



ZYMO RESEARCH

The Beauty of Science is to Make Things Simple



SafeCollect™ At-Home Sample Collection Kits

Designed Around User Experience for Self-Collection

Sample collection devices for **simple, non-invasive at-home testing**. The patented SafeCollect™ tube features a safety seal that prevents users from spilling, ingesting, or being exposed to the stabilization solution. The unique safety seal is punctured after adding a sample to the tube, releasing the stabilization solution.

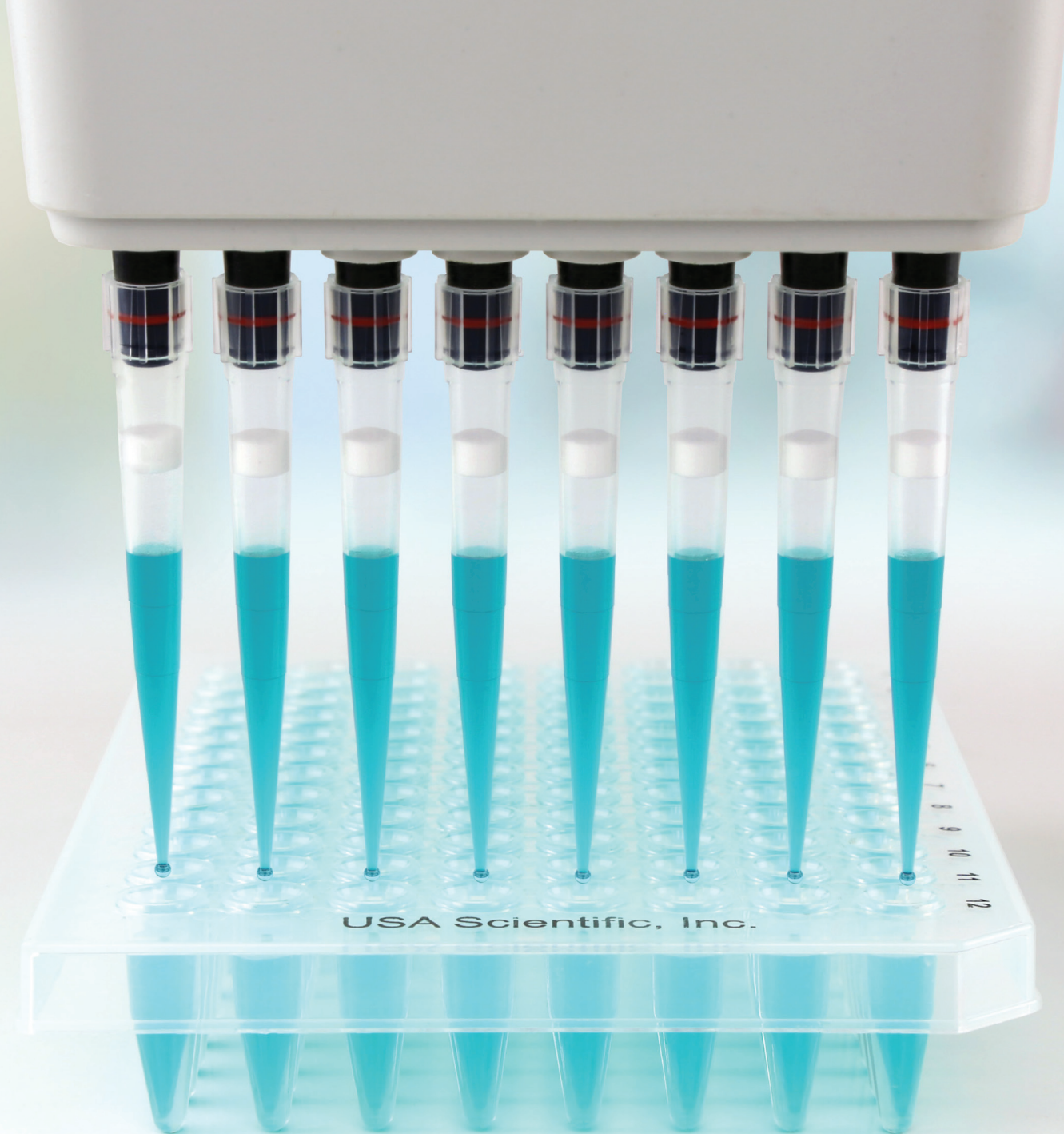


← Safety Seal



Learn more about SafeCollect™ At-Home Sample Collection Kits at
www.zymoresearch.com/pages/safecollect

www.zymoresearch.com | info@zymoresearch.com | Toll Free: (888) 882-9682



Proven to block >99% of aerosol contaminants*

Eliminate harmful aerosol transfers between samples with TipOne® filter tips. Pipetting generates aerosols that can be transferred from one sample to another. The right filter tips can prevent contamination of sensitive experiments and loss of time and/or are samples. Our ultra high density filters are proven to block >99% of aerosol contaminants.

With TipOne, your results will not be compromised by potentially bioactive ingredients.

TipOne® Filter Tips:

- Filters block >99% of aerosols*
- No additives that could interfere with samples
- Secure tip fit with low application force
- Convenient hinged racks
- Empty racks can be refilled with other TipOne tips
- Fully traceable lot numbers on each rack
- TipOne is manufactured in the USA

*Original TipOne with ultra high density filters. Additional information and product sizes available at www.usascientific.com. Sterilized and certified free of detectable RNase, DNase, DNA, and pyrogens.

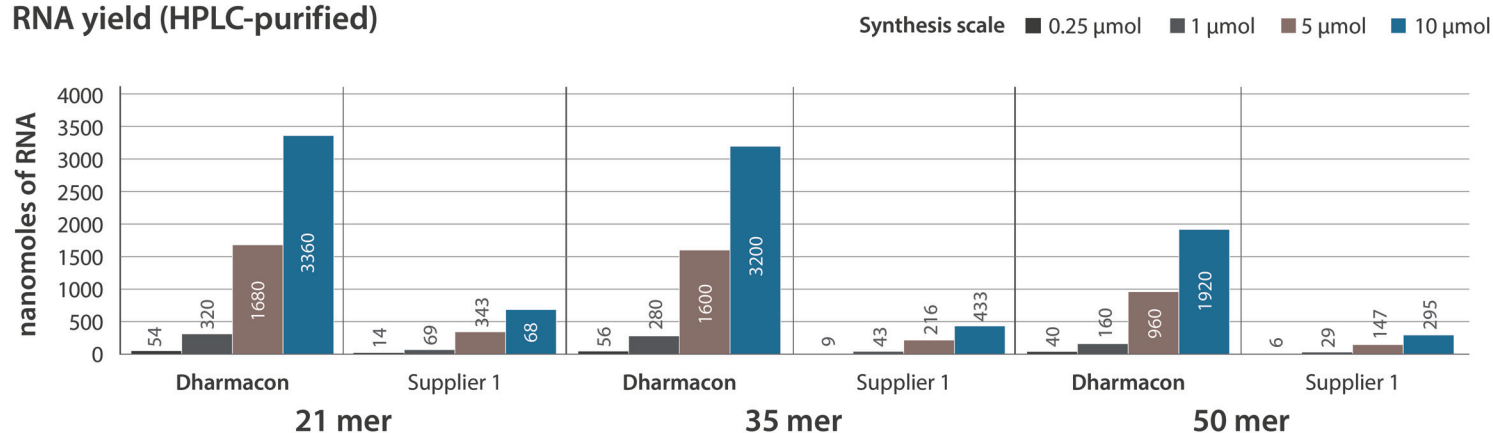
USA
SCIENTIFIC®
usascientific.com

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.



SKIP the SYNTHESIS —And the Hassle.

Get high-quality readymade mRNAs for:



Transfection
efficiency



Genome editing,
including Cas9



Antigen expression
modeling

Leading the Way in mRNA™

trilinkbiotech.com/browse/stocked-mrnas

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 **TriLink**
BIOTECHNOLOGIES
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Arraystar Small RNA Modification Arrays

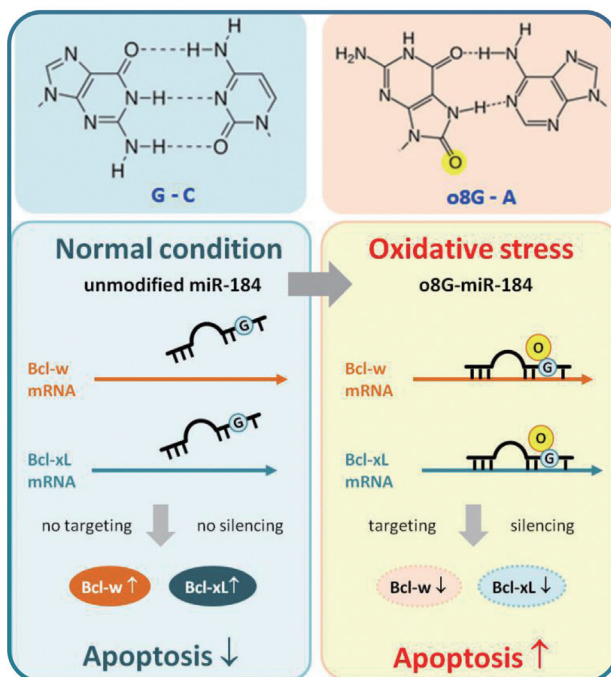
Quantifying Modifications in Small RNAs with High Sensitivity & Accuracy

- o8G/m7G/m6A/Ψ/m5C in miRNAs, pre-miRNAs & tsRNAs

Why Study Small RNA Modifications?

Small RNA modifications modulate the activities of small RNAs in diverse biological processes and play pivotal roles in pathological conditions. They can:

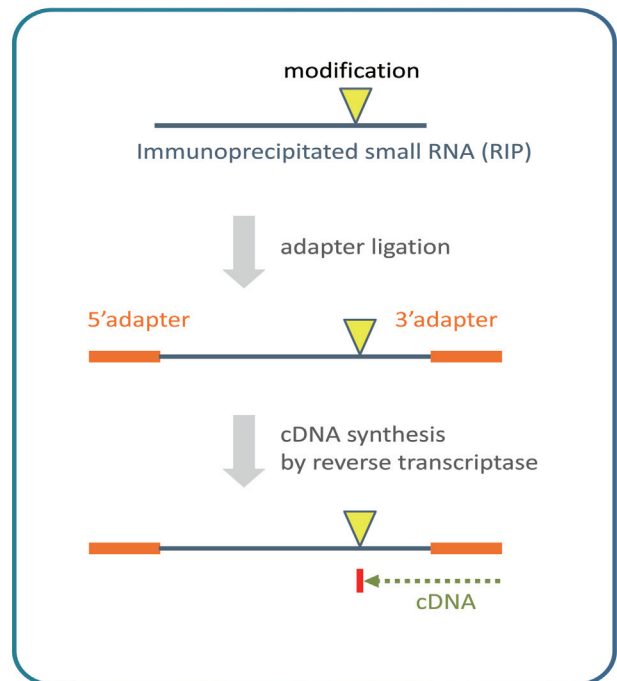
- Influence miRNA targeting
- Inhibit protein translation
- Serve as biomarkers



Oxidative modification of miR-184 enables it to target Bcl-xL and Bcl-w, based on Wang, J. X., et al. (2015) Mol Cell [PMID: 26028536]

Challenges to Quantify Small RNA Modifications Accurately

During small RNA MeRIP-sequencing library construction, the cDNA synthesis step is blocked by RNA modifications. It severely reduces the sequencing coverage and quantification accuracy.



Non-Sequencing Based Solution: Small RNA Modification Arrays

- Gold standard for accurate quantification of modified small RNAs.
- One step direct labeling that eliminates the problems of RNA modifications blocking cDNA synthesis during RNA-seq library prep.
- No PCR to distort native RNA levels.
- Low sample amount requirements.
- Array coverage of multiple small RNA classes, including miRNAs, pre-miRNAs, and tsRNAs.



FACULTY POSITION IN COMPUTATIONAL NEUROSCIENCE AT COLD SPRING HARBOR LABORATORY

Cold Spring Harbor Laboratory (CSHL) is seeking to fill a faculty position in the area of **COMPUTATIONAL/THEORETICAL NEUROSCIENCE**. Of particular interest to this search are candidates with expertise in computational and theoretical neuroscience, machine learning, and artificial intelligence. The successful candidate will have an outstanding record of research achievement and an innovative research program. They will join a highly interactive and collaborative neuroscience group working on neural circuits, neural development, neurogenetics, theoretical and computational neuroscience, artificial intelligence, synaptic function, brain disorders, rodent cognition, perception, and social behavior. Preference will be given to applicants at the Assistant Professor level, but outstanding candidates at all career stages will be considered.

Cold Spring Harbor Laboratory is a world-renowned research and educational institution with programs in cancer, neuroscience, plant biology, genomics, and quantitative biology. Located on the North Shore of Long Island 30 miles from New York City, the Laboratory has a rich and successful research environment rooted in interdisciplinary collaboration as well as an innovative graduate school that attracts talented students each year. CSHL is committed to fostering a diverse work environment that values best practices in mentorship, equity, and inclusion. Successful candidates will be expected to establish productive research programs while mentoring diverse groups of students and postdocs. Applications are strongly encouraged from groups historically underrepresented in science, including women and U.S. racial/ethnic minority populations.

To apply, please submit a cover letter, CV, description of research accomplishments, statement of future research plans, and a statement of diversity & mentoring to: <https://cshl.peopleadmin.com/postings/20153> Position ID 03299-R; letters of reference will be requested separately. The statement of diversity & mentoring should describe a candidate's mentoring philosophy, contributions to equity and inclusion in science, and prior training (as applicable) in mentoring, academic management/leadership, and antidiscrimination/antiracism. We will begin considering applications on a rolling basis on October 5, 2022, and applications will be considered until November 15. Inquiries regarding the search should be directed to: CSHLfacultyjobs@cshl.edu

CSHL is an EO/AA Employer. All qualified applicants will receive consideration for employment and will not be discriminated against on the basis of race, color, religion, sex, sexual orientation, national origin, age, disability or protected veteran status.

For more information: www.cshl.edu

2022 SCIENTIFIC CONFERENCES

Presenting the most significant research on cancer etiology,
prevention, diagnosis, and treatment

**Sixth CRI-ENCI-AACR International
Cancer Immunotherapy Conference:
Translating Science into Survival
September 28-October 1, 2022 | New York, NY**

Conference Cochairs: Özlem Türeci,
E. John Wherry, and Jedd D. Wolchok

**Colorectal Cancer
October 1-4, 2022 | Portland, OR**

Conference Cochairs: Jiyoung Ahn,
Robert J. Coffey, and Scott Kopetz

**Cancer Epigenomics
October 6-8, 2022 | Washington, D.C.**

Conference Cochairs: Scott A. Armstrong,
Howard Y. Chang, Arul M. Chinnaiyan,
and Margaret A. Goodell

**Tumor Immunology and Immunotherapy
October 21-24, 2022 | Boston, MA**

Conference Cochairs: Thomas F. Gajewski,
Jennifer A. Wargo, and Jedd D. Wolchok

**Innovation and Biomarkers in
Cancer Drug Development (IBCD):
A Joint Meeting Presented by
the EORTC, NCI, EMA, and AACR**

October 25, 2022 | Barcelona, Spain
Scientific Committee Cochairs: Roberto Salgado,
Tracy G. Lively, and David B. Solit

**EORTC-NCI-AACR Molecular Targets and
Cancer Therapeutics Symposium
October 26-28, 2022 | Barcelona, Spain**

Scientific Committee Cochairs: Ruth Plummer,
James L. Gulley, and Lillian L. Siu

**Myeloma and Plasma Cell Dyscrasias
November 3-5, 2022 | Boston, MA**

Conference Cochairs: Kenneth C. Anderson and
Irene M. Ghobrial

**2nd AACR-KCA Joint Workshop on
Precision Medicine in Cancer**

November 10-11, 2022 | Seoul, Korea
Workshop Cochairs: Nilofer S. Azad and Tae Min Kim

**Cancer Metastasis
November 14-17, 2022 | Portland, OR**

Conference Cochairs:
Fabrice Andre, Sean J. Morrison, Danny R. Welch,
and Zena Werb

**Precision Prevention, Early Detection, and
Interception of Cancer**

November 17-19, 2022 | Austin, TX
Conference Chair: Timothy R. Rebbeck
Conference Cochairs: Sangeeta N. Bhatia, Luis A.
Diaz, Jr., Ernest T. Hawk, and Philip W. Kantoff

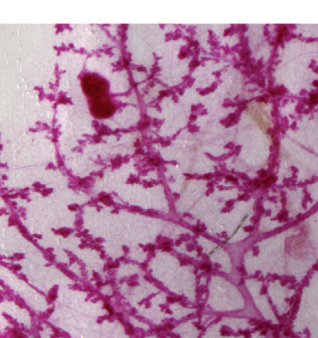
**Aging and Cancer
November 17-20, 2022 | San Diego, CA**

Conference Cochairs: Steven E. Artandi, Joanna L.
Grodén, and Eileen P. White

**San Antonio Breast Cancer Symposium
December 6-10, 2022 | San Antonio, TX**

Codirectors: Carlos L. Arteaga and Virginia G.
Kaklamani

Due to the nature of the COVID-19 pandemic, dates may be subject to change.



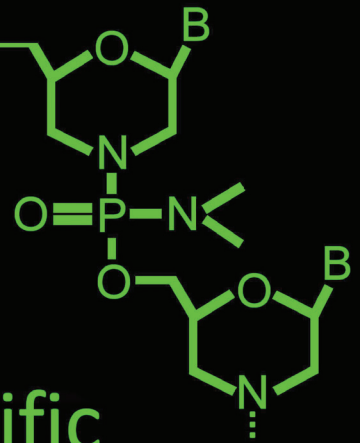
Learn more and register at
[AACR.org/Calendar](https://aacr.org/calendar)

Follow us @AACR



GENE TOOLS, LLC

www.gene-tools.com



A Morpholino oligo works like sequence-specific masking tape, blocking a section of RNA.

Halt the initiation complex.

Block snRNP binding.

Inhibit miRNA maturation.

Mask a poly-A tail signal.

Switch splice regulation.

Invade RNA secondary structure.

Proven technology:

Four FDA-approved drugs

Over 11,000 publications



All-in-one and one for all!

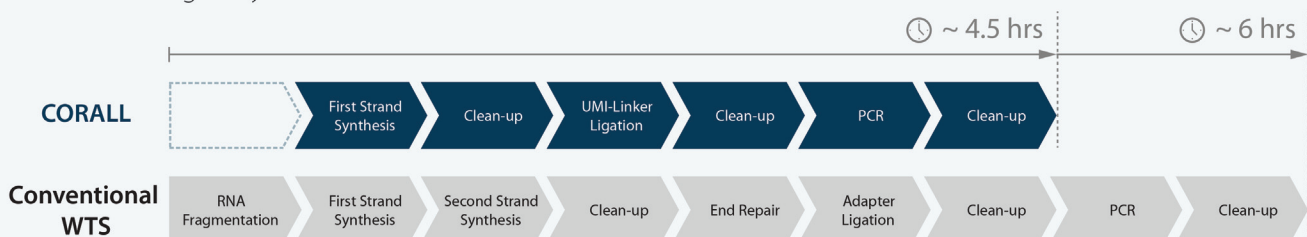
Get the best sequencing results with CORALL RNA-Seq V2 - Lexogen's all-in-one whole transcriptome RNA-Seq library preparation kit for all samples.

For more information and additional resources, please visit our website.



Fast, flexible, and fragmentation-free library prep in just 4.5 hours

CORALL RNA-Seq only requires 6 steps, saving valuable time and allowing the preparation of sequencing-ready-libraries in a single day.



Exceptional performance on low input and low quality samples

CORALL RNA-Seq V2 supports the widest input range (1 ng - 1000 ng) with excellent performance for low input RNA. The highly sensitive protocol delivers exceptional results for difficult samples, such as FFPE RNA.