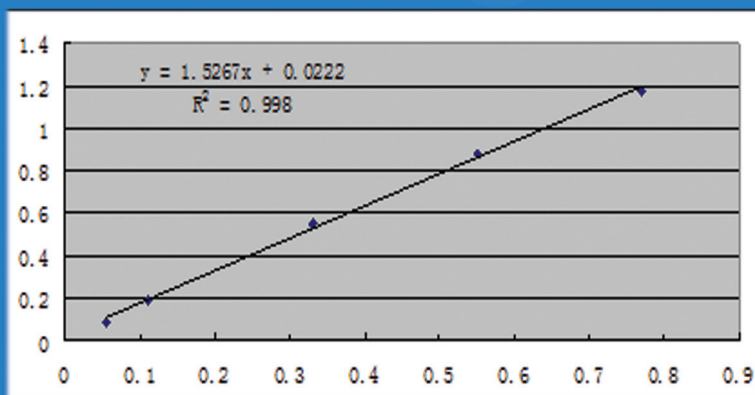


## Your reliable resource for Proteinase K

### Mutant Proteinase K US\$100/g

The application of this Mutant Proteinase K is similar to wild type Proteinase K. But this mutant one has higher specific activity and more stable at room temperature. It is a non-specific serine proteinase with broad substrates. It is active over the pH range from 4 to 12. It can be used at any situation to digest native and denatured proteins. For instance, it is used for isolating mRNA or genomic DNA from different tissues and modifying glycoprotein for structure studies. Mutant Proteinase K is active with SDS, urea and EDTA and active between 15°C and 75°C.

#### Enzyme Activity Assay:



Mutant Proteinase K is included on New Products, Science Magazine, March 8, 2019.  
Please visit: <http://science.sciencemag.org/content/363/6431/1109>

Beijing SBS Genetech Co. Ltd.

Fax: +86-10-82784290

Email: [order@sbsbio.com](mailto:order@sbsbio.com) Website: [www.sbsbio.com](http://www.sbsbio.com)

## 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<sup>1</sup>**
- **100-fold reduction of NGS library preparation volumes<sup>2</sup>**
- **Increased assembly and QC throughput**
- **Automation to easily process thousands of assemblies**

### COMPARISON OF LIQUID HANDLING METHODS<sup>2</sup>

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

<sup>1</sup>Kanigowska *et al.*, JALA, 2015.

<sup>2</sup>Shapland *et al.*, ACS Synth. Biol., 2015.



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for Cancer Research

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2020 • SAN DIEGO

APRIL 24-29

## TURNING SCIENCE INTO LIFESAVING CARE

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

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**Trials Abstract Submission Deadline:** Thursday, January 30, 2020

**Advance Registration Deadline:** Friday, February 21, 2020

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The AACR Annual Meeting highlights the work of the greatest minds in cancer science and medicine from institutions all over the world. This meeting presents the many scientific discoveries across the breadth of cancer research—from prevention, early detection, and interception; to cancer biology, translational, and clinical studies; to survivorship, population science, and advocacy. This year's program, with the theme of "Turning Science into Lifesaving Care," will be a comprehensive, cutting-edge scientific event that you will not want to miss!

**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

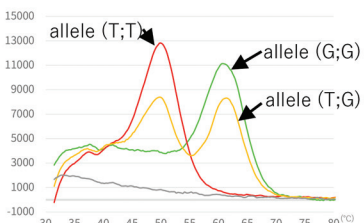
To apply, please email your CV and names of references to: [prabhakars@gis.a-star.edu.sg](mailto:prabhakars@gis.a-star.edu.sg), [arulrayan@gis.a-star.edu.sg](mailto:arulrayan@gis.a-star.edu.sg)



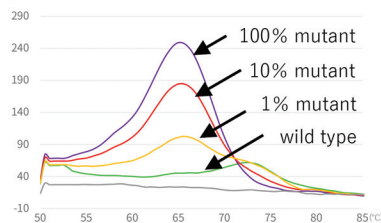
# A novel solution for SNP/somatic mutation detection

Eprobe is a **DNA-based fluorescent probe** which emits fluorescence when specifically binding to a complementary strand. Melting curve analysis after PCR can detect **SNP genotype** and **somatic mutations**. Two fluorescent dyes (thiazole orange and thiazole pink) are available.

- **High resolution SNP detection**—Increased  $T_m$  (approx.  $10^{\circ}\text{C}$ ) by the thiazole orange enables a shorter probe design and a clearer distinction of SNPs
- **Simple and highly sensitive somatic mutation detection**—sensitive detection of somatic mutations (down to 0.1%) can be achieved by suppression of PCR amplification of wild-type alleles by Eprobe (PCR clamping)
- **Compatible with most real time PCR instruments**—fluorescence emitted by Eprobe can be detected using a filter for SYBR<sup>®</sup> Green I\* \*SYBR<sup>®</sup> is a registered trademark of Molecular Probes, Inc.
- **Easy to use online design tools**—a design tool for a primer/Eprobe (E-design, [www.dnaform.com/edesign2/](http://www.dnaform.com/edesign2/)) and a thermodynamic calculation tool (ECHO, [www.dnaform.com/devel/echo/thermodynamics/](http://www.dnaform.com/devel/echo/thermodynamics/)) are available



SNP genotyping for IL28B (rs8099917 T;G) using an allele G specific Eprobe



Somatic mutation detection of KRAS G12D using an wildtype specific Eprobe.

Fluorophore (excitation/emission)	1.5 nmol	3.0 nmol	5.0 nmol	10.0 nmol
Thiazole orange (510 nm / 530 nm)	19,000 JPY <del>38,000 JPY</del>	30,000 JPY <del>60,000 JPY</del>	45,000 JPY <del>90,000 JPY</del>	70,000 JPY <del>140,000 JPY</del>
Thiazole pink (570 nm / 590 nm)	45,000 JPY	70,000 JPY	110,000 JPY	170,000 JPY

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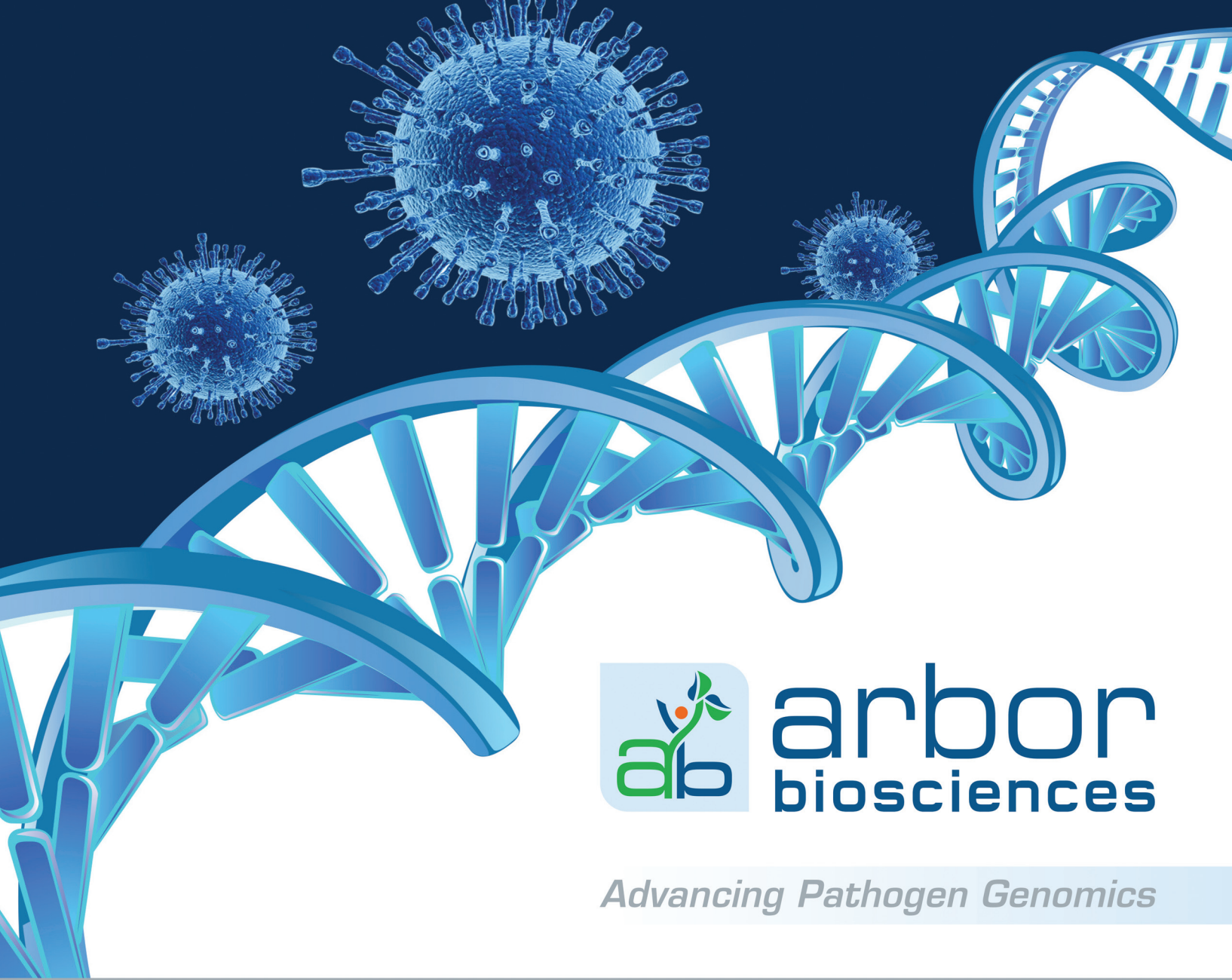
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Generate orders of magnitude enrichment of pathogen DNA or RNA from naturally complex samples, including bacterial, fungal, and viral pathogens, with hybridization-based target capture kits.

- Generate whole genome sequences of bacteria, fungi, and viruses
- Achieve >250-fold enrichment of pathogens from NGS libraries
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