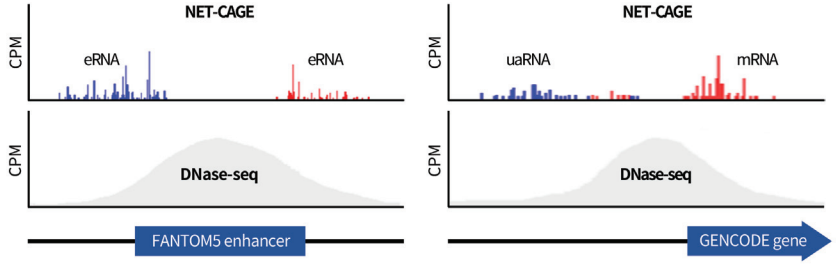


Fig.1. NET-CAGE signals around a region of FANTOM5 enhancer (left) and GENCODE gene (right).

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

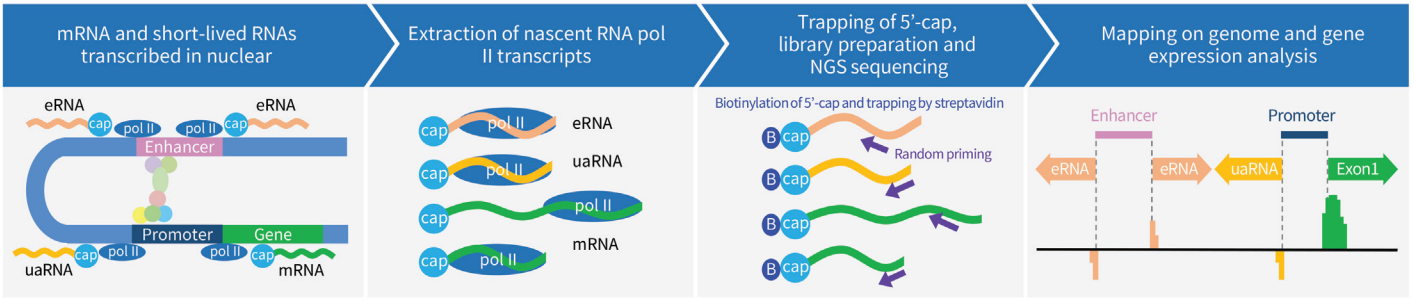
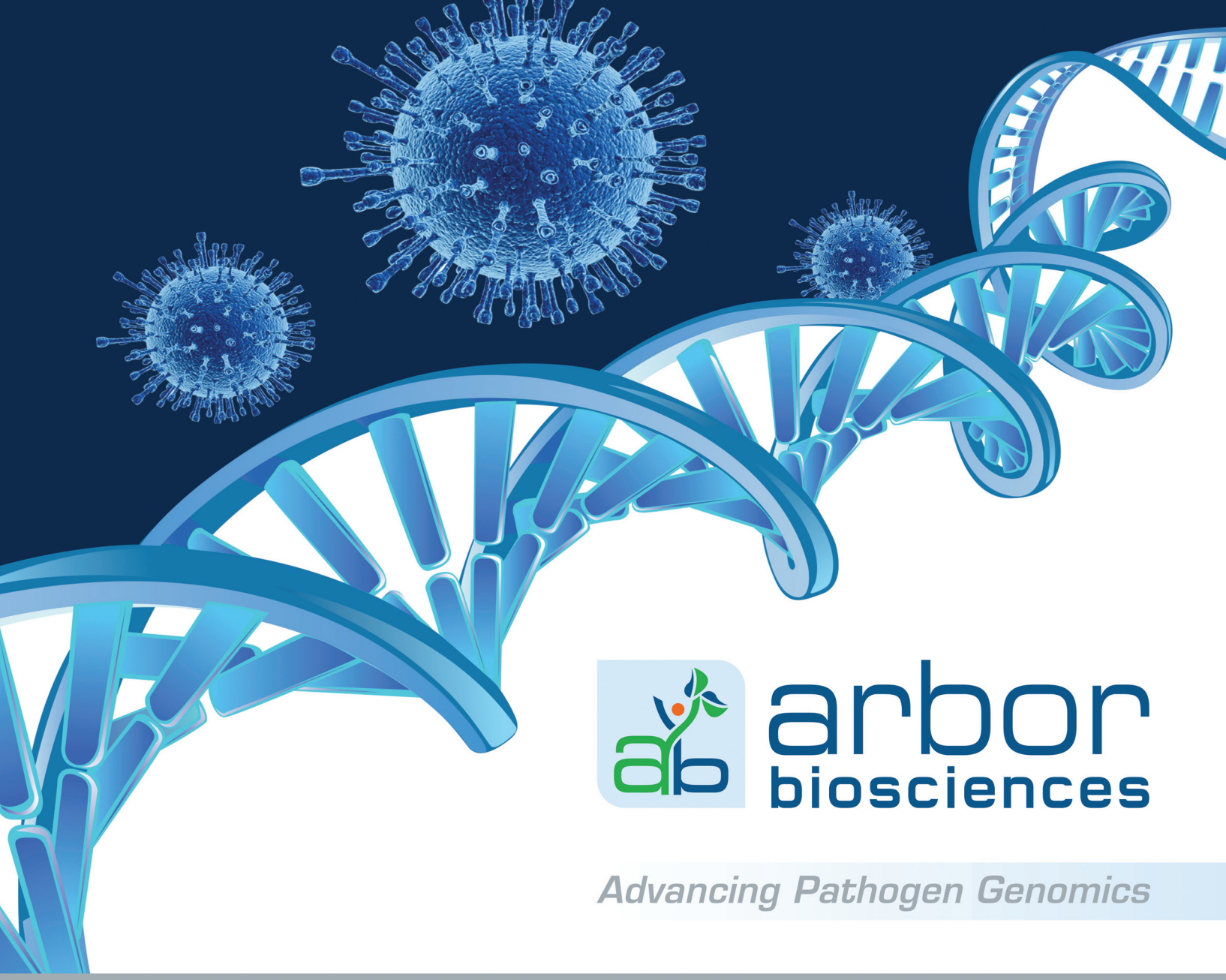


Fig.2. Workflow of the NET-CAGE. NET-CAGE is a unique NGS library preparation method using “cap-trapping” technology.

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

DNAFORM
Precision gene technologies
contact@dnaform.jp



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

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