

AUTOMATE YOUR GENOME ENGINEERING

CRISPR Done for You

Engineered Cells products deliver your desired edit in your preferred cell type with guaranteed results. We've optimized CRISPR. You focus on the discoveries.

[Synthego.com/CSHL](https://synthego.com/CSHL)

CRISPR Applications for Engineered Cells



Gene & Protein
Function



Protein Tagging and
Engineering



Assay & Antibody
Validation



Pathway
Analysis



Disease
Models



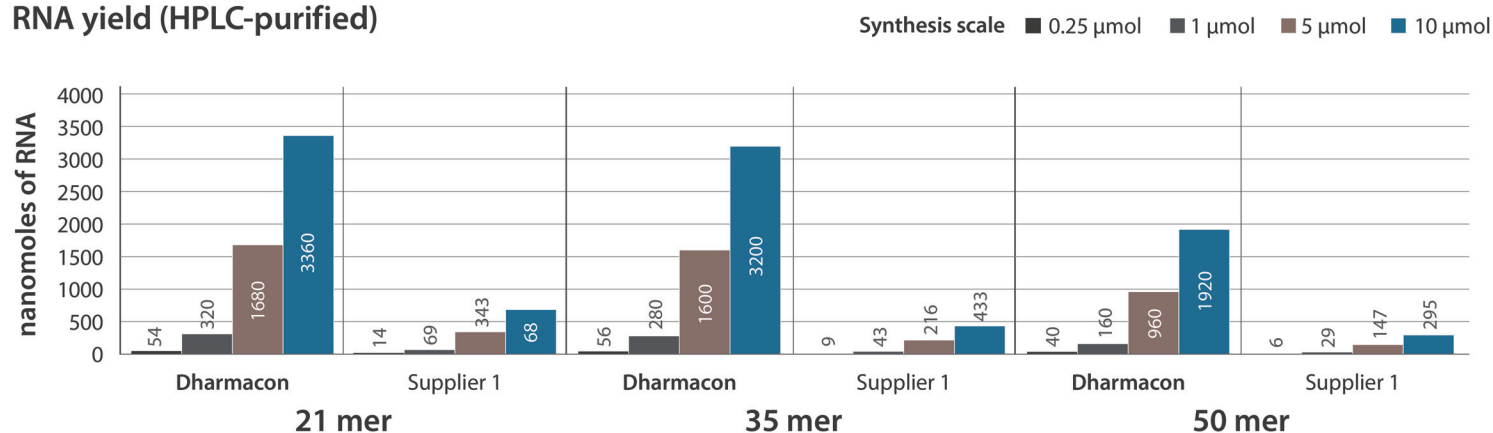
Precision
Editing

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.

Did you get the message?

In recent years, the discovery of new classes and modifications of RNA has ushered in a renaissance of RNA-focused research. Did you know that NEB[®] offers a broad portfolio of reagents for the purification, quantitation, detection, synthesis and manipulation of RNA? Experience improved performance and increased yields, enabled by our expertise in enzymology.



FEATURED PRODUCTS *for* RNA RESEARCH:

NEW Monarch[®] RNA Purification Kits –

kits available for isolation of total RNA from various sample types and for RNA cleanup following extraction, synthesis and other enzymatic reactions

NEW Luna[®] RT-qPCR products –

optimized solutions for one-step or two-step RT-qPCR, featuring the novel Luna Reverse Transcriptase

NEW NEBNext[®] Ultra[™] II RNA Library Prep Kits –

generate high quality RNA-seq libraries, even with limited amounts of RNA

HiScribe[™] *in vitro* Transcription Kits –

rapidly synthesize high yields of high quality RNA

Let NEB help streamline your **RNA-related workflows**.
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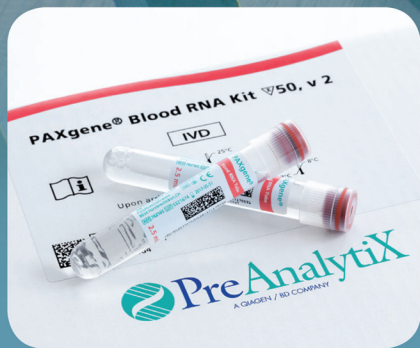
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 **MaxCyte**®



Block variability

Use the **PAXgene® Blood RNA System** to stabilize intracellular RNA upon blood collection for accurate and reproducible gene expression data



- ❖ Simplify procedures with an **integrated, standardized workflow** from blood sample to isolated RNA
- ❖ **Stabilize intracellular RNA** at the point of blood collection
- ❖ Ensure stability of transcript levels **during transport and storage**
- ❖ Streamline processing with efficient **manual or automated protocols**



The PAXgene Blood RNA System is for IVD use and consists of the PAXgene Blood RNA Tube (762165) and the PAXgene Blood RNA Kit (762164 or 762174).

Explore more at **www.preanalytix.com**

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*New customers only. Minimum sample number and quality may apply.



AACR American Association
for Cancer Research

ANNUAL MEETING

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!**

Late-Breaking Abstracts and Clinical

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!

AACR.ORG • #AACR20



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Genome Institute
of Singapore

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

Capture the entire transcriptome— in a single library.

Introducing the **new** SEQuoia Complete Stranded RNA Library Prep Kit for NGS.



It's new. It's different. And it's only from Bio-Rad.

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.

Are you ready for a new approach to transcriptomics?
Get the details at [bio-rad.com/SEQuoiaCompleteRNA](https://www.bio-rad.com/SEQuoiaCompleteRNA)

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#ScienceForward

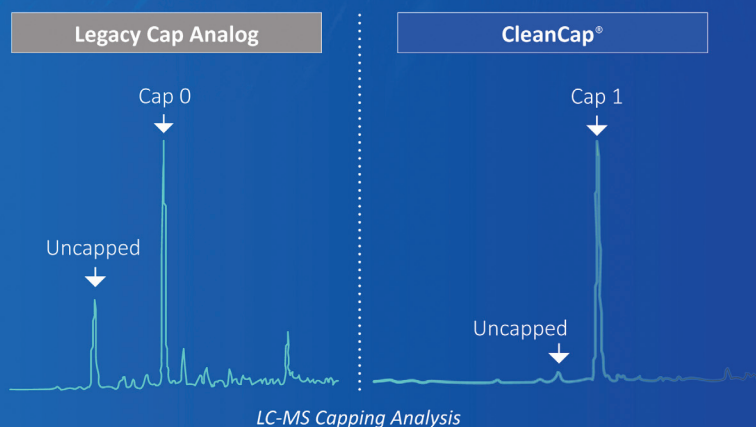
A REVOLUTION in Co-Transcriptional mRNA Capping

CleanCap® demonstrates superior performance versus legacy co-transcriptional capping methods

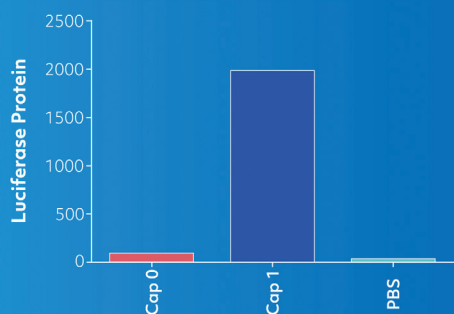
	Legacy Cap Analogs		CleanCap®	
Natural Cap	No	⊖	Yes	⊕
Immunogenic	Yes	⊖	Reduced Immunogenicity	⊕
Capping Efficiency	~70%	⊖	~95%	⊕
Yield/mL Transcription	1.5 mg/mL	⊖	4 mg/mL	⊕
Cost	3 X	⊖	1 X	⊕
Available Therapeutic Licenses	No	⊖	Yes	⊕

CleanCap®

Successful development of mRNA therapeutics relies on reproducible, high-efficiency production of capped mRNA. CleanCap® uses a new co-transcriptional chemical process for the highest level of mRNA capping:



CleanCap® gives superior activity *in vivo* by mimicking a natural cap



Luciferase mRNA was formulated with Lunar Lipids and injected by tail vein into mice. At 6 hours, luciferase was measured by western blot in mouse liver. Data courtesy of Arcturus Therapeutics.

CleanCap® results in a natural Cap 1 structure that does not stimulate the innate immune system of the host, resulting in unparalleled efficiency *in vivo*. Legacy co-transcriptional capping methods yield a Cap 0, an immunogenic cap structure that is poorly expressed *in vivo*.

The results speak for themselves: **CleanCap®, the next generation of cap analogs, provide the most active and least toxic mRNA for your *in vivo* applications.**

Be part of the revolution.

For more information visit: trilinkbiotech.com/cleancap