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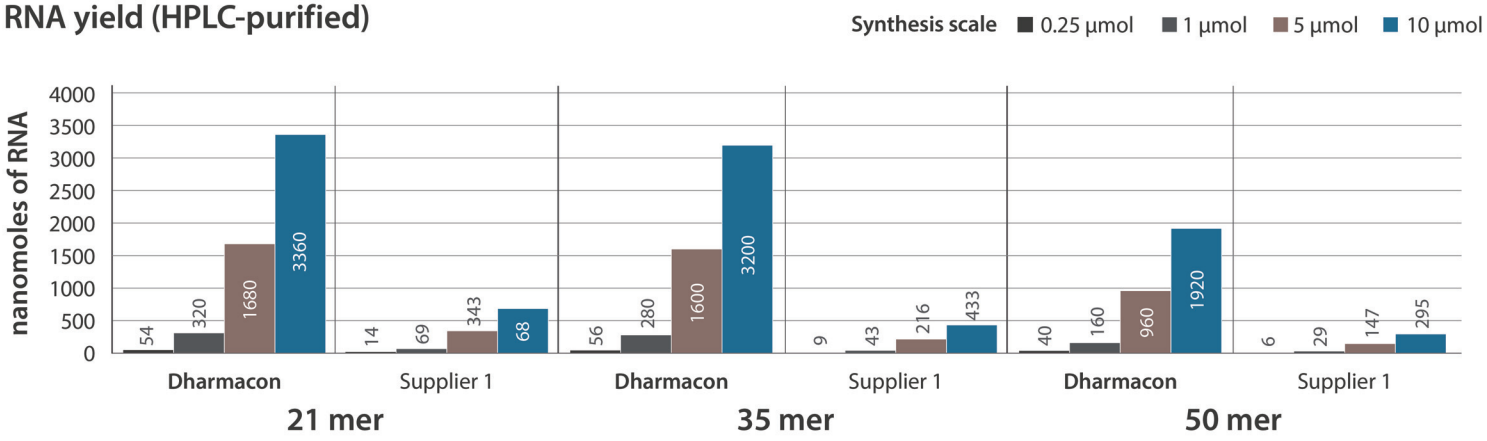
Meet your custom RNA requirements with our nearly limitless synthetic options.

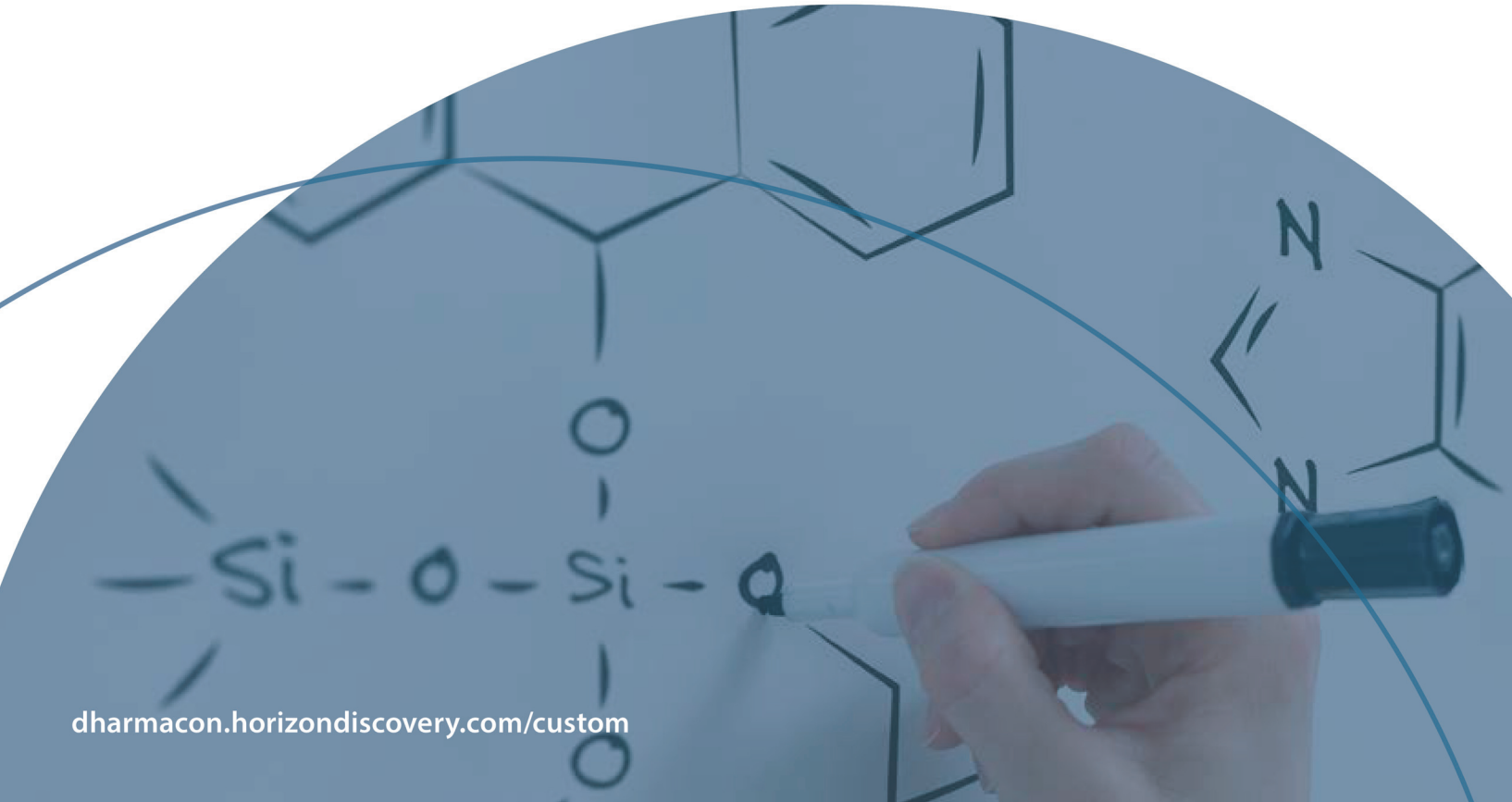
If your NMR, crystallography, or RNA binding study requires a non-standard chemical modification or a commercially unavailable modified nucleobase, we can help. For more than 20 years our chemists have utilized Dharmacon™ proprietary 2' ACE chemistry to synthesize RNA with superior yield and quality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

Description

dNTPs contain dATP, dCTP, dGTP and dTTP (monosodium salts) at a concentration of 10mM or 100mM each in sterile deionized water at pH7.5, whose purity is up to 99.5% (HPLC). It is free of RNase and DNase, and suitable for any molecular biology application that requires pure deoxynucleotides, such as PCR, DNA sequencing, cDNA synthesis and nick translation.

Stability

All of our dNTPs are very stable – we guarantee 100% stability for 2 years from the date of purchase.

Features

·Ultra-pure: >99% by HPLC
·Reliable, consistent results
·Available both as ready-to-use mix and a set

Applications

·PCR and qPCR
·cDNA synthesis
·Primer extension
·DNA sequencing
·DNA labeling
·Mutagenesis

Quality control

·Purity assay (HPLC) >99%
·Free of pyrophosphate, DNA and RNA
·DNase, RNase and nickase free
·Tested for PCR, qPCR and RT-PCR

Beijing SBS Genetech Co. Ltd.
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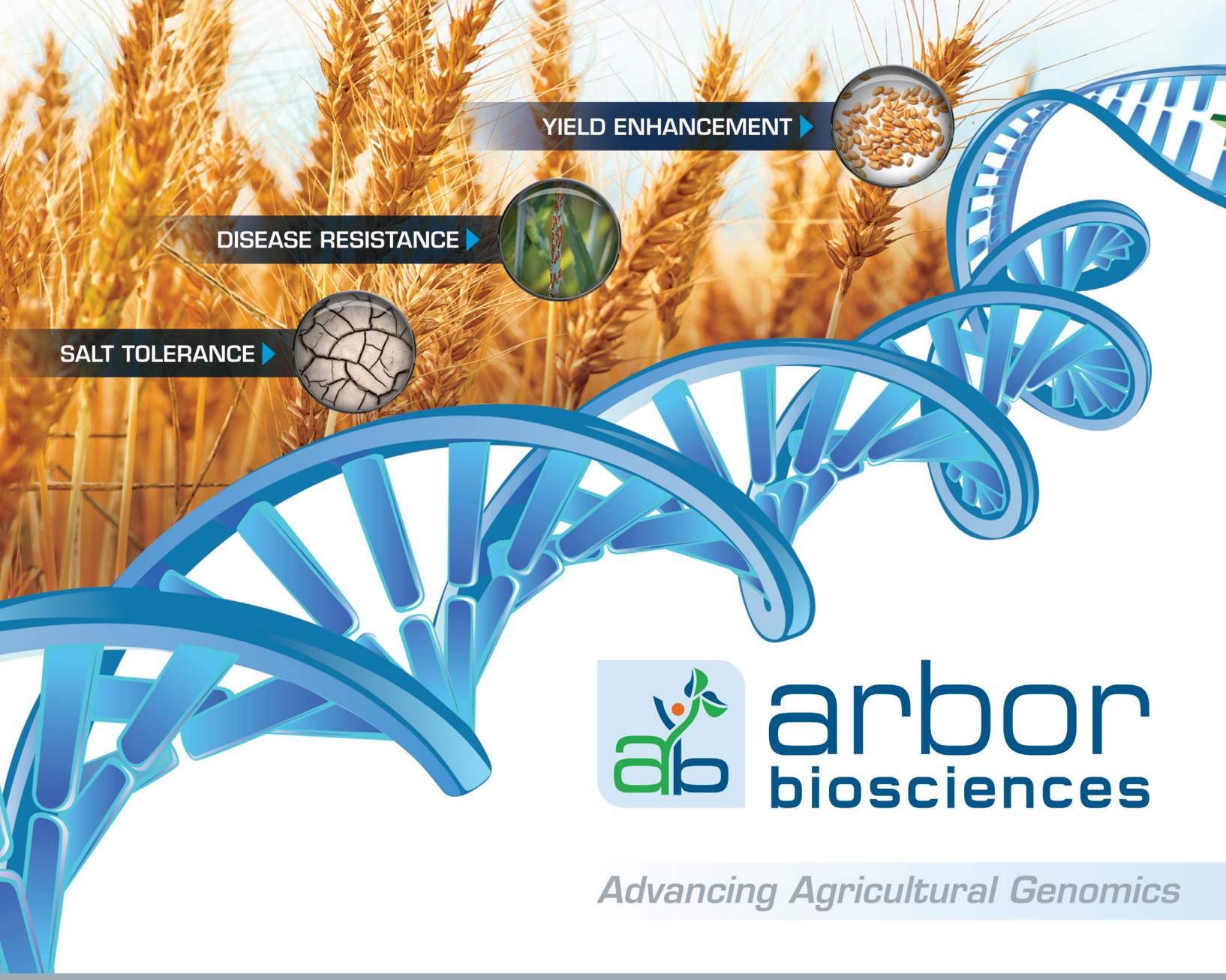

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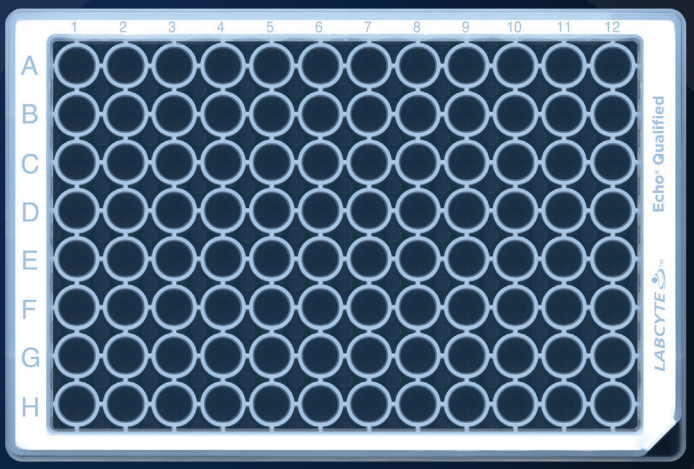

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Introducing the Echo® Qualified 96-well Microplate

A favorite for genomics applications, the Echo® 525 Liquid Handler saves reagents, sample, and time. Transfer of nanoliter volumes with high accuracy and precision enables assay miniaturization while maintaining data quality. Coming soon, Echo Qualified 96-well Microplates will link the unsurpassed performance of the Echo System with upstream sample preparation steps performed in a 96-well format.

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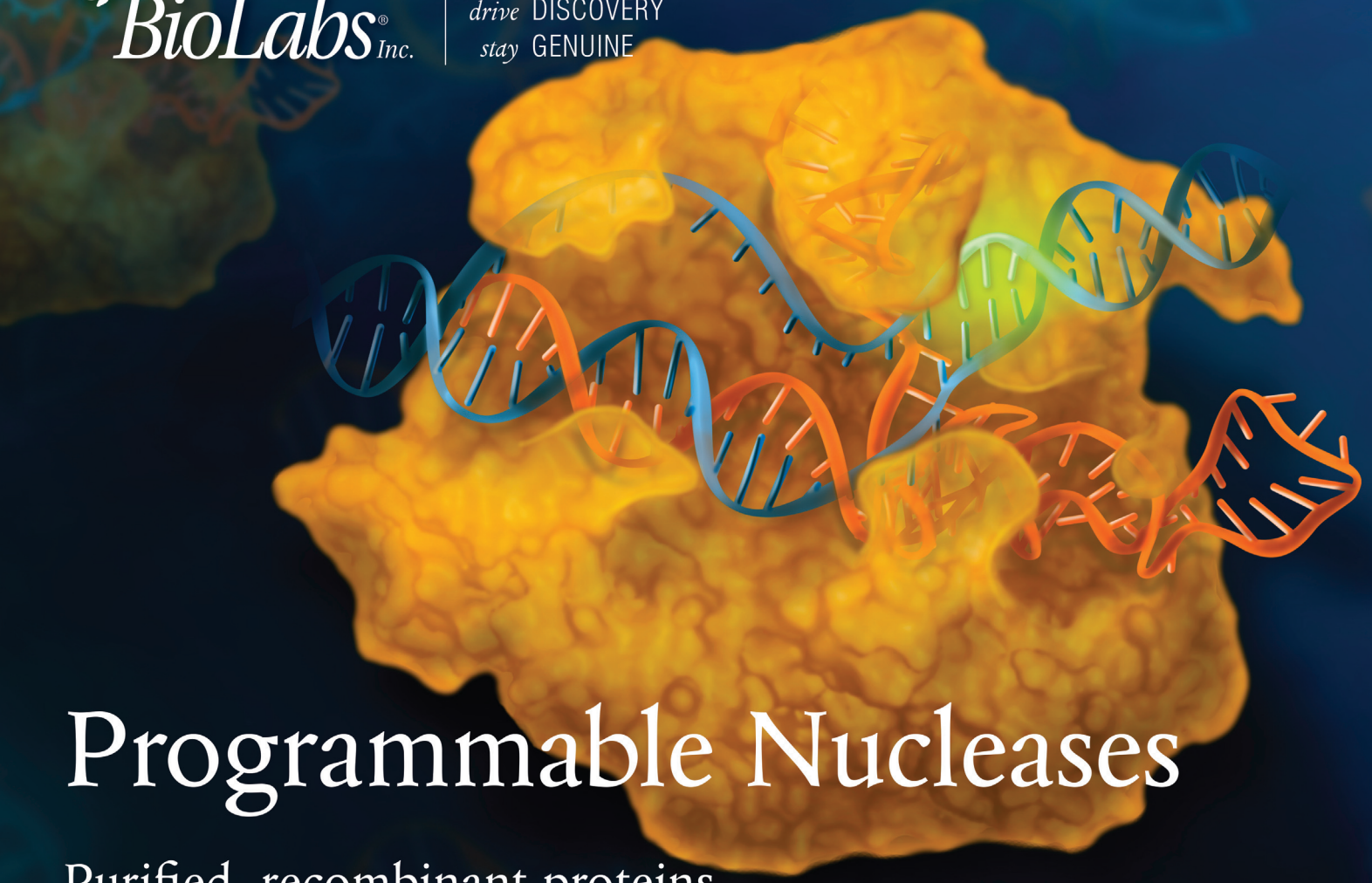

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Purified, recombinant proteins for genome editing applications

Cas nucleases, key proteins involved in CRISPR/Cas genome editing, are now available from New England Biolabs®. These Cas nucleases expand the portfolio of products from NEB® that support CRIPSR workflows, including sgRNA cloning, transcription and HDR template construction.

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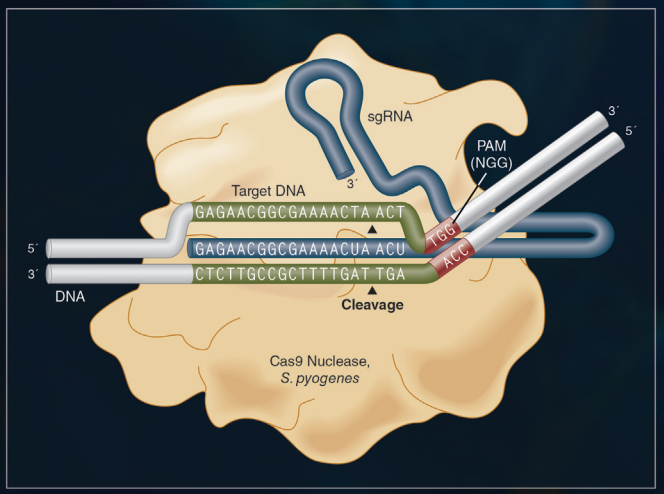
Schematic representation of Cas9 Nuclease, *S. pyogenes* sequence recognition and DNA cleavage



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:

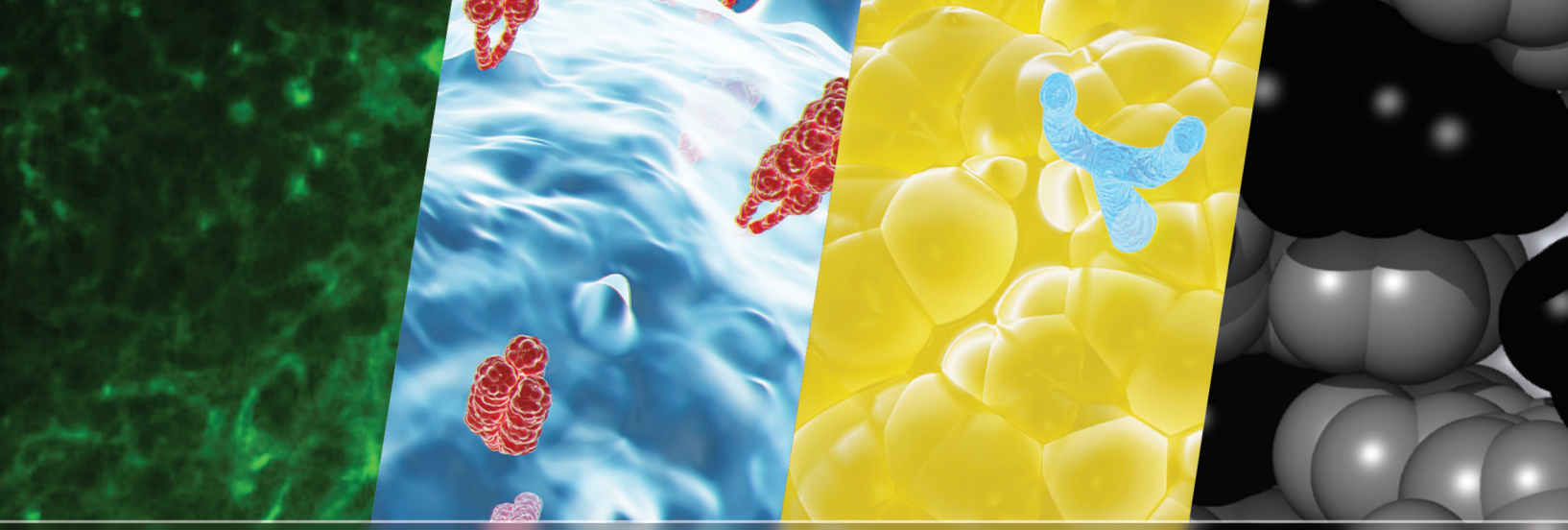
- Expertise in cancer biology, immunology, genomics or related fields
- Skilled in molecular and cellular assays
- Strong publication record
- Team player and strong communication skills (oral and written)
- The ability to work closely with clinicians and computational biologists

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



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ABOUT THIS CONFERENCE

This premier international conference featuring novel cancer therapeutics brings together over 1,500 academics, scientists, government officials, and pharmaceutical and biotech industry representatives from across the globe to discuss innovations in drug development, target selection, and the impact of new discoveries in molecular biology. This conference is the offspring of the original EORTC-NCI meetings on drug discovery and development, held biennially for three decades in Europe. The AACR partnership began in 1999 in response to the need for more frequent programs to keep pace with the rapid advancement of molecular biology and genetics and the consequent emergence of many new targets for cancer therapeutics. For all three organizations, the promotion of communication within the global scientific community is one of their key missions. This collaboration ensures that new information is exchanged regularly so that everyone in the field keeps current with the latest developments.

Learn more at
AACR.org/Targets19

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AACR American Association for Cancer Research®

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EORTC European Organisation for Research and Treatment of Cancer
The future of cancer therapy

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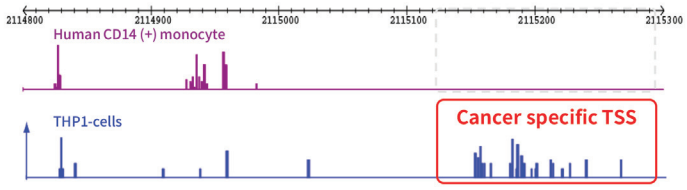
Promoter / Enhancer Annotation in the NGS era

Cap Analysis of Gene Expression (CAGE) is a new NGS library preparation method using "cap-trapping" technology which enables you to detect and quantify **transcription start site (TSS)** of RNA pol II transcripts including **mRNAs**, **lincRNAs** and **enhancer RNAs**.

- **Accurate promoter annotation**—reliable estimation of promoter posions and their activities based on precise TSS information
- **Estimation of transcription factor binding sites**—genome-wide motif search around TSS which have different expression profiles among samples
- **Detection of active enhancers**—identify active enhancers by detection of bidirectional enhancer RNAs
- **Development of new biomarkers**—TSS variants are valuable candidate of biomarkers even in the case that there are no difference at the gene expression level
- **Accurate quantification of gene expression**—PCR-free library preparation process without fragmentation allow for more reliable quantification of gene expression than RNA-seq



CAGE expression pattern of a histone H3 methyltransferase gene of human CD14(+) monocytes and THP-1 leukemia monocytic cells.

CAGE library preparation & analysis services	
Library preparation for Illumina sequencers	500 USD/sample
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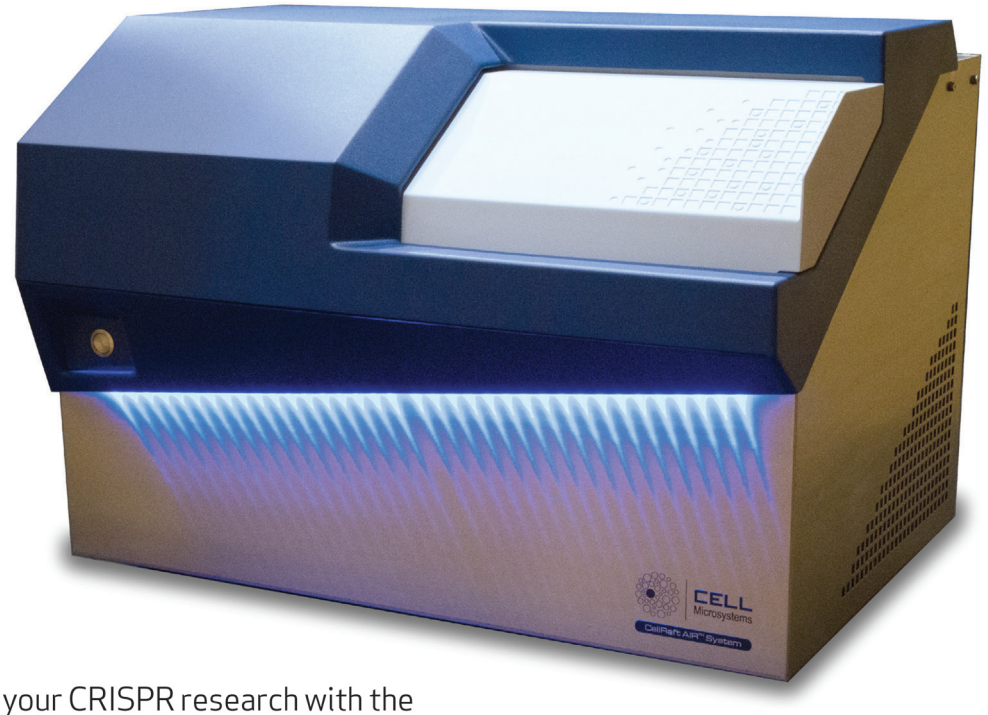
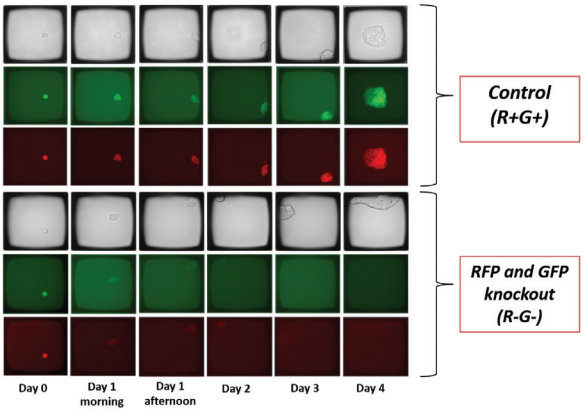


Accelerate your CRISPR research with the CellRaft AIR system.

The CellRaft AIR provides gentle sorting, cell imaging and efficient isolation – even for iPSC and hESCs.

- **Sort cells by phenotype after gRNA introduction**
- **Identify single cell founders for clonal colonies more successfully and with higher viability**
- **Accelerate colony formation; developing dozens of cell lines in one week, compared to months for traditional workflows**



Time-course imaging to verify CRISPR-edited cells are clonal and viable before collection.

Learn more about automating your CRISPR workflows at cellmicrosystems.com

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