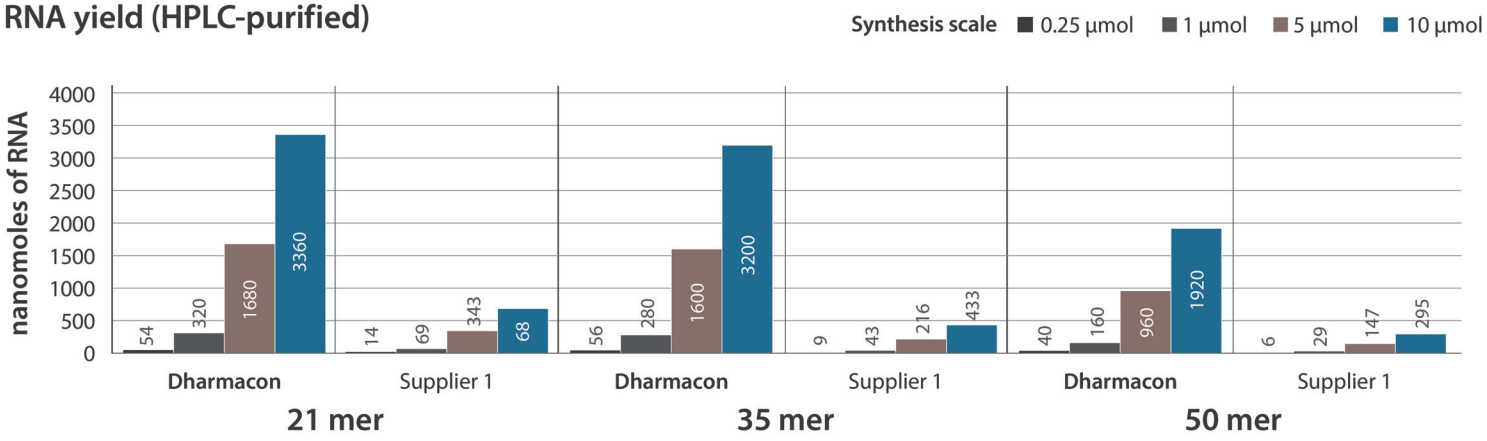
horizon
INSPIRED CELL SOLUTIONS

Meet your custom RNA requirements with our nearly limitless synthetic options.

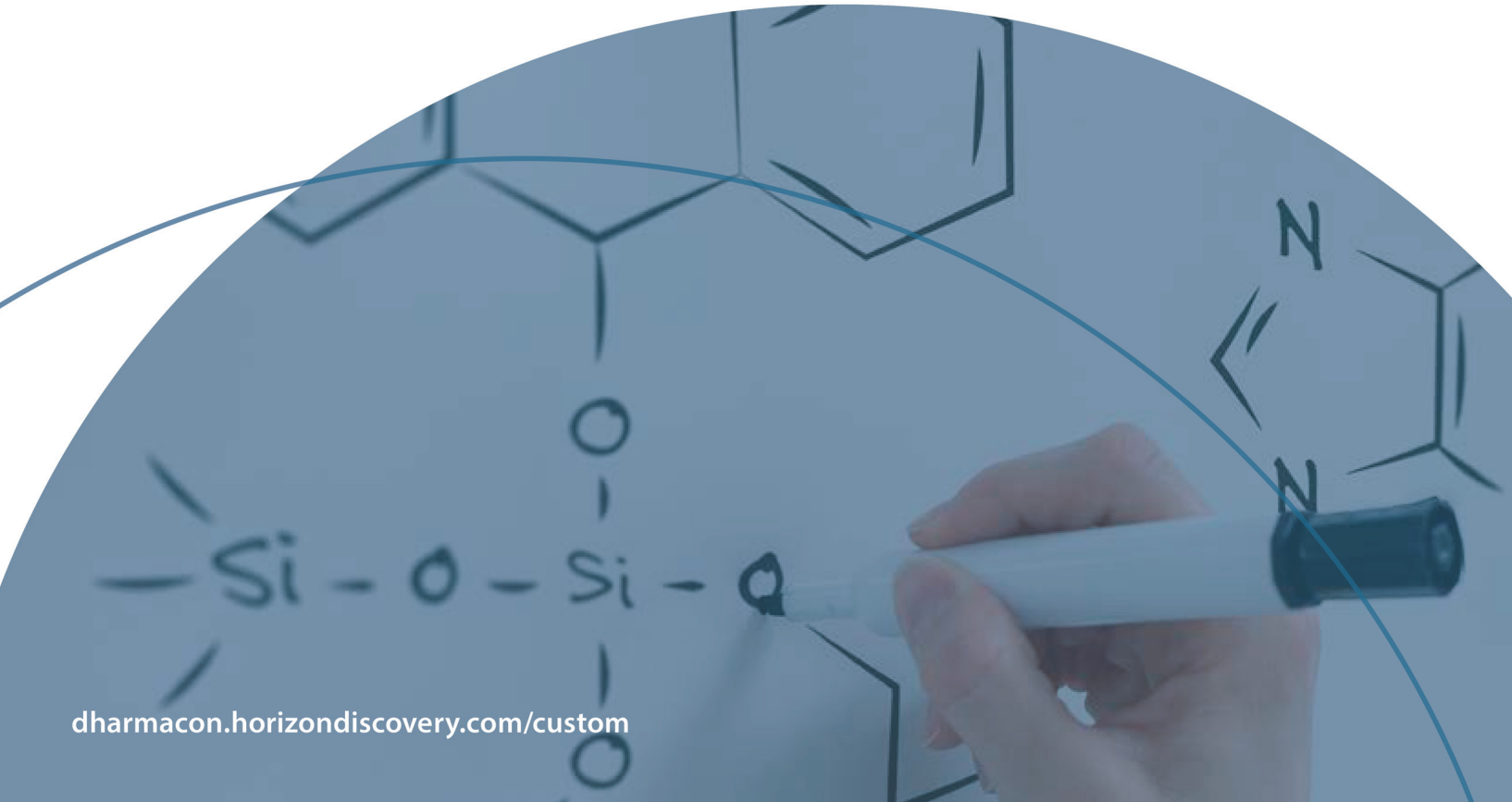
If your NMR, crystallography, or RNA binding study requires a non-standard chemical modification or a commercially unavailable modified nucleobase, we can help. For more than 20 years our chemists have utilized Dharmacon™ proprietary 2' ACE chemistry to synthesize RNA with superior yield and quality giving you the flexibility you need.

Better RNA yields give you more for your money.

RNA yield (HPLC-purified)

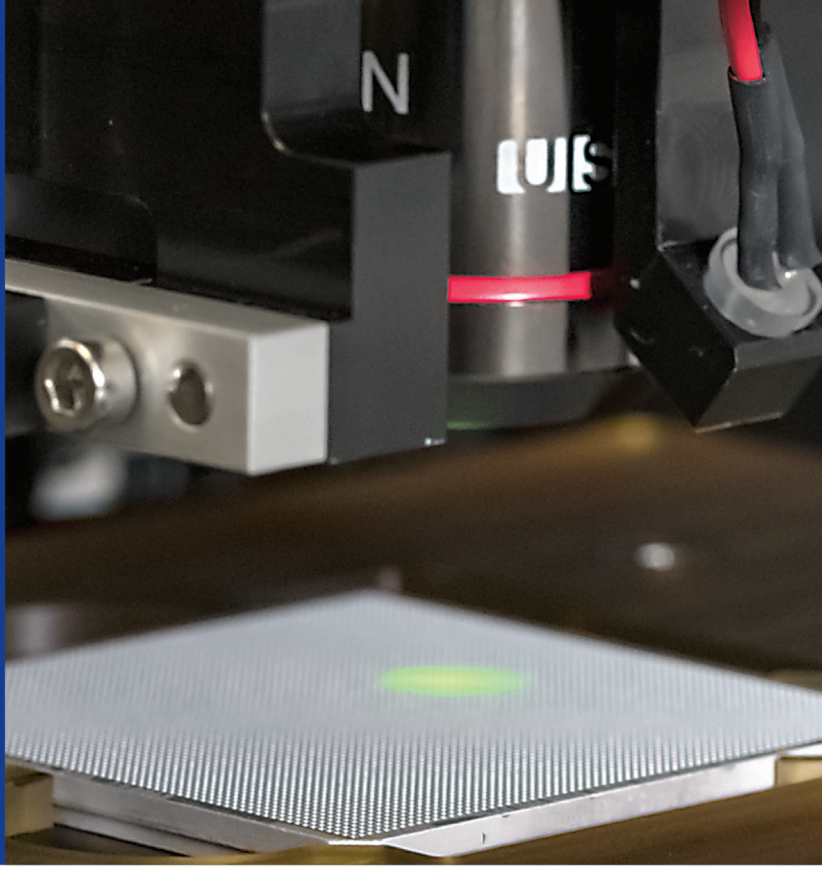


The yield for RNA oligos of three different lengths was compared for all available synthesis scales between Dharmacon and a competitor.



dharmacon.horizondiscovery.com/custom

Empowering innovation in single-cell analysis



The ICELL8® cx system enables custom application development through its open, flexible platform.

Introducing ICELL8 cx CELLSTUDIO™ open-architecture software:

- Works with ICELL8 cx CellSelect® software to allow you to proceed with only the cells you choose, following image analysis
- Provides ease of use and more control for the user to create applications with customized dispense patterns and reagent volumes
- Joins forces with our companion, user-friendly bioinformatics tools for powerful data analysis and visualization you can trust

that's GOOD science!

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takarabio.com/icell8cx

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Echo® Acoustic LIQUID HANDLING
for **SYNTHETIC BIOLOGY**

Reduce DNA Assembly and QC Costs

100-Fold

Echo® Liquid Handlers use acoustic energy to transfer DNA oligos and reagents, allowing the reduction of DNA assembly and NGS library preparation reaction volumes. Dramatically reduce reagent costs, save samples, and eliminate steps – all while improving the quality and throughput of synthetic genes.

- **100-fold reduction of Gibson or Golden Gate assembly reaction volumes**[1]
- **100-fold reduction of NGS library preparation volumes**[2]
- **Increased assembly and QC throughput**
- **Automation to easily process thousands of assemblies**

COMPARISON OF LIQUID HANDLING METHODS[2]

	Manual Pipetting	Echo® Liquid Handler
Amount of DNA	50 ng	**0.06 – 2.0 ng**
DNA volume (Rxn)	25 µL	**200 nL**
Library prep volume (Rxn)	25 µL	**300 nL**
Total volume	50 µL	**0.5 µL**
Reactions per kit	96	**9600**
Cost per reaction	$72.91	**$0.73**

[1] Kanigowska *et al.*, JALA, 2015.
[2] Shapland *et al.*, ACS Synth. Biol., 2015.

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Labcyte, now a part of Beckman Coulter Life Sciences, is revolutionizing liquid handling. Echo® Liquid Handlers use sound to precisely transfer liquids without contact, eliminating the use of pipettes. Our customers work across a wide spectrum of research, including drug discovery, genomics, proteomics, and personalized medicine.

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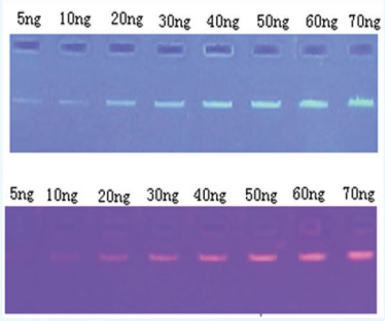
SBS Genetech Co., Ltd.

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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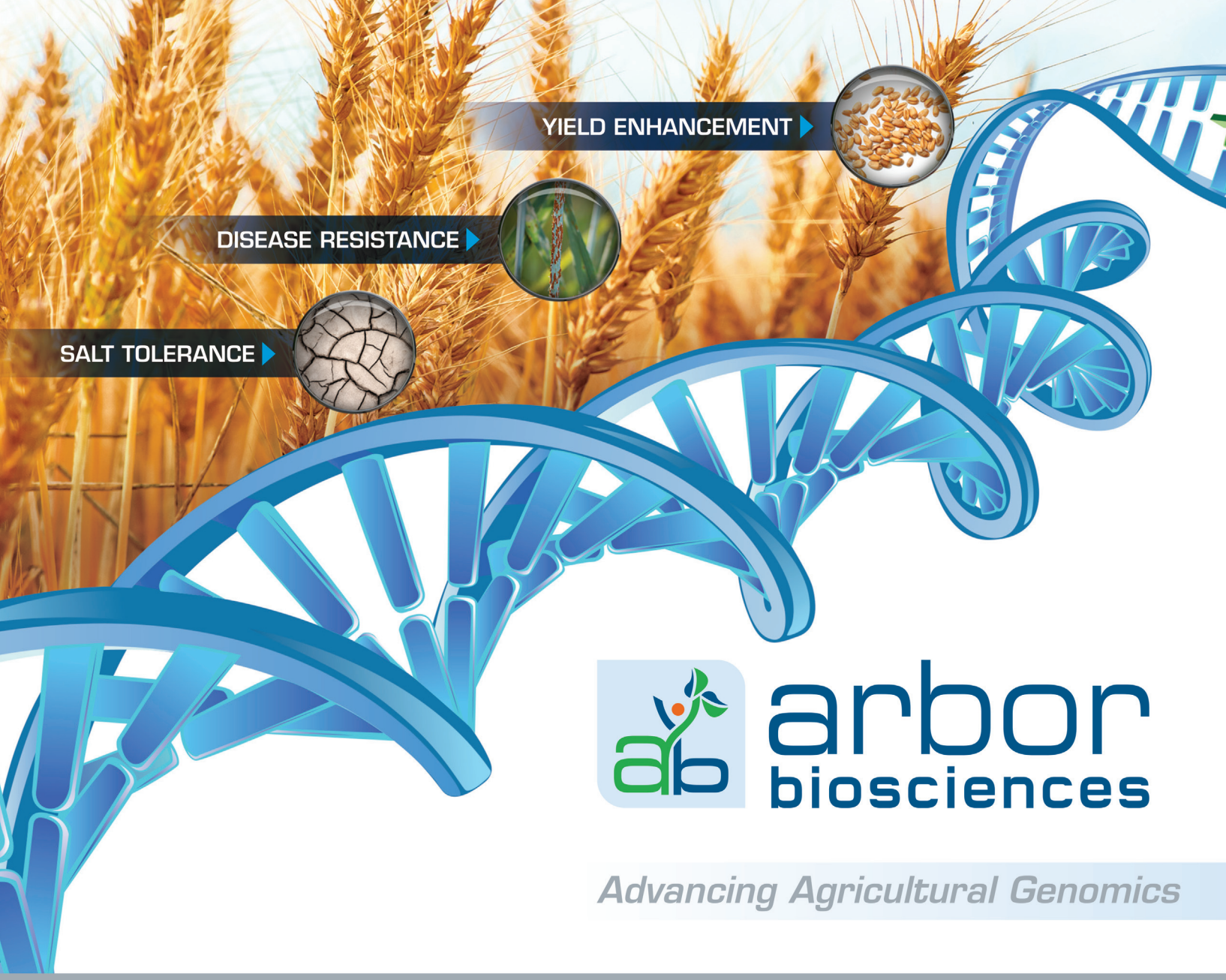

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APRIL 24-29

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Join us in San Diego for the latest innovative and inspiring cancer research from around the world...**the AACR ANNUAL MEETING 2020!**

Late-Breaking Abstracts and Clinical Trials Abstract Submission Deadline: Thursday, January 30, 2020

Advance Registration Deadline: Friday, February 21, 2020

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We look forward to seeing you!

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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.

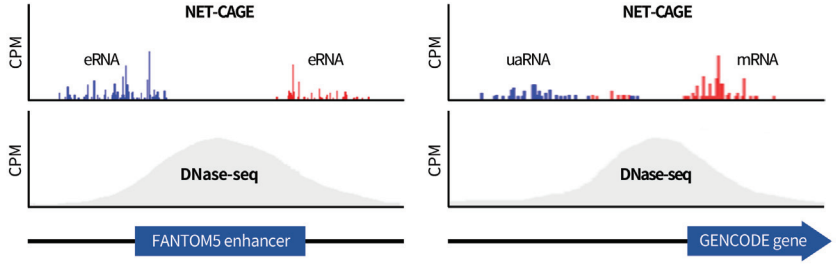

Fig.1. NET-CAGE signals around a region of FANTOM5 enhancer (left) and GENCODE gene (right).

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

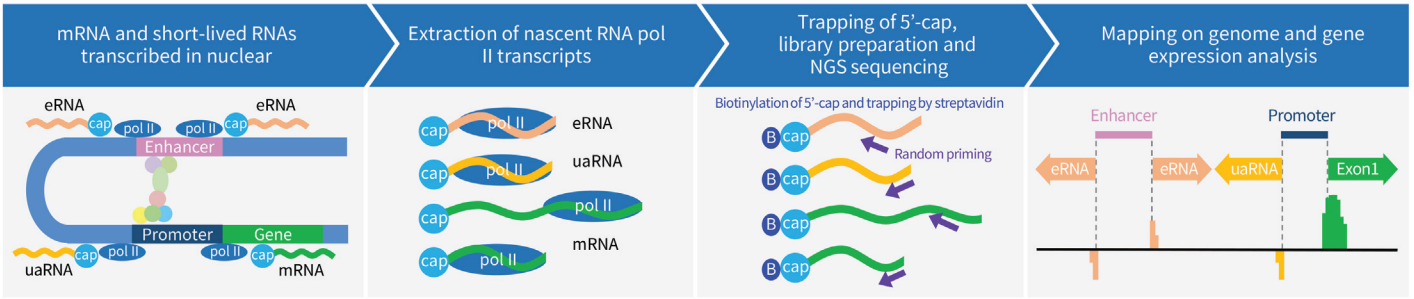

Fig.2. Workflow of the NET-CAGE. NET-CAGE is a unique NGS library preparation method using “cap-trapping” technology.

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

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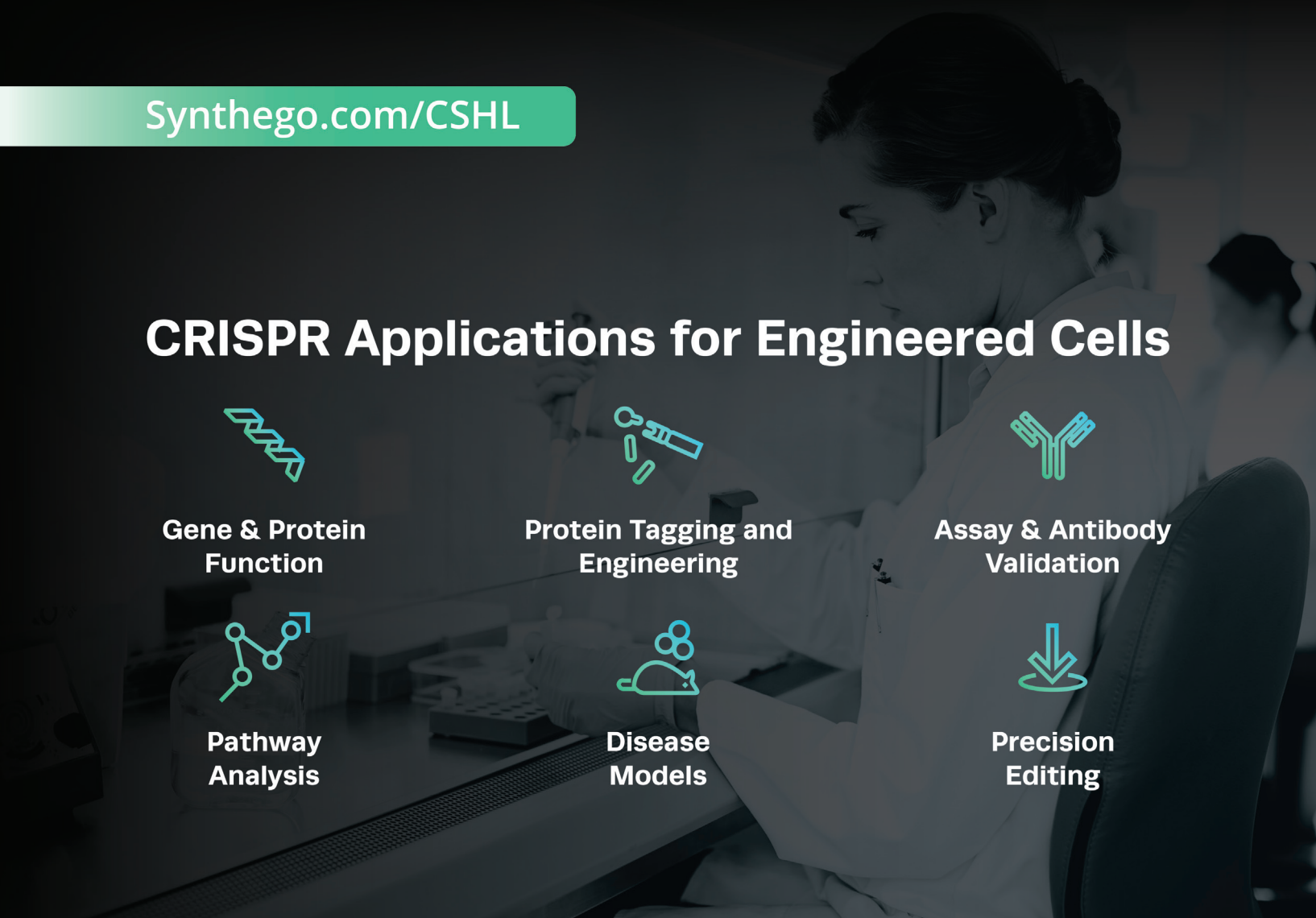

CRISPR Applications for Engineered Cells

- Gene & Protein Function
- Protein Tagging and Engineering
- Assay & Antibody Validation
- Pathway Analysis
- Disease Models
- Precision Editing