

# Join the Microbiomics Standards & Controls Initiative (M-SCI)

Labs, Worldwide Commit to Improving Microbiome Measurements



>460 Participating Labs



47 Countries



Giving Away \$1,000,000 in  
Free Standards and Controls

# M-SCI: The Microbiomics Standards & Controls Initiative

## The Problem

Because the microbiomics/metagenomics field is inundated with inaccurate or incomparable data, there is an urgent need to reduce technical bias and variations across labs.

## The Solution

Incorporating microbiome standards (e.g. defined mock community) in routine measurements and workflow benchmarking.

## What is M-SCI?

In order to help the entire field assess microbiome workflows and improve data quality, Zymo Research launched M-SCI, supplying researchers worldwide with high quality microbiome standards for free.

### Available Standards and Controls Include:

Bacterial & Fungal Mock Community | Log-Abundance Standards  
Bacterial & Fungal DNA Standards | Spike-in Controls

Sign Up for M-SCI and Get Free Standards and Controls at  
[www.zymoresearch.com/pages/m-sci](http://www.zymoresearch.com/pages/m-sci)



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Toll Free: (888) 882-9682



# Microbiomics Services

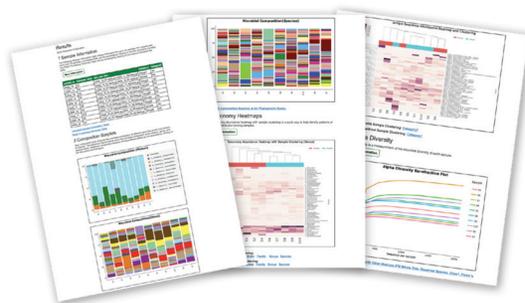
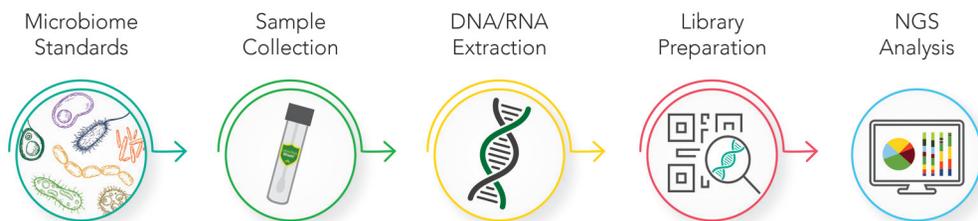
## Celebrate Your Discoveries



### 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/zymbiomic-services](http://www.zymoresearch.com/pages/zymbiomic-services) for a custom microbiomics services quote.



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# Your *Genome Research* Needs

A blue hand is shown pointing towards a white rounded square button with the word 'HELP' written in bold blue letters. The background of the entire page is a blue-toned image of a DNA double helix structure.

**HELP**

SBS Genetech offers a brand of products to support your genome research

- Muta-direct™ Site-Directed Mutagenesis Kit
- Premium™ Master Assembly Mix
- Topo Cloning Kit
- Scarlet™ Blood Direct PCR Kit
- PrimeSNP™ Genotyping Kit
- GClean™ First Strand cDNA Synthesis Kit
- PrimeTaq™ Probe One-Step RT-qPCR Kit
- SuperGold™ High Fidelity PCR EasyMasterMix
- Bst DNA/RNA Polymerase
- .....

# 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

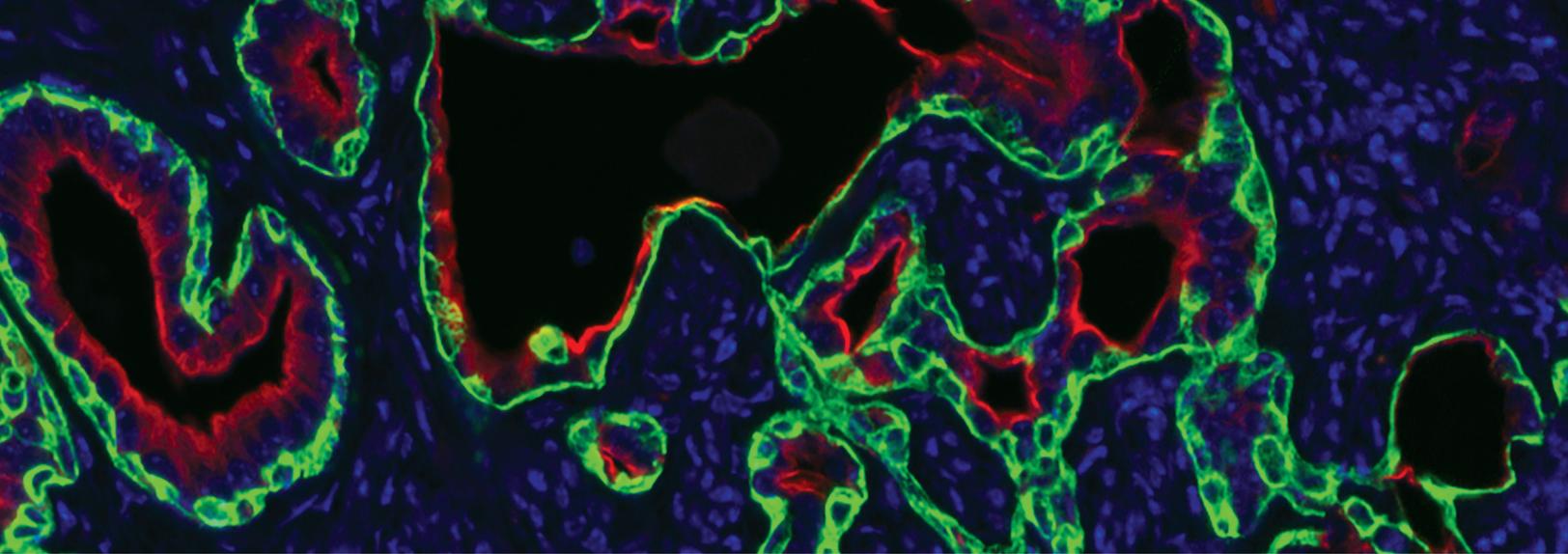


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AACR Virtual Special Conference:

# Endometrial Cancer: New Biology Driving Research and Treatment

November 9-10, 2020

Register Online!

## CONFERENCE COCHAIRS



**Victoria L. Bae-Jump**  
University of North Carolina,  
Chapel Hill, NC



**Blake Gilks**  
University of British Columbia,  
Vancouver Coastal Health Research Institute,  
Vancouver, BC, Canada



**Douglas A. Levine**  
New York University Perlmutter  
Cancer Center, New York, NY

## ABOUT THIS CONFERENCE

This AACR Virtual Special Conference on Endometrial Cancer will explore New Biology Driving Research and Treatment. A broad range of topics will be discussed, from basic research in model systems, exploration of cause, and early detection and characterization to novel immunologic therapies, precision, and targeted therapeutics. The Conference Cochairs have developed a multidisciplinary program that will appeal to laboratory scientists and clinical oncologists committed to understanding and eliminating endometrial cancer.



Continuing Medical Education (CME) Activity  
AMA PRA Category 1 Credits™ available

Learn more and register at  
[AACR.org/EndoCan20](https://AACR.org/EndoCan20)

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### Bisulfite Pyrosequencing

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

### Targeted Bisulfite NGS

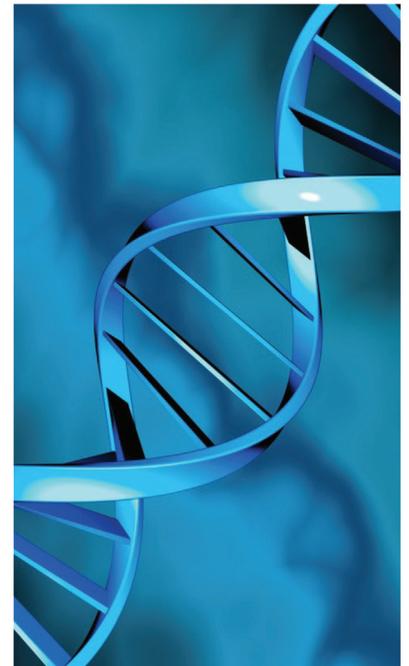
Quantify DNA methylation in multiple targets simultaneously at single basepair resolution.

### Custom Assays

Study DNA methylation level at request target genes.

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- **Simplify Lysis**

Deparaffinize, lyse, and de-crosslink in a single reaction without using harsh chemicals

- **Eliminate Bias**

Extract targeted nucleic acid regardless of fragment length or GC content

- **Minimize User Involvement**

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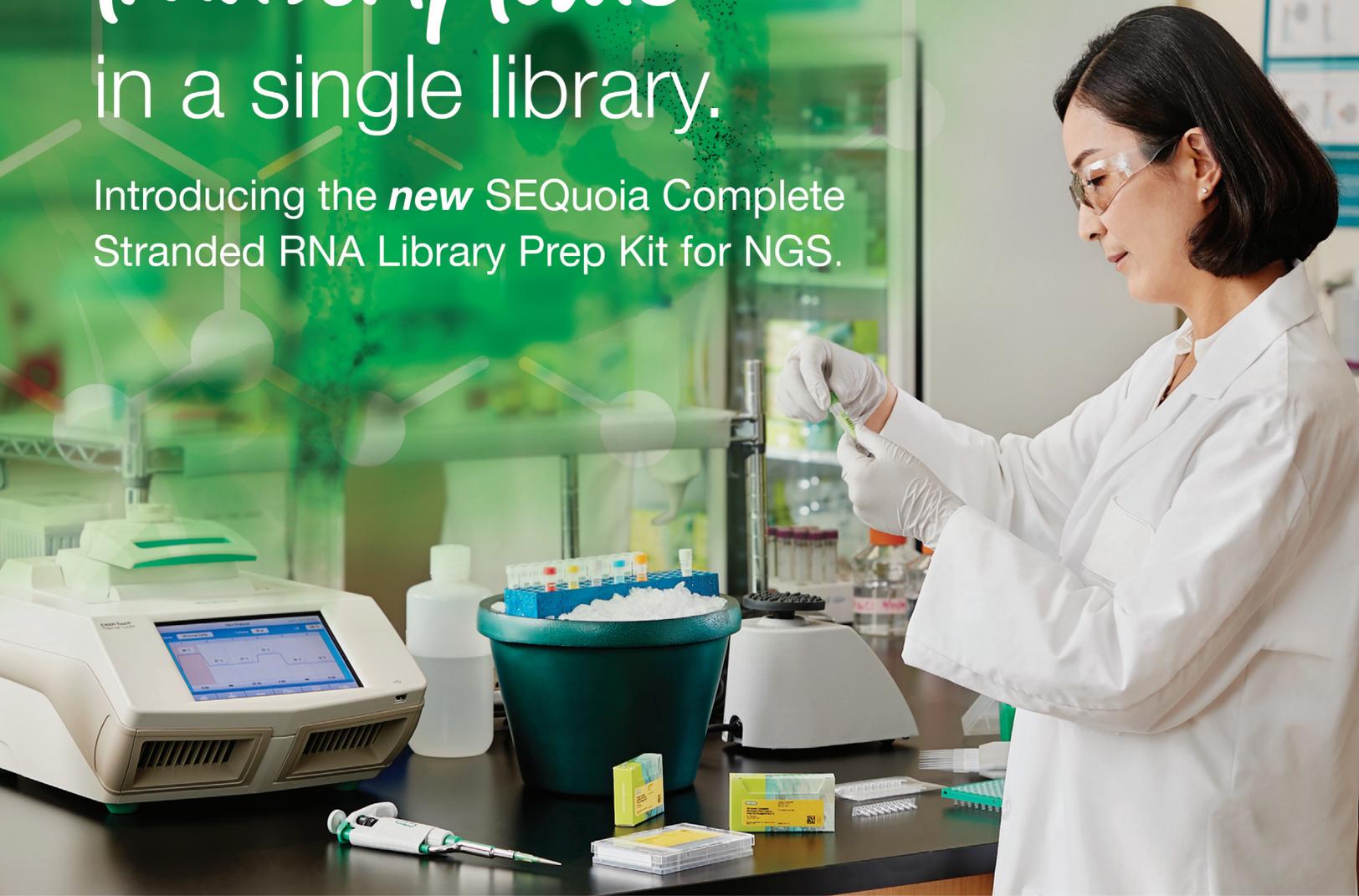
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The SEQuoia Complete Stranded RNA Library Prep kit gives you a truly holistic view of the transcriptome, capturing all types of RNAs (long, short, and everything in between) from all types of samples in less than 4 hours. With unparalleled uniformity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

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Get the details at [bio-rad.com/SEQuoiaCompleteRNA](https://www.bio-rad.com/SEQuoiaCompleteRNA)

#ScienceForward

**BIO-RAD**

# 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.

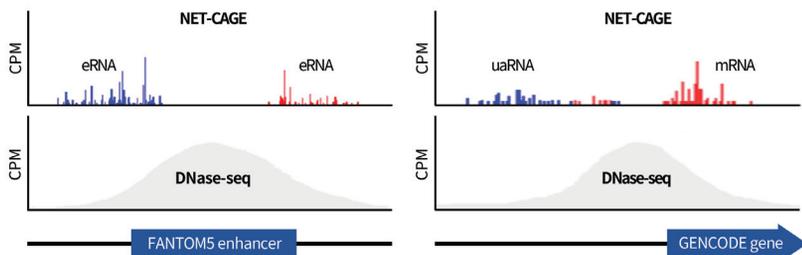


Fig.1. NET-CAGE signals around a region of FANTOM5 enhancer (left) and GENCODE gene (right).

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

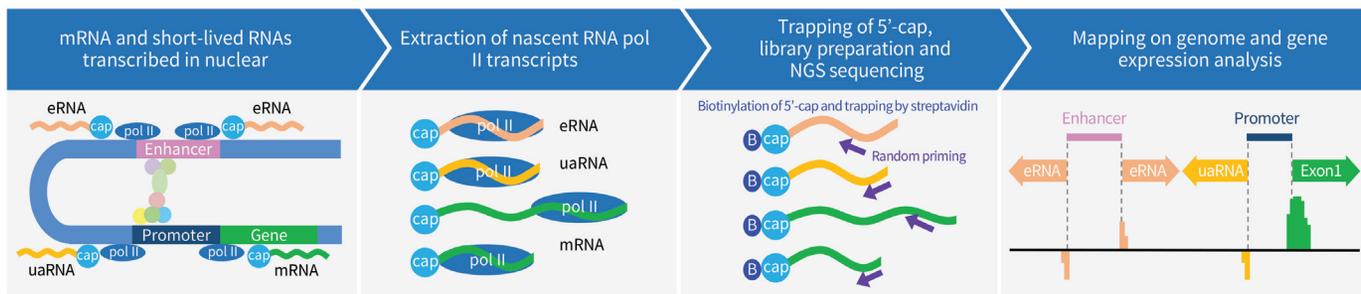
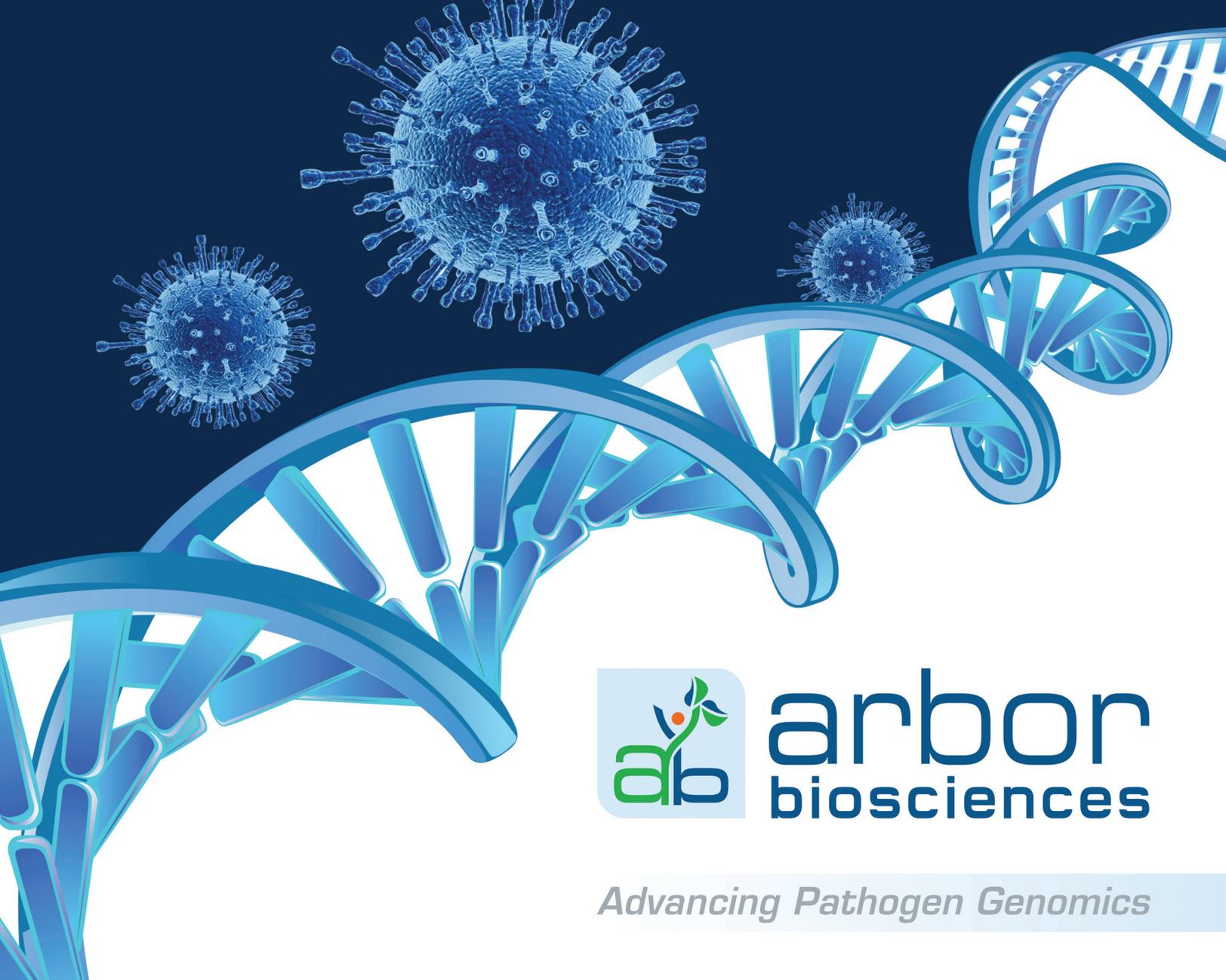


Fig.2. Workflow of the NET-CAGE. NET-CAGE is a unique NGS library preparation method using “cap-trapping” technology.

More than 250 papers using CAGE have been published!  
 Learn more about CAGE at [cage-seq.com](http://cage-seq.com)



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