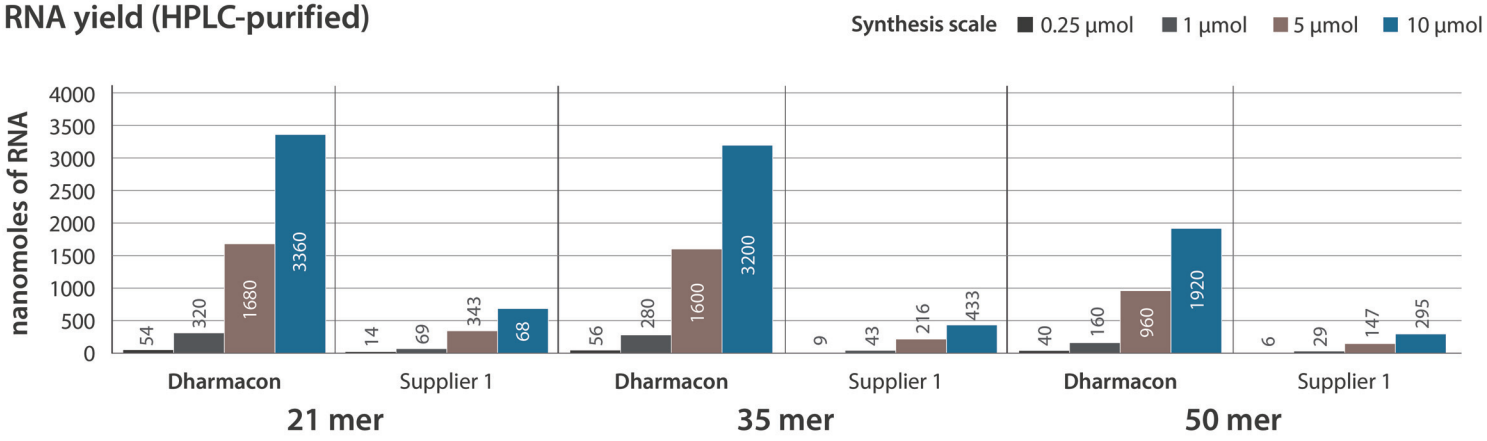
horizon
INSPIRED CELL SOLUTIONS

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

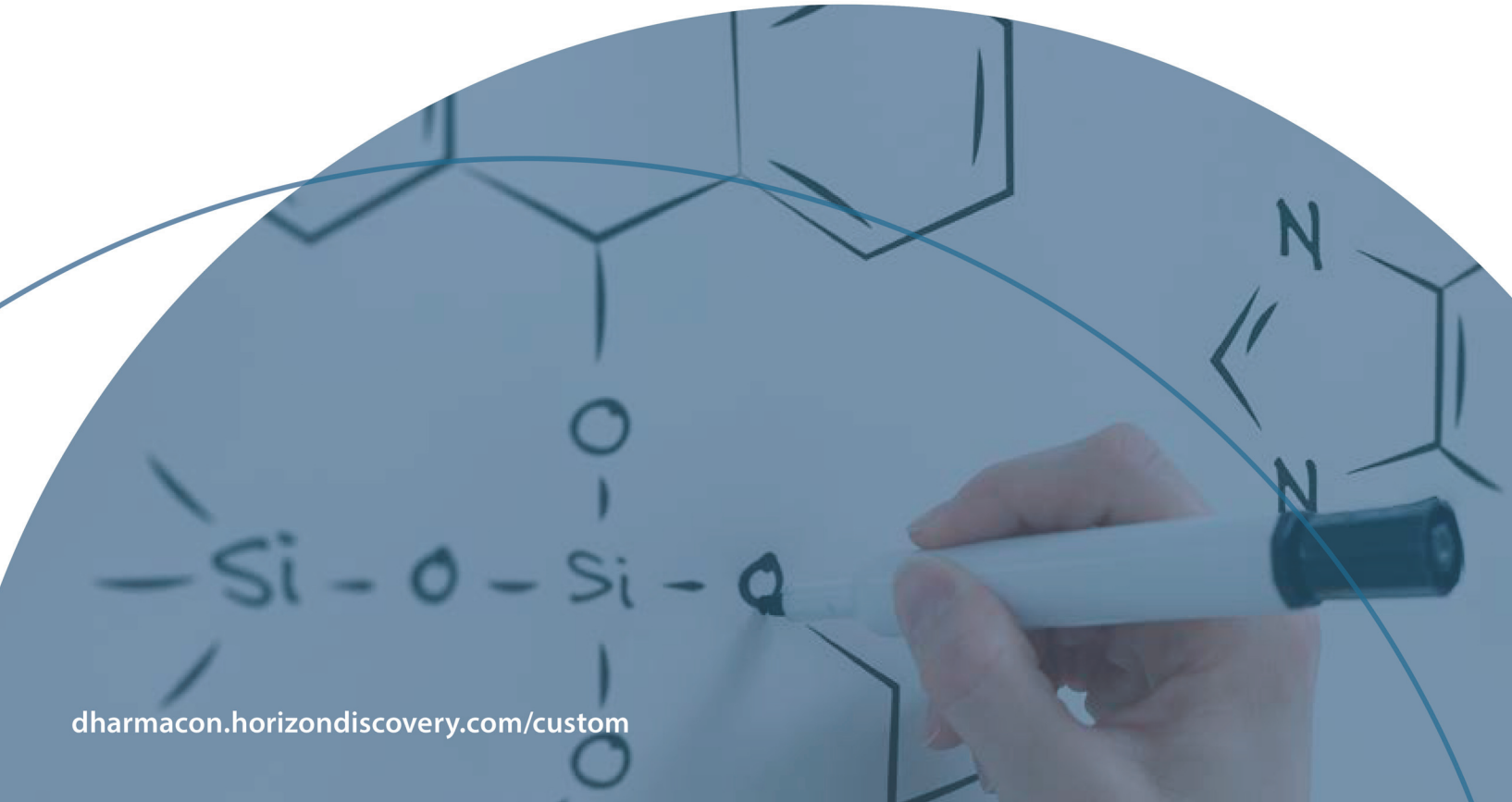
If your NMR, crystallography, or RNA binding study requires a non-standard chemical modification or a commercially unavailable modified nucleobase, we can help. For more than 20 years our chemists have utilized Dharmacon™ proprietary 2' ACE chemistry to synthesize RNA with superior yield and quality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



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Takara Bio has the solutions you need.

- **SMART-Seq® HT kit**—streamlined full-length cDNA library prep
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SMARTer NGS

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takarabio.com/SMARTerNGS

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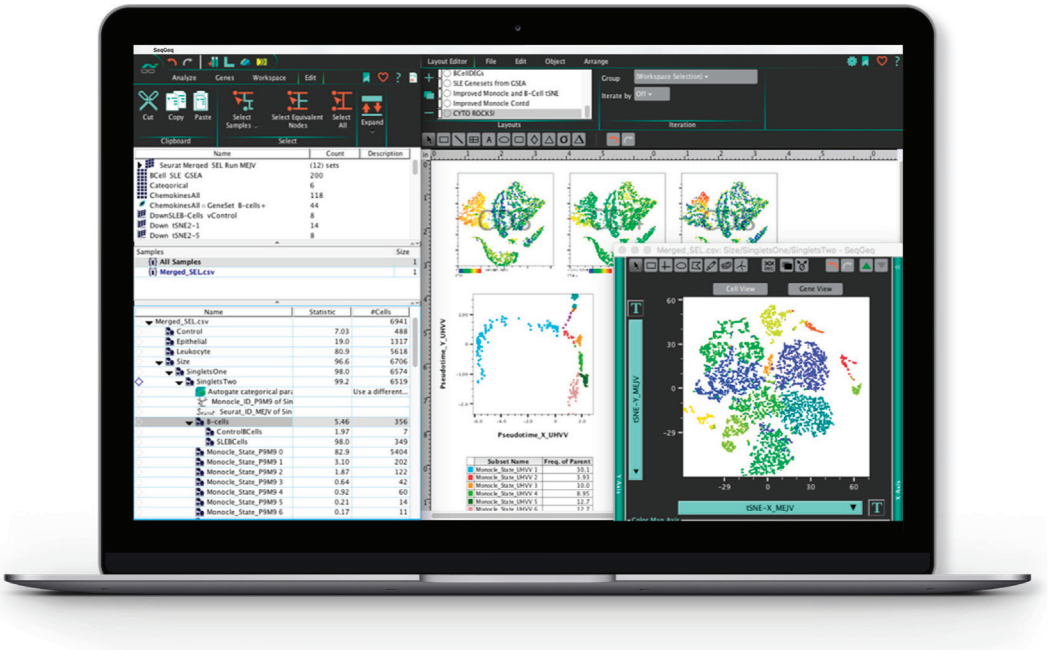
SeqGeq (seek-geek) is a desktop bioinformatics platform that makes complex scRNA seq analysis accessible with an intuitive interface. With SeqGeq, you control your analysis—no more writing R scripts to visualize your data.



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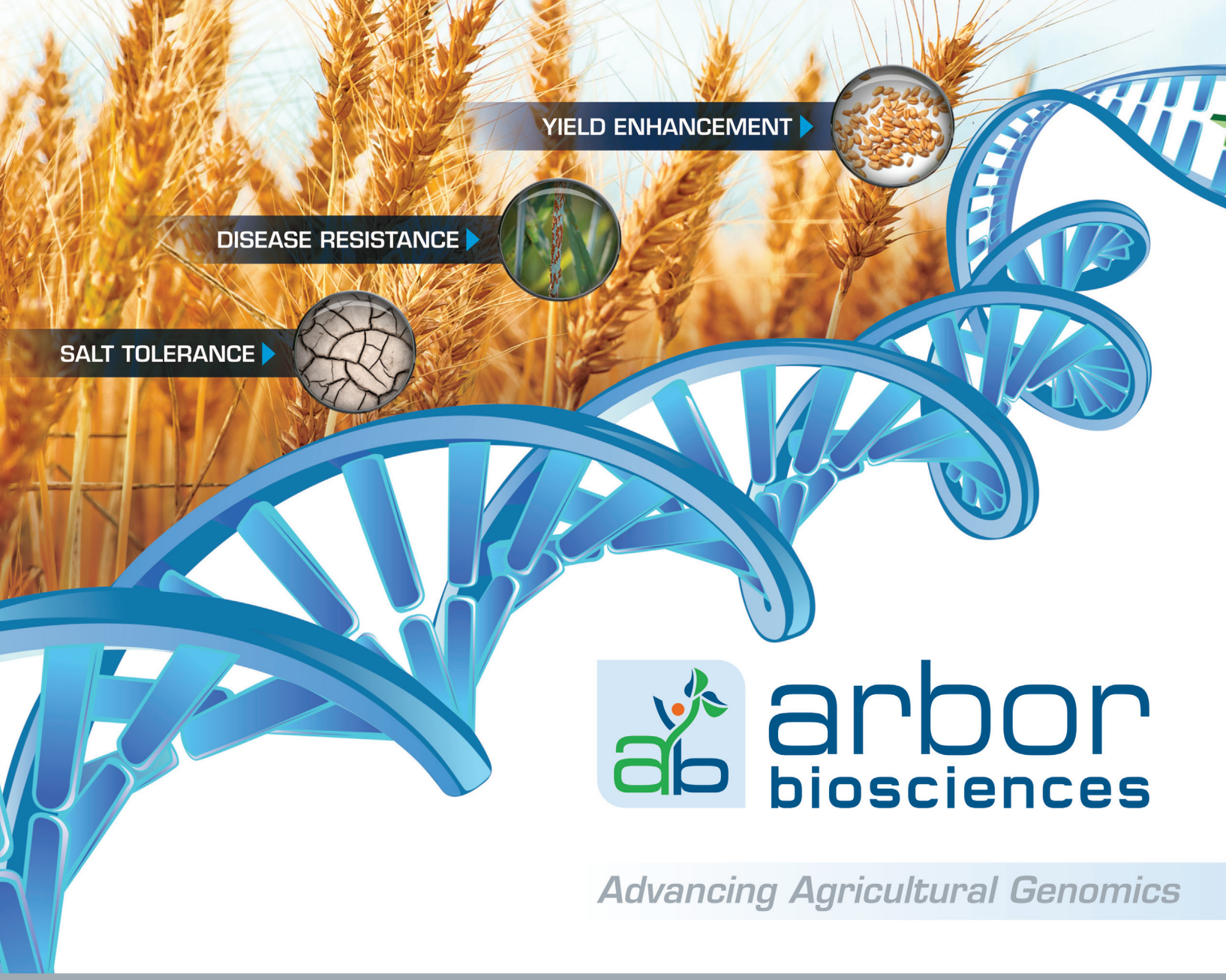

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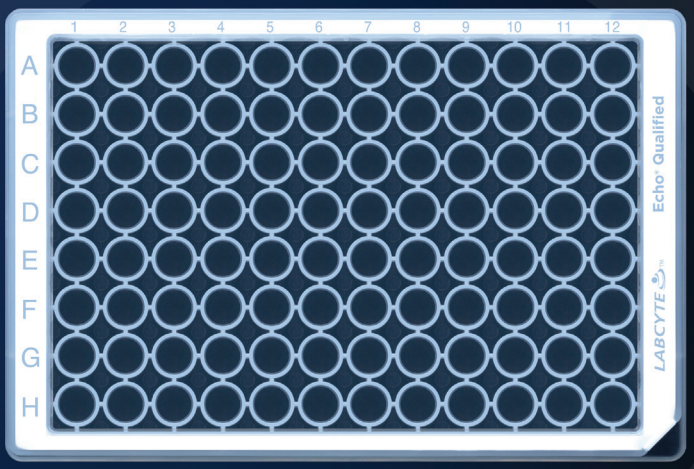
Coming soon...



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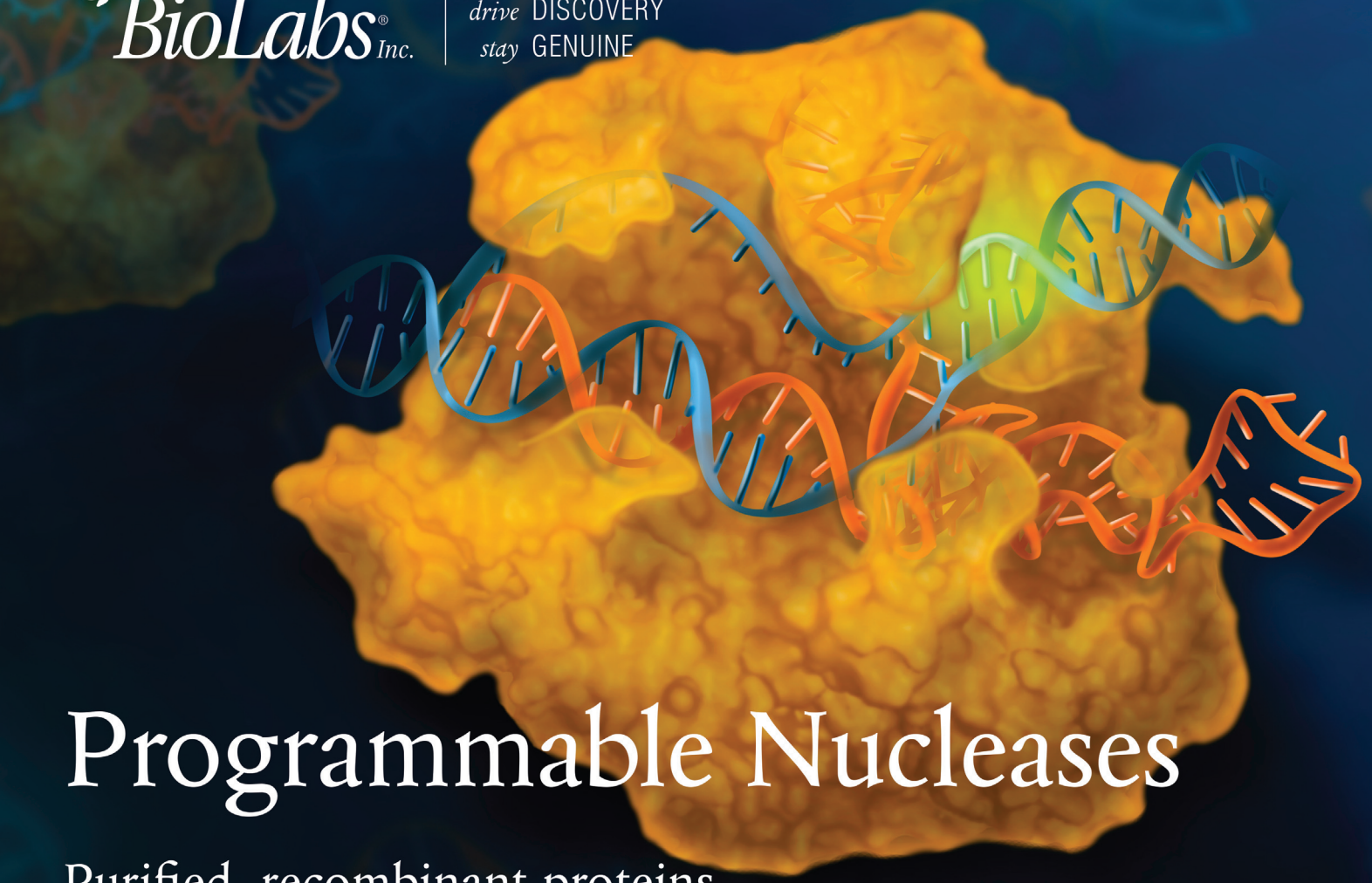

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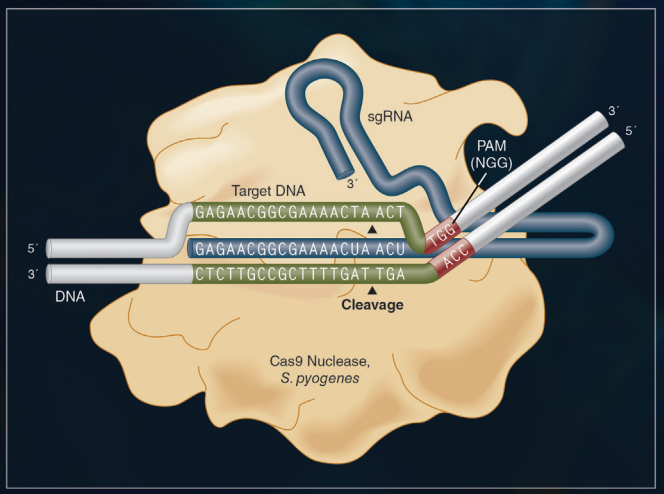
Schematic representation of Cas9 Nuclease, *S. pyogenes* sequence recognition and DNA cleavage



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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.

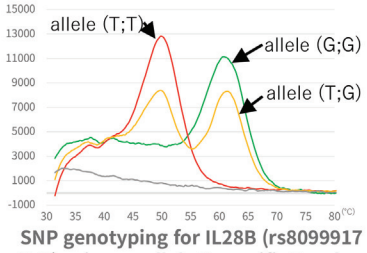
How to Apply
To apply, please email your CV and names of references to: prabhakars@gis.a-star.edu.sg, arulrayan@gis.a-star.edu.sg

Eprobe® / Eprimer™ fluorescent probe

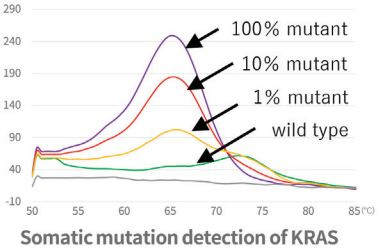
A novel solution for SNP/somatic mutation detection

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 Tm (approx.10°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® Green I* *SYBR® 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/) and a thermodynamic calculation tool (ECHO, 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.

Fluorphore (excitation/emission)	1.5 nmol	3.0 nmol	5.0 nmol	10.0 nmol
Thiazole orange (510 nm / 530 nm)	19,000 JPY ~~38,000 JPY~~	30,000 JPY ~~60,000 JPY~~	45,000 JPY ~~90,000 JPY~~	70,000 JPY ~~140,000 JPY~~
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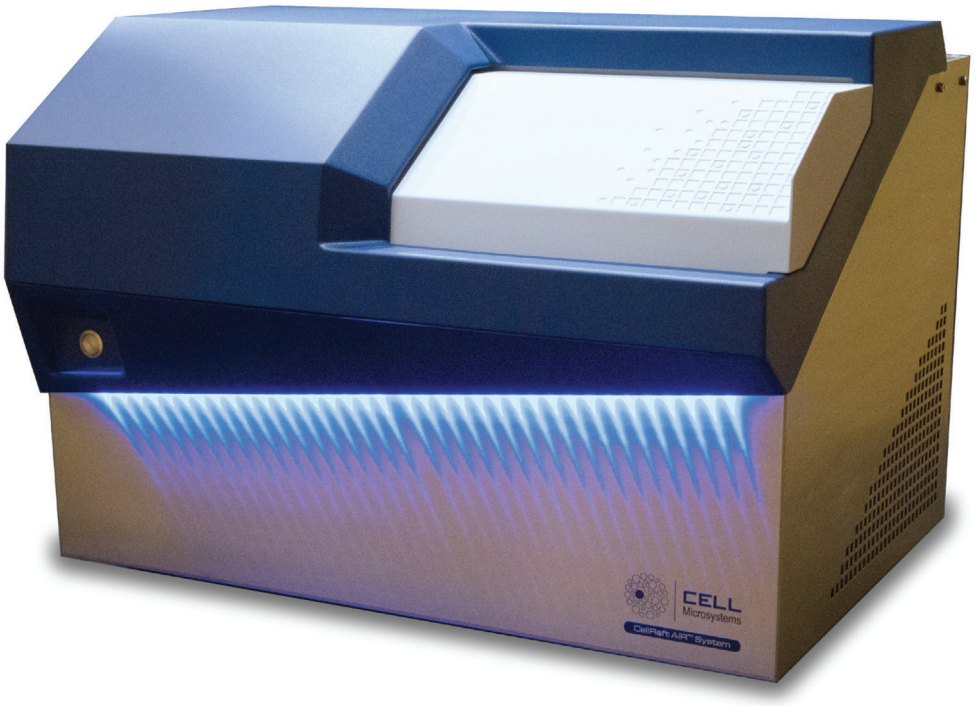
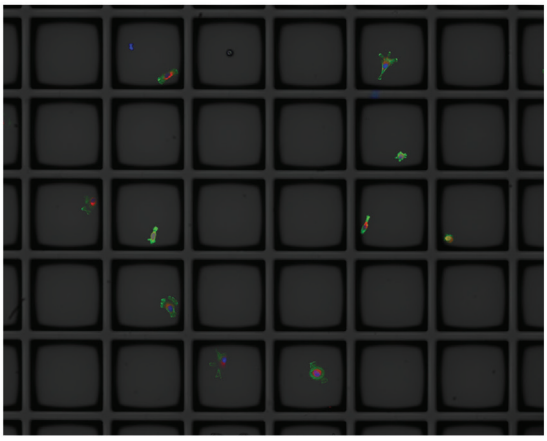


Expand your single cell analysis research with imaging-based sorting.

The CellRaft AIR System integrates single cell imaging and viable cell isolation, with no minimum input requirement – and works with virtually any cell type.



- **Phenotyping by imaging provides more information than RFUs alone**
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- **Verify live single cells and eliminate empties, doublets, or dying cells**
- **Flexible for any downstream process – NGS, multi-omics, expansion culture**
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